

Intelligent, artificially

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Dairy farming in the era of artificial intelligence: Trend or a real game changer?

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Mexico, Iran, China, Finland, Spain, Egypt, Italy, USA, UK

Abstract

Artificial Intelligence (AI) is reshaping the world as we know it, impacting all aspects of modern society, basically due to the advances in computer power, data availability, and AI algorithms. The dairy sector is also on the move, from the exponential growth in AI research, to ready to use AI-based products, this new evolution to Dairy 4.0 represents a potential “game-changer” for the dairy sector, to confront challenges regarding sustainability, welfare and profitability. This research reflection explores the possible impact of AI, discusses the main drivers in the field and describes its origins, challenges and opportunities. Further, we present a multidimensional vision considering factors that are not commonly considered in dairy research, such as geopolitical aspects and legal regulations that can have an impact on the application of AI in the dairy sector. This is just the beginning of the third tide of AI, and a future is still ahead. For now, the current advances in AI at on-farm level seem limited and based on the revised data, we believe that AI can be a “game-changer” only if it is integrated with other components of Dairy 4.0 (such as robotics) and is fully adopted by dairy farmers.

Bayesian-genome wide association study and post-GWAS on reproductive traits of Holstein dairy cattle

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Iran

Abstract

Bayesian multiple regression models are often used for genomic selection, where all markers are adjusted simultaneously as random effects to reduce the false discovery rate. The purpose of this research was to identify individual candidate genes for some reproductive traits in Holstein cattle through genome wide association studies (GWAS) using a Bayesian method

in combination with post-GWAS analysis. Reproductive traits included: days open (DO), pregnancy rate (PR), calving interval (CI) and age at first calving (AFC). The animals were genotyped using single nucleotide polymorphism (SNP) panels of different densities imputed to a 50K SNP density. After quality control, we included 2400 genotyped animals. According to the Bayesian analysis, there were 19 windows with an explained additive genetic variance of >0.1 percent for CI, DO, AFC and PR in Holstein cattle, which were 3, 3, 6 and 7, respectively. Using Bayesian analysis, 79 genes were located within or nearby (250-kb) 19 significant SNPs/windows in the *Bos taurus* autosomes. Among these genes, we identified 25 candidate genes for reproductive traits, namely CHD7, CLVS1, EVX2, MAT2B, NUDCD2, GPR39, NCKAP5, LYPD1, HOXD13, SEMA5B, CCNG1, SEMA5A, BRF1, PSEN2, CACHD1, SUGTA, ELF1, SNORA70, AKT1, TM2D1, SLF1, MCTPA, PAB2A, MTRF1 and ADCY2. Additionally, another 9 candidate genes (CLVS1, GPR39, CENPF, AMOT, ARF1, CCDC186, ADCY2, BDP1 and AMOTL1) were identified in the network cluster analysis as hub genes for reproductive traits. The results of gene set enrichment analysis (GSEA) and pathway analysis, suggest that the most important gene ontology term involving cellular metabolic process was related to the AFC trait. To summarise, Bayesian methods were used to identify SNPs and candidate genes that could be useful in genomic selection to improve reproductive traits of Holstein dairy cattle

Substituting imported soybean meal with locally produced novel yeast protein in concentrates for Norwegian Red dairy cows: Implications for rumen microbiota and fatty acid composition

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Norway

Abstract

This research paper addresses the hypothesis that substituting soybean meal with locally produced yeast protein from *Cyberlindnera jadinii* in barley-based concentrates for Norwegian Red (NR) dairy cows does not have adverse effects on milk fatty acid (FA) composition, rumen microbiota and sensory quality of milk. As soybeans also represent valuable protein sources for human consumption, alternative protein sources need to be investigated for animal feed. A total of 48 NR dairy cows were allocated into three feeding treatments, with the same basal diet of grass silage, but different concentrates. The concentrates were all based on barley, but 7% of the barley in the barley-concentrate (BAR; negative control) was replaced by either soybean meal (SBM; conventional control) or yeast microbial protein (YEA). The experiment lasted for a total of 10 weeks, including 2 weeks of adaptation with the soybean meal concentrate. Analysis of the feed revealed some

differences in the FA composition of the YEA concentrate compared to the SBM and BAR concentrates. In milk, only two FAs (C17:1*n*-8*cis*9 and an unidentified isomer of C18:3) were significantly different between the YEA- and SBM-group, while six FAs differed between the BAR- and SBM-group. However, the amount of these FAs was low compared to the entire FA profile (< 0.7 g/100g). The experimental diets did not affect rumen microbiota nor the milk sensory quality. This study shows that *C. jadinii* can replace soybean meal as a protein source in concentrates (7% inclusion) for NR dairy cows fed a diet composed of grass silage and concentrates without any effects on rumen microbiota, and without compromising the FA composition or sensory quality of milk.

Productive performance and milk composition of dairy ewes supplemented with corn silage (*Zea mays L.*), sunflower (*Helianthus annuus*) silage and their mixture.

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Mexico, Iran and UK

Abstract

The work reported in the Research Communication investigated *in vitro* rumen gas kinetics and fermentation profile as well as *in vivo* performance of lactating ewes fed corn silage (CS), sunflower silage (SFS) and their 50:50 mixture (CS-SFS). For the *in vivo* experiment, nine early-lactation Suffolk × Texel ewes were grouped in a replicated 3 × 3 latin square design of three 21-d periods. Treatments were based on *ad libitum* CS, SFS, and CS-SFS supplemented with concentrate at 48 g/kg LW^{0.75}. *In vitro* results showed that the CS had the highest dry matter degraded substrate and microbial crude protein production followed by CS-SFS. The *in vivo* data showed that animals fed on CS had higher digestibility of dry matter and organic matter than CS-SFS, while SFS were intermediate. Nitrogen (N) intake, fecal N excretion, and urine N excretion were similar between groups, however, milk N excretion was lower in SFS than CS. Milk yield was higher for CS and CS-SFS than SFS group, however, SFS-fed ewes had higher milk fat content than either CS or CS-SFS (all differences reported here were significant, *P*<0.05 or better). Overall, CS-SFS could be used as dietary roughage for dairy ewes without deleterious effects on nutrient intake, N-balance and milk yield whilst potentially offering a more sustainable alternative to CS.

Effects of fibrolytic and amylolytic compound enzyme preparation on rumen fermentation, serum parameters and production performance in primiparous early-lactation dairy cows

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China and the Netherlands

Abstract

This research communication reports the effects of a compound enzyme preparation consisting of fibrolytic (cellulase 3500 CU/g, xylanase 2000 XU/g, β -glucanase 17500 GU/g) and amylolytic (amylase 37000 AU/g) enzymes on nutrient intake, rumen fermentation, serum parameters and production performance in primiparous early-lactation (47 ± 2 d) dairy cows. Twenty Holstein-Friesian cows in similar body condition scores were randomly divided into control (CON, $n = 10$) and experimental (EXP, $n = 10$) groups in a completely randomized single-factor design. CON was fed a basal total mixed ration diet and EXP was dietary supplemented with compound enzyme preparation at 70 g/cow/d. The experiment lasted 4 weeks, with 3 weeks for adaptation and then 1 week for measurement. Enzyme supplementation significantly increased diet non-fibrous carbohydrates (NFC) content as well as dry matter intake (DMI) and NFC intake ($P < 0.05$). EXP had increased ruminal butyrate and isobutyrate percentages ($P < 0.01$) but decreased propionate and valerate percentages ($P < 0.05$), as well as increased serum alkaline phosphatase activity and albumin concentration ($P \leq 0.01$). Additionally, EXP had increased milk yield (0.97 kg/d), 4% fat corrected milk yield and energy corrected milk yield, as well as milk fat and protein yield ($P < 0.01$). In conclusion, dietary supplementation with a fibrolytic and amylolytic compound enzyme preparation increased diet NFC content, DMI and NFC intake, affected rumen fermentation by increasing butyrate proportion at the expense of propionate, and enhanced milk performance in primiparous early-lactation dairy cows.

Prepartum supplementation of dairy cows with inorganic selenium, organic selenium or rumen-protected choline does not affect carotenoid composition or colour characteristics of bovine colostrum or transition milk.

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Ireland

Abstract

Minerals are supplemented routinely to dairy cows during the dry period to prevent metabolic issues postpartum. However, limited information exists on the impacts of mineral

supplementation on colostrum carotenoids. This study aimed to determine the effects of prepartum supplementation with three micro-nutrients; inorganic selenium (INORG), organic selenium (ORG) or rumen-protected choline (RPC) on the carotenoid content of bovine colostrum and transition milk (TM) from pasture-based dairy cows. A total of 57 (12 primiparous and 45 multiparous) Holstein-Friesian (HF) and HF × Jersey (JEX) cows were supplemented daily for 49 ± 12.9 days before calving. Colostrum samples were collected from all cows immediately postpartum and TM samples were collected from a sub-set of 15 cows (five per treatment group) at each of 5 consecutive milkings postpartum. Carotenoid concentration was determined using ultra-high performance liquid chromatography–diode array detection. With the use of transmittance, the colour index and colour parameters a^* , b^* and L^* were used to determine colour variations over this period. Prepartum supplementation did not have a significant effect on colostrum β -carotene concentration or colour. Positive correlations between β -carotene and colour parameter b^* ($R^2 = 0.671$; $P < 0.001$) and β -carotene and colour index ($R^2 = 0.560$; $P < 0.001$) were observed. Concentrations of β -carotene were highest in colostrum ($1.34 \mu\text{g/g}$) and decreased significantly with each milking postpartum (TM5 $0.31 \mu\text{g/g}$). Breed had a significant effect on colostrum colour with JEX animals producing a greater b^* colostrum than HF animals ($P < 0.05$). Primiparous animals produced colostrum with the weakest colour compared to second or \geq third parity animals ($P < 0.05$). Despite statistical increases in the b^* parameter in colostrum from JEX cows and multiparous cows, β -carotene concentrations did not significantly increase suggesting that other factors may influence colostrum colour. The b^* parameter may be used as an indicator for estimating carotenoid concentrations in colostrum and TM, particularly when assessed via transmittance spectroscopy.

Relationship between body weight and hip width in dairy buffaloes (*Bubalus bubalis*)

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Mexico and Brazil

Abstract

The objective of the present study was to evaluate the relationship between body weight (BW) and hip width (HW) in dairy buffaloes (*Bubalus bubalis*). HW was measured in 215 Murrah buffaloes with a BW of 341 ± 161.6 kg, aged between three months and five years, and raised in southeastern Mexico. Linear and non-linear regressions were used to construct

the prediction models. The goodness of fit of the models was evaluated using the Akaike information criterion (AIC), Bayesian information criterion (BIC), coefficient of determination (R^2), mean squared error (MSE), and root MSE (RMSE). Additionally, the developed models were evaluated through internal and external cross-validation (k-folds) using independent data. The ability of the fitted models to predict the observed values was assessed based on the root mean square error of prediction (RMSEP), R^2 , and mean absolute error (MAE). The relationship between BW and HW showed a high correlation coefficient ($r = 0.96$, $P < 0.001$). The chosen fitted model to predict BW was: $-176.33 (\pm 40.83^{***}) + 8.74 (\pm 1.79^{***}) \times HW + 0.04 (\pm 0.01^*) \times HW^2$, because it presented the lowest MSE, RMSE, and AIC values, which were 1228.64, 35.05 and 1532.41, respectively. Therefore, with reasonable accuracy, the quadratic model using hip width may be suitable for predicting body weight in buffaloes.

Potential utility of RSAD2 transcript and protein in early detection of pregnancy in buffaloes

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India

Abstract

This study investigates a novel early pregnancy marker in water buffaloes, focusing on RSAD2 mRNA expression, known to be upregulated by interferon-tau (IFNT) during pregnancy. While RSAD2 is primarily recognized for its antiviral effect, we hypothesized its role as a conceptus-induced component in regulating pregnancy in buffaloes. Given its differential expression compared to other IFNT-induced genes in cows, *RSAD2* may serve as a biomarker for early pregnancy detection in buffaloes. RNA, cDNA, and plasma samples were obtained from archived samples collected before insemination (d0) and at d20, d25 and d40 after insemination. Twelve RNA samples, having optimal optical density and concentration, from six pregnant and six non-pregnant buffaloes were selected. The cDNA was analysed to measure the abundance of *RSAD2* mRNA using real-time quantitative PCR (RT-qPCR) and plasma for protein expression analysis using Western blot. The RT-qPCR analysis showed a transcript of *RSAD2* increased significantly by 7-fold and 6-fold on d20d and d25, compared to both d0 and d40-day in the pregnant group only. At d20, the sensitivity of *RSAD2* was 100% and the specificity was 83.3%, and at d25-d both the sensitivity and specificity was 100%, indicating low incidences of misdiagnosing early pregnancy in buffaloes. In the non-pregnant group, *RSAD2* expression remained low and did not change after insemination. Western blot analysis revealed an immunoreactive RSAD2 protein band. Densitometry analysis of the RSAD2-specific protein band, based on gray mean value, showed significantly increased expression of RSAD2 at d25 compared to d0 in the pregnant group. In conclusion, these results indicated that RSAD2 expressions at both the mRNA and protein levels show promising potential for detecting pregnancy at d25 post-insemination.

Effects of prepartum positive and negative dietary cation/anion differences on postpartum calcium concentration and risk factors for subclinical hypocalcemia in Holstein cows

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Iran and South Korea

Abstract

Insufficient data is available about the association between prepartum risk factors including dietary cation-anion difference (DCAD) status and postpartum outcomes of Holstein dairy cows within commercial management systems. The first objective of this experiment was to assess the association between postpartum serum calcium (Ca) dynamics and the risk of metritis development. The second objective was to identify the association of risk factors, including DCAD status of prepartum ration, prepartum serum macrominerals and parity, with the development of subclinical hypocalcemia (SCH) in two commercial herds. Herd A (n = 32) fed a negative DCAD close-up ration and herd B (n = 30) fed a positive DCAD close-up diet. A receiver operating characteristic (ROC) curve was run to evaluate the association of serum Ca concentration at 1, 2, and 4 DIM with the risk of developing metritis. A second ROC curve was also created to assess the association of prepartum serum Mg, P, and Ca concentration with the postpartum serum Ca concentration dichotomized into normocalcemic (>8.82 mg/dL) and subclinical hypocalcemic (\leq 8.82 mg/dL). A logistic regression model was created to assess prepartum DCAD status (negative vs. positive) and parity (classified into a 3-level variable as first, second and third or greater lactations) as potential predictors of SCH classification. Serum Ca concentration at DIM 4 was a significant predictor of metritis (area under the curve = 0.87; $P < 0.01$). Cows fed positive vs. negative prepartum DCAD diet were more likely to be classified as SCH at 4 DIM (odds ratio = 2.71; 95% confidence interval = 0.87 to 8.41). Parity did not show a significant association with the classification of SCH at 4 DIM. Our results demonstrate the importance of the DIM of blood Ca concentration assessment in connection with the diagnosis of metritis, which is crucial for the most accurate categorization of SCH and the related risk factors.

Investigating the relationship between heat load and shade seeking behavior in dairy buffaloes

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Pakistan

Abstract

The study presented in this Research Communication aimed to investigate the relationship between physiological responses, body surface temperature and shade-seeking behavior in Nili Ravi dairy buffaloes during summer months. We enrolled 60 buffaloes, and each animal was observed for three consecutive days starting before sunrise until they moved towards the shade structures. A repeated measures ANOVA was employed to assess the changes in physiological parameters and body surface temperature between the early morning and the occurrence of shade-seeking behavior. The average temperature humidity index and heat load index during the behavioral monitoring period (0400 to 1200 h) were 81.3 ± 6.5 and 92.9 ± 17 , respectively (mean \pm SD). There was no significant difference in core body temperature between sunrise and the time of shade-seeking event. However, the buffaloes had a slightly higher respiration rate at the time of shade-seeking (19.2 vs. 22.4 breaths/min). In addition, body surface temperature, measured at the flank region, shoulder, base of the ear and forehead was significantly higher at the occurrence of shade-seeking behavior compared to the early morning. On average, the buffaloes sought shade when the surface temperature was 2°C higher than the temperature recorded before sunrise. Overall, the current findings suggest that body surface temperature, rather than core body temperature was strongly associated with shade-seeking behavior in dairy buffaloes. These findings could be useful in developing strategies to mitigate the effects of heat stress in dairy buffalo herds and thereby improve animal welfare.

The concentration of free glycerol in goat milk increases during feed restrictions

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Denmark

Abstract

This Research Communication introduces a novel enzymatic-fluorometric analytical procedure for glycerol and glycerol 3-phosphate in milk. Milk from thirty-seven goats was analysed during 9 consecutive days during which a two-day feed restriction was introduced. Fractional milk triacylglyceride and free glycerol increased significantly while glycerol 3-phosphate reacted more moderately. The energy status of the mammary cell is discussed.

Potential biomarkers for lameness and claw lesions in dairy cows: A scoping review

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Malaysia

Abstract

One of the major challenges in lameness management is prompt detection, especially before visible gait disturbance. This scoping review describes the potential biomarkers for lameness in dairy cows reported in the literature, their relevance in lameness diagnosis, identifying cows at risk of developing claw lesions and monitoring recovery after treatment. Using specific keywords, a comprehensive literature search was performed in three databases: PubMed, Google Scholar and ScienceDirect to retrieve relevant articles published between 2010 and 2022. A total of 31 articles fulfilling the inclusion criteria were analysed. The categories of potential markers for lameness reported in the literature included acute phase proteins (APPs), nociceptive neuropeptides, stress hormones, proteomes, inflammatory cytokines and metabolites in serum, urine and milk. Cortisol, APPs (serum amyloid A and haptoglobin) and serum, urinary and milk metabolites were the most studied biomarkers for lameness in dairy cows. While APPs, nociceptive neuropeptides and blood cortisol analyses assisted in elucidating the pain and stress experienced by lame cows during diagnosis and after treatment, evidence-based data are lacking to support their use in identifying susceptible animals. Meanwhile, metabolomic techniques revealed promising results in assessing metabolic alterations occurring before, during and after lameness onset. Several metabolites in serum, urinary and milk were reported that could be used to identify susceptible cows even before the onset of clinical signs. Nevertheless, further research is required employing metabolomic techniques to advance our knowledge of claw horn lesions and the discovery of novel biomarkers for identifying susceptible cows. The applicability of these biomarkers is challenging, particularly in the field, as they often require invasive procedures.

Genotypic insights to Panton-Valentine leukocidin positive methicillin-resistant *Staphylococcus aureus* isolated from cattle mastitis

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Pakistan

Abstract

In this research communication we investigate the prevalence and antimicrobial susceptibility of *S. aureus* harboring virulent genes responsible for mastitis in cattle of Punjab, Pakistan. A total of 690 milk samples were collected from commercial dairy farms for analysis of the prevalence of subclinical and clinical mastitis and isolation of *S. aureus*. Virulence ability and methicillin resistance in *S. aureus* (MRSA) was determined by targeting the *pvl* and *mecA* genes, respectively. A total of 175 *S. aureus* isolates exhibiting prevalence of *pvl* gene (6.28%) and *mecA* gene (22.28%) were determined. Antimicrobial susceptibility testing of *pvl* positive and negative MRSA against different classes of antibiotics revealed 100% resistance against β -lactams while 100% sensitivity towards tylosin and linezolid.

Udder health, bacterial isolation and antimicrobial sensitivity of *Staphylococcus* species from non-dairy goats on smallholder farms in the Hong Kong Special Administrative Region

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China

Abstract

This research communication describes an investigation into the udder health, bacterial isolation and antimicrobial sensitivity of three staphylococcal species isolated from the milk of non-dairy goats, suckling their kids, on two smallholder farms in the Hong Kong Special Administrative Region. Udder lesions were visually noted in 21 of 34 goats and two goats had palpable abnormalities. Collected milk samples grew a total of 11 bacterial organisms and the most frequently isolated organism was *Staphylococcus chromogenes*. Selected isolates of *S. aureus*, *caprae* and *simulans* from both farms were tested by antimicrobial sensitivity testing for 23 antimicrobials and all isolates showed antimicrobial resistance to doxycycline and tetracycline. Less common resistance was shown to ampicillin, chloramphenicol, penicillin and rifampicin. This preliminary study confirms the presence of udder lesions and mastitis bacteria in non-dairy goats in Hong Kong, along with the first information on the antimicrobial profile of three common *Staphylococcus* species bacteria affecting goats.

In vitro antimicrobial and antibiofilm activity of phage cocktail against *Mammaliococcus sciuri*, a causative agent of bovine mastitis

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India

Abstract

In this research paper the *in vitro* antimicrobial and antibiofilm activity of phage cocktail against the coagulase negative *Mammaliococcus sciuri* was investigated. Three *M. sciuri* isolates obtained from clinical bovine mastitis samples were characterized and identified by 16S rRNA gene sequencing. Bacteriophages with lytic activity against *M. sciuri* isolates were isolated from dairy farm effluents. Two typical phages were isolated using standard enrichment and plaque assay techniques, purified by polyethylene glycol precipitation, and morphologically characterised based on shape and size using transmission electron microscopy. This was followed by determination of host range using spot tests and stability to varying temperature, pH and UV treatment.. The phage cocktail suppressed bacterial activity within 30 minutes of exposure. Crystal violet assay showed that the tested phages and their cocktail significantly reduced the biofilm biomass of all three *M. sciuri* strains compared to the untreated control *in vitro* within 24h with a single dosing. Transmission electron micrography of the purified phage particle revealed an icosahedral head and a rigid contractile tail, characteristic of the class *Caudoviricetes*. The findings open new avenues in phage-based antimicrobial approaches for controlling contagious and teat skin opportunistic bacteria causing bovine mastitis.

Geometry of milk liners affects milking performance in dairy cows

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New Zealand

Abstract

The geometry of milk liners may affect milking performance and cow comfort as the milk liner is the only part of the milking machine that comes into contact with the teat. To determine the effect of alternative shape of milk liners we compared square (SQR) versus the conventional round (RND) teat cup liner on milking performance and comfort of dairy cows. Treatment milk liners were randomly allocated to clusters within each side of the 12 a side double up-herringbone dairy shed in a complete randomised block design over two periods. Milking performance data from a total of 10,065 (late stage of lactation and once-a-day milking frequency, LATE) and 18,048 (early stage of lactation and twice-a-day milking

frequency, EARLY) milking events were automatically recorded by a DeLaval milk meter, and separately analysed for LATE and EARLY, respectively. In EARLY, cow comfort behaviour was also recorded during afternoon milking sessions. Across the two study periods, average milk flow rate, milk flow rate during 0-15, 15-30 and 30-60s after cluster attachment, and milk flow rate at cluster take-off were higher in SQR compared to RND treatment. Proportion of time in a milking session with low milk flow rate and duration of milking session were less in SQR compared to RND treatment. However, effect of geometry of milk liner on peak milk flow rate was inconsistent across the two-study periods. Peak milk flow rate was higher ($P<0.001$) in SQR than RND in LATE, but higher ($P<0.001$) in RND than SQR in EARLY. Stomping and kicking behaviours of cows were similar between treatments. Results of this study suggest that square milk liners potentially improve milking performance, without adverse effect on cow comfort compared to conventional round liners. Long-term, multi-site studies are required to confirm potential teat-end health benefits associated with square milk liners and further verify these results.

A novel shiga toxigenic *E. coli* sequence type harbouring multidrug resistance isolated from raw milk

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India

Abstract

The objective was to examine the prevalence of extended-spectrum β -lactam (ESBL) resistance among Shiga toxigenic *Escherichia coli* (STEC) isolated from raw milk. The findings from disc diffusion analysis and polymerase chain reaction revealed a high occurrence of ESBL resistance, specifically to penicillins, cephalosporins, and carbapenems, in isolated STEC strains. Additionally, a distinct sequence type of STEC was also identified in milk through comparative analysis.

Variation in bovine milk stability according to lactational stage and genetic group

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Brazil

Abstract

We address the hypothesis that at early and late lactation milk presents low ethanol stability due to high acidity and ionic calcium values. Our aim was to evaluate the functional traits of milk (focusing on milk ethanol stability: MES, acidity and ionic calcium: iCa) according to lactation stage in different genetic groups. Raw milk samples were collected from August

2021 to August 2022, from Jersey (n = 271), Holstein (n = 248) and Jersey x Holstein crossbred cows (n = 82), raised on five commercial farms located in the state of Paraná, Brazil. Milk composition, somatic cell count (SCC), milk urea nitrogen (MUN), MES, pH, acidity and iCa were determined. Days in milk (DIM) were categorized into four classes: 1-60, 61-150, 151-305 and over 305 DIM. Data were submitted to analysis of variance. Fixed and random effects were incorporated into the model, in a repeated measures in time arrangement using the mixed models methodology. Significant interactions between DIM class and genetic groups were detected for MES, MUN, acidity, iCa, fat, and total solids. The comparison between each combination of genetic group and DIM class showed that at the beginning of lactation, Holsteins produced milk with higher MES than Jersey and crossbreds. Also, at 105-300 DIM Holstein milk presented higher MES than Jersey, while beyond 300 DIM Holstein milk showed higher MES than crossbred cows. At the beginning of lactation acidity was higher in Holstein milk and crossbreds compared with Jersey, while acidity was lower in Holstein milk compared with Jersey and crossbreds in the other lactation stages. Ionic calcium was highest after lactation peak (61-150 DIM) for Holstein, but did not vary between lactation stages for Jersey and crossbreds. Functional characteristics of bovine raw milk such as MES, iCa and acidity varied between lactation stages in a distinct manner according to genetic groups. Moreover, early and end lactation stages are challenging in terms of low stability, especially for Jersey and crossbreds.

Two major bovine milk whey proteins induce distinct responses in IEC-6 intestinal cells

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Japan

Abstract

α -lactalbumin (α -LA) and β -lactoglobulin (β -LG) are major whey proteins in bovine milk. We studied the effects of these molecules on the intestinal cell response by comparing the native form with the denatured form containing oligomers obtained by treatment with 2,2,2-trifluoroethanol (TFE). We previously reported that proteins in native and TFE-treated forms exhibited cell growth stimulation and cytotoxicity, respectively, in undifferentiated rat crypt IEC-6 and human colon Caco-2 cells. However, neither whey protein showed cytotoxicity even in the TFE-treated form in differentiated Caco-2 cells. Only undifferentiated immature intestinal cells can distinguish between these native and denatured proteins. Moreover, α -LA and β -LG exhibited different oligomer formation characteristics during the TFE treatment. In the present study, we compared the effects of native and TFE-treated whey proteins on IEC-6 cells in more detail. The native forms of both whey proteins exhibited cell proliferative effects in a concentration-dependent manner. For the TFE-treated forms, α -LA showed rapid

and potent cytotoxicity, whereas β -LG altered cell responses depending on its concentration and exposure time; lower concentration/shorter exposure and higher concentration/longer exposure induced cell growth stimulation and cytotoxicity, respectively. Pre-treatment of the cell membrane with cholesterol suppressed the effects on the cell response only in TFE-treated β -LG. In a preliminary examination using inhibitors of signal transduction, TFE-treated α -LA acted on the intrinsic apoptosis pathway via Bcl-2-associated X and p53, whereas the action of TFE-LG did not require this pathway. Tyrosine phosphorylation is necessary for the cell proliferation effect of both native whey proteins; however, native α -LA, but not native β -LG, also required activation of the pathway with selective epidermal growth factor receptor tyrosine kinase and Janus kinase 2/3. In summary, the two major bovine milk whey proteins induced similar yet discrete responses in undifferentiated intestinal cells. Even when oligomers are formed, β -LG may be much less hazardous to immature intestinal cells than α -LA.