COLLECTED ABSTRACTS

Editorial: the need for consideration of environmental implications in developing countries' dairy research

Long Cheng
Australia

The global human population reached 7.7 billion in 2020 and it is expected to increase close to 9 billion in the next 30 years. This substantial population growth is associated with improvements in human life expectancy, growing urbanization, and increasing demand on our limited environmental resources. These facts challenge the way we farm dairy cattle and require dairy production to be managed sustainably, with environmental protection as a major factor to consider. There are many components involved in sustainable dairy production and two major components will be discussed in this short Editorial: environmental pollution quantification and mitigation.

Individual dairy cow management: achievements, obstacles and prospects

Ephraim Maltz
Israel

Abstract

This review deals with the prospects and achievements of individual dairy cow management (IDCM) and the obstacles and difficulties encountered in attempts to successfully apply IDCM into routine dairy management. All aspects of dairy farm management, health, reproduction, nutrition and welfare are discussed in relation to IDCM. In addition, new IDCM R&D goals in these management fields are suggested, with practical steps to achieve them. The development of management technologies is spurred by the availability of off-the-shelf sensors and expanded recording capacity, data storage, and computing capabilities, as well as by demands for sustainable dairy production and improved animal wellbeing at a time of increasing herd size and milk production per cow. Management technologies are sought that would enable the full expression of genetic and physiological potential of each cow in the herd, to achieve the dairy operation's economic goals whilst optimising the animal's wellbeing. Results and conclusions from the literature, as well as practical experience supported by published and unpublished data are analyzed and discussed. The object of these efforts is to identify knowledge and management routine gaps in the practical dairy operation, in order to point out directions and improvements for successful implementation of IDCM in the dairy cows' health, reproduction, nutrition and wellbeing.

Identification and verification of differentially expressed genes in yak mammary tissue during early lactation

Mao Yuan, Wei Xia, Xiaolei Zhang, Yongtao Liu and Mingfeng Jiang
China

Abstract

Yaks (*Bos grunniens*) live primarily in the Qinghai-Tibetan plateau (altitude: 2000-5000 m). Their milk presents unusual characteristics, containing large amounts of solids including fat and protein, and it is, therefore, important to understand the genetic makeup of the yak. To identify potentially critical genes playing a role in yak mammary tissue from colostrum to mature milk phase of lactogenesis, the early lactation (colostrum) stage (ELS; day 1 after parturition) and mature lactation (milk) stage (MLS; day 15) were chosen for comparison. An ELS-specific cDNA library was established by suppression subtractive hybridization and 25 expressed sequence tags at ELS were identified by sequencing and alignment. To further confirm our results the expression levels of 21 genes during the lactation cycle were measured using quantitative real-time RT-PCR (qRT-PCR). The qRT-PCR results confirmed 9 significantly up-regulated genes at ELS vs. MLS in yak mammary tissue, in which the L-amino acid oxidase 1 *(LAO1)* and collagen, type I, alpha I (*COL1A1)* were the most significantly up-regulated. During the lactation cycle, the highest expression of some milk fat genes (i.e., *XDH* and *FABP3*) in yak mammary tissue appears earlier than that in dairy cow. Our data also indicate *MYC* potentially playing a central role through putative regulation of *COL1A1*, *CD44*, *SPARC*, *FASN* and *GPAM*.

Variation in the yak lipin-1 gene and its association with milk traits

Xin Wang, Huitong Zhou, Jon G.H. Hickford, Shaobin Li, Jiqing Wang, Xiu Liu, Jiang Hu and Yuzhu Luo
China and New Zealand

Abstract

The aim of this research was to identify variation in the yak lipin-1 gene (*LPIN1*) and determine whether this variation affects milk traits. PCR-single stranded conformational polymorphism (PCR-SSCP) analysis was used to detect variation in the 5' untranslated region of *LPIN1* in 500 yaks, from four populations: Tianzhu white yaks, Qinghai yaks, wild × domestic-cross yaks, and Gannan yaks. Four unique PCR-SSCP patterns, representing four different DNA sequence variants (named *A, B, C* and *D*), were observed. These contained six single nucleotide polymorphisms. Female Gannan yaks with *BC* genotypes produced milk with a higher fat content ($P < 0.001$) and total milk solids ($P < 0.001$), than those with the *AA*, *AB* and *BB* genotypes. These results would suggest that *LPIN1* is having an effect on yak milk fat synthesis.

The functions and mechanisms of sequence differences of DGAT1 gene on milk fat synthesis between dairy cow and buffalo

Dinesh Bhattarai, Rahim Dad, TesfayWorku, SutongXu, Farman Ullah, Min Zhang, Xianwei Liang, Tingxian Den, MingxiaFan and Shujun Zhang
China

Abstract

In this research communication we describe the DGAT1 sequence and promoter region in dairy cows and buffalo and compare the activities of DGAT1 between the two species in order to increase knowledge of the cause of milk fat variation. pGL-3 basic vectors were used to construct the reporter gene. Based on the predicted promoter region, 4 truncated plasmid vectors were constructed in cow-DGAT1 and 3 plasmid vectors in buffalo-DGAT1. Each reporter plasmid was transfected into the bovine mammary epithelial cell (BMEC), 293T cell, and CHO cells to analyze the activity using Dual-Luciferase Reporter Assay System. The results show that the region between -93 to -556bp was essential for cow promoter activity while -84 to -590bp was essential for buffalo promoter activity revealing these regions contain core promoter. The buffalo has higher promoter activity than cow yet it was not statistically significant. Comparison of candidate mutation K232A between cow and buffalo population revealed the presence of both the allelic population in dairy cows (lysine and alanine) however, only K (lysine) allelic amino acid was found in buffalo population. The absence of the alanine allelic population from buffalo explains the higher fat content of buffalo milk.

Contrasting effects of high-starch and high-sugar diets on cattle

Andrea Francesio, Lorenzo Viora, Matt J Denwood, Will Tulley, Nicola Brady, Peter Hastie, Andrew Hamilton, Christopher Davison, Craig Michie and Nicholas N Jonsson
UK and Denmark

Abstract

The experiment reported in this research paper aimed to determine whether clinical and subclinical effects on cattle were similar if provided with isoenergetic and isonitrogenous challenge diets in which carbohydrate sources were predominantly starch or sugar. The study was a 3 × 3 Latin square using six adult Jersey cows with rumen cannulae, over 9 weeks. In the first 2 weeks of each 3 week experimental period cows were fed with a maintenance diet and, in the last week, each animal was assigned to one of three diets: a control diet (CON), being a continuation of the maintenance diet; a high starch (HSt) or a high sugar (HSu) diet. Reticuloruminal pH and motility were recorded throughout the study period. Blood and ruminal samples were taken on day-1 (TP-1), day-2 (TP-2) and day-7 (TP-7) of each challenge week. Four clinical variables were recorded daily: diarrhoea, inappetence, depression and ruminal tympany. The effects of treatment, hour of day and day after treatment on clinical parameters were analysed using linear mixed effects (LME) models. Although both challenge diets resulted in a decline in pH, an increase in the absolute pH residuals and an increase in the number of minutes × day under pH 5.8, systemic inflammation was only detected with the HSt diet. The challenge diets differentially modified amplitude and period of reticuloruminal contractions compared with CON diet and both were associated with an increased probability of diarrhoea. The HSu diet reduced the probability

of an animal consuming its complete allocation. Because the challenge diets were derived from complex natural materials (barley and molasses respectively), it is not possible to assign all the differential effects to the difference in starch and sugar concentration: non-starch components of barley or non-sugar components of molasses might have contributed to some of the observations. In conclusion, substituting much of the starch with sugar caused no substantial reduction in the acidosis load, but inflammatory response was reduced while feed rejection was increased.

Selenium biofortified alfalfa hay fed in low quantities improves selenium status and glutathione peroxidase activity in transition dairy cows and their calves

Shana Jaaf, Brandon Batty, Angela Krueger, Charles T. Estill and Massimo Bionaz
USA

Abstract
The study hypothesizes that feeding a relatively low amount of Se biofortified alfalfa hay during the dry period and early lactation would improve selenium status and glutathione peroxidase activity in dairy cows and their calves. Ten Jersey and 8 Holstein primiparous dairy cows were supplemented with Se biofortified (TRT; n=9) or non-biofortified (CTR; n=9) alfalfa hay at a rate of 1 kg/100 kg of BW mixed with the TMR from 40 days prior parturition to 2 weeks post-partum. Se concentration in whole blood, liver, milk, and colostrum, the transfer of Se to calves, and the glutathione peroxidase (GPx) activity were assessed. TRT had 2-fold larger ($P<0.05$) Se in blood vs. CTR that resulted in larger Se in liver and colostrum but not milk and larger GPx activity in plasma and erythrocytes but not in milk. Compared to CTR, calves from TRT had larger Se in blood but only a numerical ($P=0.09$) larger GPx activity in plasma. A positive correlation was detected between Se in the blood and GPx activity in erythrocytes and plasma in cows. Our results demonstrated that feeding pregnant primiparous dairy cows with a relatively low amount of Se-biofortified alfalfa hay is an effective way to increase Se in the blood and liver, leading to greater antioxidant activity via GPx. The same treatment was effective in improving Se concentration in calves but had a modest effect on their GPx activity. Feeding Se biofortified hay increased Se concentration in colostrum but not in milk.

Skin surface temperature of the mammary gland, measured by infrared thermography, in primiparous Girolando cows fed diets containing different lipid sources

Alysson M Wanderley, Luís CV Ítavo, Geraldo T dos Santos, Camila CBF Ítavo, Alexandre M Dias, Rodrigo G Mateus, Luiz C Pereira, Ariadne B Gonçalves, Endyara S Kohl and Celso RC Lima
Brazil

Abstract
This research communication describes the influence of diet, mammary quarter position and milking process on the temperature of teats and udder of cows fed diets containing different lipid sources. Five primiparous cows were fed diets containing cottonseed, sunflower seed, soybeans or soybean oil as a source of lipids and a reference diet without the inclusion of lipid sources in a 5 × 5 Latin Square design. Milk yield was determined in the last five days of each period. Milk samples were collected for SCC analysis on the last two days of each experimental period. The images of the mammary gland were obtained using an infrared camera and were analyzed with appropriate computer software. Milk yield was 14.8% higher for cows fed soybeans as a source of lipids. Diets

and somatic cell counts did not influence the temperature of teats and udder. The milking process reduced the temperature of teats and udder by 0.79 ºC. Rear teats and rear quarters had higher surface temperatures than front teats and fore quarters. Changes in temperature of teats and mammary quarters occurred as a function of the milking process and quarter position. However, the diet and the SCC did not influence the temperature of teats and mammary quarters in this experiment.

Opportunities and limitations of milk mid-infrared spectra-based estimation of acetone and β-hydroxybutyrate for the prediction of metabolic stress and ketosis in dairy cows

Monica de Oliveira Caldeira, Denisa Dan, Anna-Lena Neuheuser, Remo Stürmlin, Christoph Weber, Daniel L. Glauser, Martin Stierli, Urs Schuler, Juerg Moll, Silvia Wegmann, Rupert M. Bruckmaier and Josef J. Gross
Switzerland

Abstract
Subclinical (SCK) and clinical (CK) ketosis are metabolic disorders responsible for big losses in dairy production. Although Fourier-transform mid-infrared spectrometry (FTIR) to predict ketosis in cows exposed to great metabolic stress was studied extensively, little is known about its suitability in predicting hyperketonemia using individual samples, e.g. in small dairy herds or when only few animals are at risk of ketosis. The objective of the present research was to determine the applicability of milk metabolites predicted by FTIR spectrometry in the individual screening for ketosis. In experiment 1, blood and milk samples were taken every two weeks after calving from Holstein (n = 80), Brown Swiss (n = 72) and Swiss Fleckvieh (n = 58) cows. In experiment 2, cows diagnosed with CK (n = 474) and 420 samples with blood β-hydroxybutyrate [BHB] < 1.0 mmol/L were used to investigate if CK could be detected by FTIR-predicted BHB and acetone from a preceding milk control. In experiment 3, correlations between data from an in farm automatic milk analyser and FTIR-predicted BHB and acetone from the monthly milk controls were evaluated. Hyperketonemia occurred in majority during the first eight weeks of lactation. Correlations between blood BHB and FTIR-predicted BHB and acetone were low (r = 0.37 and 0.12, respectively, $P < 0.0001$), as well as the percentage of true positive values (11.9% and 16.6%, respectively). No association of FTIR predicted ketone bodies with the interval of milk sampling relative to CK diagnosis was found. Data obtained from the automatic milk analyser were moderately correlated with the same day FTIR-predicted BHB analysis (r = 0.61). In conclusion, the low correlations with blood BHB and the small number of true positive samples discourage the use of milk mid-infrared spectrometry analyses as the only method to predict hyperketonemia at the individual cow level.

From six to zero percent *Mycobacterium avium* subsp. *paratuberculosis* milk ELISA positivity in three years – probably induced by *Mycobacterium vaccae*

Daniel Elad, Inna Lysnyansky, Rama Falk, Shlomo E. Blum, Limor Weisbelith, Inna Mikula and Adin Shwimmer
Israel

Abstract

This research communication reports the results of a study aimed at investigating the effects of introducing *Mycobacterium vaccae* on paratuberculosis carriage in a dairy herd. *M. vaccae* is a non-pathogenic member of the *Mycobacteriaceae*, with immunomodulatory and immunotherapeutic capabilities, acting by stimulating the cellular immune system, important in protection against paratuberculosis. Starting in 2014 we administered, by gavage, 10^{10} live *M. vaccae* bacteria to all new-born heifers on a dairy farm, first within 24 hours of birth and again 2 weeks later. Paratuberculosis carriage was monitored yearly by milk ELISA. Faecal samples of 50% of cows, aged 3 years, born 1, 2 or 3 years before the experiment's onset, were tested by qPCR for MAP shedding and compared to 100% treated cows of the same age. Within 3 years, milk ELISA positivity was reduced from 6% to 0% and remained unchanged for the subsequent 2 years (last checked in February 2019). One qPCR positive control cow was found each year for a total of 3 animals (2.46%). One positive cow (1%) was found among the treated cows. Two of the 3 positive control animals, still present on the farm at the end of 2019, tested negative whereas the positive test cow continued shedding MAP. *M. vaccae* shedding heifers mixing with adult cows were the probable means of the microorganism's propagation. The results of this investigation indicate that the introduction of live *M. vaccae* may be an inexpensive and fast alternative to current paratuberculosis control practices, justifying further exploration of the topic.

Bulk tank milk quality data is unlikely to give useful information about dairy cow welfare at herd level

Jessica Ginestreti, Rosa Maria Strano, Valentina Lorenzi, Francesca Fusi, Alessandra Angelucci, Giandomenico Ferrara, Giorgio Galletti, Stefania Bergagna, Giuseppe Bolzoni, Giorgio Zanardi, Elena Buffoli, Antonio Marcolini and Luigi Bertocchi
Italy

Abstract

This research communication explores the value of routinely collected bulk tank milk quality data for estimating dairy cattle welfare at herd level. Selected bulk tank milk quality parameters (somatic cell count, total bacterial count, urea, protein and fat contents) recorded during the years 2014-2016 in 287 Italian dairy farms were compared with the animal welfare data of each farm. The welfare assessment data were extracted from the database of the Italian Reference Centre for Animal Welfare (CReNBA), which includes the outputs of the application of the CReNBA welfare assessment protocol for dairy cows, used at national level for on-farm controls. The statistical analysis was carried out using the correlation coefficient for Kendall's Tau ranks, in order to investigate the presence of a categoric relationship between the selected bulk tank milk quality parameters and the overall animal welfare score or the scores of the single areas A (farm management and staff training, B (housing) and C (animal-based measures). Somatic cell count,

total bacterial count, urea and proteins demonstrated only a few statistically significant and very weak correlations with farm animal welfare data, while no significant correlations were obtained for milk fat content. Given the weak correlations found, the selected bulk tank milk parameters seems to be able to provide only limited information about the welfare level of the herd, thus it could be difficult to use them for drawing up a pre-screening model for identifying herds at risk of poor welfare.

High levels of fatty acids inhibit β-casein synthesis through suppression of the JAK2/STAT5 and mTOR signaling pathways in mammary epithelial cells of cows with clinical ketosis

Xin Shu, Zhiyuan Fang, Yuan Guan, Xiying Chen, Juan J Loor, Hongdou Jia, Jihong Dong, Yazhe Wang, Rankun Zuo, Guowen Liu, Xiaobing Li, and Xinwei Li
China and USA

Abstract

Ketosis is a metabolic disease of dairy cows often characterized by high concentrations of ketone bodies and fatty acids, but low milk protein and milk production. The Janus kinase 2 (JAK2)-signal transducer and activator of transcription 5 (STAT5) and the mechanistic target of rapamycin (mTOR) signaling pathways are central for the regulation of milk protein synthesis. The effect of high levels of fatty acids on these pathways and β-casein synthesis are unknown in dairy cows with clinical ketosis. Mammary gland tissue and blood samples were collected from healthy (n = 15) and clinically-ketotic (n = 15) cows. In addition, bovine mammary epithelial cells (BMEC) were treated with fatty acids, methionine (Met) or prolactin (PRL), respectively. In vivo, the serum concentration of fatty acids was greater ($P > 0.05$) and the percentage of milk protein ($P > 0.05$) was lower in cows with clinical ketosis. The JAK2-STAT5 and mTOR signaling pathways were inhibited and the abundance of β-casein was lower in mammary tissue of cows with clinical ketosis ($P > 0.05$). In vitro, high levels of fatty acids inhibited the JAK2-STAT5 and mTOR signaling pathways ($P > 0.05$) and further decreased the β-casein synthesis ($P > 0.05$) in BMEC. Methionine or PRL treatment, as positive regulators, activated the JAK2-STAT5 and mTOR signaling pathways to increase the β-casein synthesis. Importantly, the high concentration of fatty acids attenuated the positive effect of Met or PRL on mTOR, JAK2-STAT5 pathways and the abundance of β-casein ($P > 0.05$). Overall, these data indicate that the high concentrations of fatty acids that reach the mammary cells during clinical ketosis inhibit mTOR and JAK2-STAT5 signaling pathways, and further suppress β-casein synthesis.

Introducing a sinusoidal equation to describe lactation curves for cumulative milk yield and composition in Holstein cows

Navid Ghavi Hossein-Zadeh, Hassan Darmani Kuhi, James France and Secundino López
Iran, Canada and Spain

Abstract

The aim of the work reported here was to investigate the appropriateness of a sinusoidal function by applying it to model the cumulative lactation curves for milk yield and composition in primiparous Holstein cows, and to compare it with three conventional growth models (linear, Richards and Morgan). Data used in this study were 911,144 test-day records for milk, fat and

protein yields, which were recorded on 834 dairy herds from 2000 to 2011 by the Animal Breeding Centre and Promotion of Animal Products of Iran. Each function was fitted to test-day production records of dairy cows using appropriate procedures in SAS (PROC REG for the linear model and PROC NLIN for the Richards, Morgan and sinusoidal equations) and the parameters were estimated. The models were tested for goodness of fit using adjusted coefficient of determination (R^2_{adj}), root mean square error (RMSE), Akaike's information criterion (AIC) and the Bayesian information criterion (BIC). R^2_{adj} values were generally high (>0.999), implying suitable fits to the data, and showed little differences among the models for cumulative yields. The sinusoidal equation provided the lowest values of RMSE, AIC and BIC, and therefore the best fit to the lactation curve for cumulative milk, fat and protein yields. The linear model gave the poorest fit to the cumulative lactation curve for all production traits. The current results show that classical growth functions can be fitted accurately to cumulative lactation curves for production traits, but the new sinusoidal equation introduced herein, by providing best goodness of fit, can be considered a useful alternative to conventional models in dairy research.

Examination of methionine stimulation of gene expression in dairy cow mammary epithelial cells using RNA-sequencing

Xiaoming Hou, Minghui Jiang, Jinyu Zhou, Shuyuan Song, Feng Zhao and Ye Lin
China

Abstract
In this research communication, a cell model with elevated β-CASEIN synthesis was established by stimulating bovine mammary epithelial cells with 0.6 mM methionine, and the genome-wide gene expression profiles of methionine-stimulated cells and untreated cells were investigated by RNA sequencing. A total of 458 differentially expressed genes (DEGs; 219 upregulated and 239 downregulated) were identified between the two groups. Gene Ontology (GO) analysis showed that the two highest-ranked GO terms in "molecular function" category were "binding" and "catalytic activity", suggesting that milk protein synthesis in methionine-stimulated cells requires induction of gene expression to increase metabolic activity. Kyoto Encyclopedia of Genes and Genomes analysis revealed that within the "environmental information processing" category, the subcategory that is most highly enriched for DEGs was "signal transduction". cGMP-PKG, Rap1, calcium, cAMP, PI3K-AKT, MAPK, and JAK-STAT are the pathways with the highest number of DEGs, suggesting that these signaling pathways have potential roles in mediating methionine-induced milk protein synthesis in bovine mammary epithelial cells. This study provides valuable insights into the physiological and metabolic adaptations in cells stimulated with methionine. Understanding the regulation of this transition is essential for effective intervention in the lactation process.

MicroRNA-212 targets *SIRT2* to influence lipogenesis in bovine mammary epithelial cell line

Xubin Lu, Hailei Xia, Jingyi Jiang, Xin Xu, Mingxun Li, Zhi Chen, Yujia Sun, Huimin Zhang and Zhangping Yang
China

Abstract

In this research paper we filter and verify miRNAs which may target silent information regulator homolog 2 *(SIRT2)* gene and then describe the mechanism whereby *miRNA-212* might regulate lipogenic genes in mammary epithelial cell lines via targeting *SIRT2*. Bioinformatics analysis revealed that the bovine *SIRT2* gene is regulated by three miRNAs: *miR-212*, *miR-375* and *miR-655*. The three miRNAs were verified and screened by qRT-PCR, western blot, and luciferase multiplex verification techniques and only *miR-212* was shown to have a targeting relationship with *SIRT2.* The results of co-transfecting *miR-212* and silencing RNA (siRNA) showed that by targeting *SIRT2*, *miR-212* can regulate the expression of fatty acid synthetase (*FASN*) and sterol regulatory element binding factor 1 (*SREBP1*) but not peroxisome proliferator-activated receptor gamma (*PPARγ).* Measurement of triglyceride (TAG) content showed that *miR-212* increased the fat content of mammary epithelial cell lines. The study indicates that *miR-212* could target and inhibit the expression of the *SIRT2* gene to promote lipogenesis in mammary epithelial cell lines.

Application of triplex-PCR with an innovative combination of 3 pairs of primers for the detection of milk's animal origin in cheese and yoghurt

Evanthia Tsirigoti, Zoi Katsirma, Athanasios I. Papadopoulos, Georgios Samouris, Loukia V. Ekateriniadou and Evridiki Boukouvala
Greece

Abstract

In the research communication we describe an innovative protocol that combines three pairs of primers, two from the literature and one designed in our laboratory, for application in triplex-PCR on somatic cell DNA to enable identification of the species origin (cow, sheep, goat) of cheeses and yogurts with a detection limit of 0.1%. Mislabeling was detected in 15 out of 40 cheeses and in 18 out of 40 yogurts tested. The suggested procedure is a quick and reliable tool for identifying the animal origin of cheeses and yogurts and it can be used to certify product reliability on the domestic and international market. Additionally, in combination with a serological test it can offer a reliable tool for detecting the presence of cow's whey.

Assessment of physico-chemical changes in UHT milk during storage at different temperatures

Suvartan Ranvir, Rajan Sharma, Kamal Gandhi and Bimlesh Mann
India

Abstract

This research communication describes enzymatic and physico-chemical changes during storage of UHT milk. The UHT milk sample was stored at 5 and 30°C for 4 months and analyzed regularly at an interval of one month. During storage of UHT milk, there was a significant ($p<0.001$) increase in non-protein nitrogen, non-casein nitrogen, soluble calcium, soluble magnesium and proteolysis,

while a significant ($p<0.001$) decrease in pH was observed. There was a slight change in the particle size and zeta potential of casein micelles. Changes were more pronounced in milk sample stored at 30°C than that stored at 5°C. During storage, there occurred changes in pH, viscosity, salt balance and nitrogenous components which adversely affected its quality. It was concluded that the proteolysis led to the acidification which had destabilizing effect on the milk.

Diafiltration affects the gelation properties of concentrated casein micelle suspensions obtained by filtration

Zhengtao Zhao, Isis Renhe, Robert Fu and Milena Corredig
Canada and Denmark

Abstract
Using membrane filtration it is possible to selectively concentrate proteins and, in the case of microfiltration, concentrate casein micelles. During filtration, water is often added and this practice, called diafiltration, causes further release of permeable components and maintains filtration efficiency. Filtration causes changes in composition of the protein as well as the soluble phase, including soluble calcium, which is a critical factor controlling the gelation properties of the casein micelles in milk. It was hypothesized that concentrates obtained using membrane filtration with or without diafiltration would have different gelation behavior. To test this hypothesis, two concentrates of similar casein micelle volume fraction were prepared, using spiral wound polymeric microfiltration membranes with a 800 kDa molecular weight cutoff, with or without diafiltration. The concentrates showed a gelation behavior comparable to that of skim milk, with a similar gelation time and with a higher firmness, due to the higher number of protein linkages in the network. In contrast, the hydrolysis of κ-casein by chymosin and casein aggregation were inhibited in diafiltered casein micelle suspensions. When the concentrates were recombined with the original skim milk to a final concentration of 5% protein, which re-established a similar soluble phase composition, differences in gelation behavior were no longer observed: both treatments showed similar gelation time and gel firmness. These results confirmed that membrane filtration can result in concentrates with different functionality, and that ionic environmental conditions are critical to the aggregation behavior of casein micelles. This is of particular significance in industrial settings where these fractions are used as a way to standardize proteins in cheese making.

Effect of carbonation and probiotic addition on the physicochemical, microbiological and sensory characteristics of whey dairy beverage

Carla Salete Jadão Alves, Simone Andreoti Mendes Floriano, Verônica Parassen Voltarelli, Christiane Maciel Vasconcellos Barros de Rensis, Tatiana Colombo Pimentel, Giselle Nobre Costa and Priscila Cristina Bizam Vianna
Brazil

Abstract
This research communication addresses the impact of the addition of *Lactobacillus casei* and/or carbonation (CO_2) on the chemical composition, physicochemical characteristics, probiotic survival, and sensory acceptance of passion-fruit flavored whey dairy beverages (70% milk/30% whey) during storage (30 days/4°C). The addition of *Lactobacillus casei* and/or carbonation did not impact on the chemical composition, pH values, and acceptance (flavor and overall impression) of the products, but increased the acidity, and decreased the aroma acceptance. The carbonation process did not affect the probiotic survival but decreased the acidity of the products during storage. It can be concluded that it is possible to develop a probiotic passion-fruit flavored carbonated whey dairy beverage with suitable chemical composition, acidity, sensory acceptance (> 6 in 9-point hedonic scale) and probiotic viability (>7 log cfu/mL) that could be refrigerated stored for 30 days. This is the first report considering a probiotic non-fermented carbonated whey dairy beverage.

Technological properties of beneficial bacteria from the dairy environment and development of a fermented milk with the beneficial strain *Lactobacillus casei* MRUV6

Monique Colombo, Svetoslav D. Todorov, Antonio F. Carvalho and Luís A. Nero
Brazil and South Korea

Abstract
In this research paper we describe the technological properties of beneficial lactic acid bacteria (LAB) obtained from a dairy production chain and the development of a fermented milk produced with *Lactobacillus casei* MRUV6. Fifteen LAB isolates (*Lactobacillus* sp., *Pediococcus* sp. and *Weissela* sp.) presented acidifying abilities (pH ranges from 0.73 to 2.11), were able to produce diacetyl (except by 5 isolates) and exopolysaccharides, and two were proteolytic. *L. casei* MRUV6 was selected for producing a fermented milk, stored up to 35 days at 4 and 10 °C. Counts on MRS agar with added vancomycin (10 mg/L) and MRS agar with added bile salts (1.5% w/v) ranged from 9.7 to 9.9 log CFU/g, independently of the tested conditions, indicating stability and intestinal resistance of *L. casei* MRUV6, despite some significant differences ($p < 0.05$). The study demonstrated the technological potential of a potential probiotic candidate strain, *L. casei* MRUV6, to be used as a starter culture in the dairy industry.

Identification of bacterial hazards in the production of artisan fresh cheese in Cuba

Ailin Martínez, Nivian Montes de Oca, Mabelín Armenteros, Odalys Uffo, Yamilka Riverón, Dayaimi González, Dianys Remón, Severino Beneone Páez Barbosa, Manoel Adriao, Soraya Farías de Andrade Freitas and Alejandra Villoch
Cuba and Brazil

Abstract

Artisan fresh cheese producing farms from six provinces of Cuba were studied to identify the presence of bacterial hazards and the results are presented in this research communication. The bacterial hazards identified in milk and cheese respectively were: *Listeria* spp. (9.5% and 18.9%), *Bacillus cereus* (23.2% and 24.2%), *Escherichia coli* O157 (12.6% and 13.7%), *Salmonella* spp. (10.5% and 17.9%), and *Staphylococcus aureus* (29.5% and 51.6%). *Listeria monocytogenes* was not detected. Nine *Salmonella* serotypes corresponding to *Salmonella* enterica subsp. enterica and *Salmonella* enterica subsp. arizonae were isolated, whereas *Salmonella* Anatum was present most often. Biofilm formation by the isolated species and enterotoxin production by *S. aureus* strains demonstrated the pathogenic potential of the identified bacterial hazards. Results proved the presence of bacterial hazards in the raw milk and cheeses analyzed, so that good manufacturing practices must be accomplished throughout the entire production process in order to avoid the occurrence of foodborne diseases in the population.

Oestrogens in milk and breast cancer: a cause for concern…or not?

Malcolm Peaker
UK

Abstract

In this short Research Reflection I address and refute the suggestion that oestrogens consumed in milk might contribute in a significant way to endogenous levels and thereby have a physiological action, possibly resulting in adverse consequences including increased breast cancer risk. Quantitative analysis based on published data shows that, even in worst case scenarios, oestrogen consumption in milk is considerably less than regulatory bodies regard as entirely safe.