

Challenges for the science of animal production in the changing world

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Hormonal control of the mammary blood-milk barrier and its role in establishing and maintaining milk production

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Abstract

The blood-milk barrier (BMB) forms at parturition when the gland switches from a non-lactating state to one of copious milk production and becomes leaky again when milk removal ceases and mammary involution is initiated. In this review the importance of the BMB in milk production and, in particular, its hormonal regulation is explored. Tight junctions (TJ) between adjacent mammary epithelial cells form a barrier to the two-directional paracellular movement of small molecules between the blood and milk and are responsible for establishing and maintaining the BMB. They form part of the cell's junctional complex and consist of transmembrane proteins that are linked to the mammary cell's cytoskeleton. This means that when, during lactation, TJ become "leaky" the resulting perturbation of the cytoskeleton interferes with the cell's secretory function. As such, TJ are involved in regulating and maintaining milk production. Mammary TJ are under hormonal control, with progesterone, glucocorticoids, prolactin, parathyroid hormone-related peptide (PTHrP) and serotonin (5-HT) being the key hormones. Progesterone prevents closure of TJ and the immediate prepartum drop in its concentration is a prerequisite for TJ closure. A simultaneous increase in the levels of glucocorticoids and prolactin is necessary for full TJ closure and initiation and maintenance of lactation. Both PTHrP and 5-HT are important hormones in maintaining extracellular calcium concentrations, a requirement for maintaining TJ integrity. Whereas PTHrP reduces TJ permeability, necessary for establishing and maintaining milk production, 5-HT has an opening effect on TJ. The latter may help speed up mammary involution and facilitate the movement of immune factors into the gland, preventing intramammary infections. In summary, mammary TJ make up the BMB and play a role in establishing and maintaining milk production and are under hormonal control, with progesterone, glucocorticoids, PTHrP and 5-HT being key regulatory hormones and prolactin probably playing a supporting role.

Effect of feeding increasing levels of whole cottonseed on milk production, milk components and milk fatty acids profile in lactating dairy goats

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Brazil

Abstract

We assessed the feeding behavior, intake, apparent total tract digestibility, blood parameters, milk yield, milk composition and milk fatty acid profile in dairy goats fed diets containing increasing levels of whole cottonseed (WCS), specifically a control diet with no WCS and diets containing 120, 150 and 180g WCS/kg DM. Eight lactating dairy goats were distributed in a replicated 4 × 4 Latin square design with four 21-day periods. Rumination and total chewing time increased linearly with WCS inclusion levels. However, no effects on dry matter intake or digestibility were observed. Milk production was similar among treatments, but milk fat and lactose concentration increased linearly with WCS dietary levels, as did monounsaturated and polyunsaturated FA and conjugated linoleic acid concentration in milk fat. This study demonstrates that increasing the inclusion of WCS in the diets of dairy goats offers potential nutritional benefits without negatively impacting intake, digestibility, or ruminal fermentation. Notably, WCS-enhanced diets led to improved milk fat composition, with increased concentrations of beneficial FA. These results support the use of WCS as an effective feed ingredient to enhance milk quality in dairy goats, leveraging both the high-energy content and fiber structure of WCS, which promotes rumen health and function without reducing DMI. Dairy goat producers can incorporate up to 180 g WCS/kg DM in diets to produce milk with a healthier fat profile, potentially enhancing its marketability.

Residue from the extraction of cassava starch in dairy cows feeding: nutrient digestibility and performance

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Brazil

Abstract

The effect of different levels of residue from the extraction on cassava starch (REAM) in the diet of multiparous lactating Holstein cows was investigated. The experiment was carried out at the Universidade Estadual do Oeste do Paraná. Five multiparous Holstein cows, with mean

milk production of 30.65 ± 1.17 kg/day were distributed into five treatments, using Latin squares (5×5). Treatments consisted of inclusion (0, 8, 16, 24 and 32% dry matter basis) of REAM in the diet. Intake, digestibility, milk production and composition as well as blood parameters were measured. Except for ether extract and total digestible nutrients, the intake variables did not differ significantly between treatments. Except for the digestibility of crude protein, all digestibility values decreased progressively with inclusion levels of REAM. The inclusion of REAM in feeding of lactating Holstein cows up to 32% of the diet reduced milk production by 15%, however, it did not alter milk production efficiency, fat, total solids and blood parameters. We conclude that up to 16% of REAM can be included in the diet; however, higher levels may lead to a significant fall in productivity.

Lack of effect of stevia (*Stevia rebaudiana*) and hemp (*Cannabis sativa*) by-products on milk yield, milk fatty acid profile and milk oxidative stability in dairy cows

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Abstract

This experiment assessed the effects of adding hemp (seeds or hay) and stevia by-products to dairy cow diets on milk yield and on the fatty acid profile and oxidative stability of the milk. Additional analyses included composition, total phenolic content and total antioxidant capacity of milk samples as well as blood serum parameters. Thirty-five Holstein dairy cows were involved for 60 days, divided into five groups: control, hemp seed, hemp hay, stevia and a combination of hemp seeds and stevia leaves. No significant changes were observed in milk yield or composition. While monounsaturated fatty acid (MUFA) content did not differ significantly between control and experimental diets, milk from cows fed hemp seeds had higher MUFA compared to those fed hemp hay. Further research is recommended to determine the optimal proportion of these by-products in cow diets.

Assessment of lactoferrin supplementation in milk replacer on calf growth, feed efficiency and scouring incidence preweaning and postweaning

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Abstract

We investigated the hypothesis that supplementing milk replacer (MR) with exogenous lactoferrin (LF) would improve average daily gain (ADG) and feed efficiency and decrease scouring incidence in dairy calves. Lactoferrin is an antimicrobial and anti-inflammatory glycoprotein naturally found in bovine colostrum and milk that is low in MR. Previous studies suggest that supplementing LF to MR enhances ADG and feed efficiency while reducing disease occurrence in pre-weaning dairy calves. In our experiment, 103 Holstein heifer calves were randomly assigned to 1 of 4 treatments in a randomized complete block design from birth to d 56 of age. Each calf received 340.1 g/d of 24% protein, 20% fat basal MR fed twice daily from d 1 to 42 and once daily from d 43 to 49, supplemented with 0 (L0), 1 (L1), 2 (L2) or 4 (L4) g/hd/d of LF treatment (45% purity). Calves were weaned at 49 d of age. Body weight was measured at d 1, 14, 28, 42, 49 and 56 of age. Fecal scores were measured weekly. Milk replacer and calf starter intake was measured daily and calculated biweekly. Data were analyzed using a linear mixed model with fixed effects of LF inclusion, and random effects of source herd and nursery room. In the first two weeks of life, L4 tended to increase ADG and gain-to-feed ratio (G:F) compared with L1 and L2, but this effect was not maintained throughout the rest of the pre-weaning period or entire experiment. Average fecal score during the entire 56 d experiment was greater in L2 compared with L0, L1, and L4, although fecal scores of all treatment groups were generally low. Under the conditions of the present study, LF supplementation at the inclusion levels provided showed minimal effects on feed intake, growth rate or calf health.

Description of innate immunity and hematological changes in Holstein calves during the gradual weaning process

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Brazil and USA

Abstract

The weaning process negatively affects the hematological parameters and innate immune response of dairy calves, even when managed under an intensive milk program. Here we describe hematological and innate immunity changes in 47 Holstein calves aged 69-85 days subjected to a gradual weaning process. Blood samples were collected at six (D-6), four (D-4), and two (D-2) days before and on the weaning day (D0) for the phagocytosis assay and to measure the production of reactive oxygen species (ROS) after stimulation with *Staphylococcus aureus*, *Escherichia coli*, and *Mannheimia haemolytica*, in addition to total protein (TP), haptoglobin (Hp), and iron concentration. The highest mean neutrophil number was recorded at D-2. The absolute number of monocytes was initially high on D-6 and D-4 but declined as the calf progressed to weaning. The number of basophils decreased rapidly,

reaching a low value on D-4, and remained low for the remainder of the study period. The TP, Hp, and Fe concentrations decreased. Overall, PMN phagocytosis activity induced by *S. aureus* and *E. coli* decreased from D-6 to D-2, indicating persistence of the low phagocytosis rate for *S. aureus*. ROS production was constant for all bacterial stimulations from D-6 to D-2, followed by an increase on D0. Phagocytosis and ROS production indicate that the weaning process dampens the innate immune response relative to exposure to these common pathogenic bacteria in dairy calves. Phagocytosis and the corresponding indicators of intracellular killing activities (ROS production and myeloperoxidase index) represent the most accepted core mechanisms for the early elimination of pathogenic microorganisms in calves. Despite a slow gradual weaning management system, the study concluded that intensive milk production programs contribute to innate immune response suppression during weaning.

Large scale subclinical ketosis risk assessment in dairy herds using predicted milk acetone and β -hydroxybutyrate via MIR technology

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Abstract

Sub-clinical ketosis (SCK) significantly affects post-partum dairy cow performance and welfare. A total of 11,327,959 test-day (TD) records over two years on 1.76 million Holstein cow lactations and 2840 farms were processed to ascertain thresholds for milk acetone (mACE) and β -hydroxybutyrate (mBHB) as indicators of SCK on the basis of a significant milk yield loss at the TD. The set thresholds for mACE and mBHB were 0.10 mmol/L and 0.14 mmol/L, respectively. The prevalence of SCK in the population during the first 60 days in milk (DIM) was estimated based on herd size and milk yields, utilizing one or both of these metabolites surpassing their respective thresholds. Analyzing both mACE and mBHB together revealed a higher occurrence of SCK in small herds (fewer than 100 cows) and a lower occurrence in the two most productive milk categories. The prevalence had an inverse relationship with the daily milk yield at 60 DIM, indicating a surprisingly high frequency of low-productivity herds in the risk classes exceeding 30%. These results suggest that assessing SCK prevalence through the combined evaluation of mACE and mBHB is a more effective approach than using the milk fat to protein ratio, especially when considering different herd sizes and daily milk yield at 60 DIM.

Prediction of body weight of growing dairy buffaloes from body volume

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Abstract

Among body measurements, body weight (BW) is one of the most important within the buffalo production system, due to its association with economic characteristics. In previous research, we have shown that body volume (BV) is an effective predictor of BW in lactating adult water buffalo. As there are no equations to predict BW through BV for growing dairy buffaloes (young animals), we hypothesized that equations should be developed to meet this need. BW, body length (BL) and heart girth (HG) data were collected in 160 growing dairy buffaloes raised in commercial farms in southern Mexico, with body volume (BV) then estimated from BL and HG. The ratio between BV and BW was determined by linear, quadratic and allometric equations. The goodness-of-fit of the regression models was evaluated using the Akaike information criterion (AIC), the Bayesian information criterion (BIC), the coefficient of determination (R^2), the mean square error (MSE) and the root MSE (RMSE). After this, the k -folds cross-validation was performed to indicate a better fit. Our results showed that the growing dairy buffaloes presented a BW of 256.6 ± 96.82 kg and a BV of 155.3 ± 74.87 dm³. High and positive correlation were observed among all variables studied. All parameters (R^2 , MSE, RMSE, AIC and BIC) used to evaluate the regression equations showed that the quadratic regression model was more effective than the linear and allometric models for estimating BW using BV. The criteria for evaluating and validating models showed that the quadratic model presented a better predictive performance. Based on these findings, we conclude that body volume data to estimate body weight of growing dairy buffaloes were best fitted using the quadratic regression model.

Prediction of different physiological conditions of Riverine buffaloes (*Bubalus bubalis*) based on their vocal cues through machine learning algorithms and a conventional statistical model

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Abstract

To understand the requirements of animals their calls can be analysed. This potentially enables specific and more precise individual care under different emotional and physiological conditions. This study was conducted to identify three different conditions (estrus, delayed milking and isolation) of buffaloes based on vocalization patterns. A total of 600 acoustic samples of buffaloes for each condition were collected under different conditions consisting of 300 records for confirming and 300 for non-confirming of a particular condition. Important acoustic features like amplitude (P), total energy (P^2s), pitch (Hz), intensity (dB), formants (Hz),

number of pulses, number of periods, mean period (sec) and unvoiced frames (%) were extracted using the MFCC (mel frequency cepstrum coefficients) technique. Algorithms (model) were trained by partitioning the acoustic data into training and validation sets to develop predictive models. Three different ratios were assessed: 60%-40%, 70%-30% and 80%-20%. Decision tree models were optimized based on decision and average square error (probability) options and other parameters were set to default values of the software package to develop the best model. The performance of algorithms was evaluated on the parameter accuracy rate. Decision tree models predicted the physiological conditions estrus, isolation and delayed milking with an accuracy of 66.1, 84.3 and 71.3%, respectively, while the logistic regression model predicted with an accuracy rate of 59.5, 71.1 and 65.7%, respectively, and the artificial neural network (ANN) model predicted these three conditions with 77.7, 85.2 and 79.4% accuracy, respectively. The ANN model was found to be best on the basis of minimum misclassification rate (on 80%-20% portioning). However, decision tree algorithms also provided the additional information that intensity (maximum), amplitude (minimum) and formant (F1) are the most important features of vocal signals to identify physiological conditions like estrus, isolation and delayed milking respectively in dairy buffalo.

Functional impact of c.V15M variation in LH β gene on silent estrus behavior in river buffalo of Pakistan

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Pakistan

Abstract

Buffalo are shy breeders and poor fertility traits are a major hindrance in exploiting the production potential of the animal. This study hypothesizes that polymorphisms in LH β gene can affect the estrus behavior in buffaloes. A total of 100 animals were screened by calculating the heat index (threshold-50) and animals were categorized into two groups (Group1 >50, Group2 <50). Animals were subjected to blood sampling, genomic DNA isolation, specific primer based polymerization and sequencing of amplicons. A total of six genomic variations were identified in the gene. c.V15M was a non synonymous mutation found in line with the Hardy Weinberg Equilibrium and was significantly associated with the trait. Functional impact of the variation was determined by three-dimensional structure of the protein. Effect of c.V15M on the functionality of the gene was evident and hypothesis was supported so this can potentially be used as a marker for the future development of superior animal breed or regulating the expression of the gene to get the optimal estrus cyclicity in river buffalo of Pakistan.

Single-step Bayesian regression methods for genomic evaluation of milk yield of Murrah buffaloes

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Abstract

In this Research Communication we describe the application of single-step Bayesian regression (ssBR) models to predict milk yield of Murrah buffaloes. Milk production records of 2,026 cows in their first lactation were used. Using 270-day cumulative milk yield records as phenotype, genomic breeding values were predicted and their accuracies and dispersions were calculated by five methods: BayesA (ssBA), BayesB (ssBB), BayesC (ssBC); Bayesian Lasso (ssBL); and Bayesian ridge regression (ssBRR). For models based on mixture distributions (ssBB and ssBC), the proportions of markers having effect (π) were assumed as fixed, with respective values of 99% or 90%, or as unknown, where two approaches to estimate π were applied (ssBayesB π and ssBayesC π). The accuracy values found ranged from 0.550 (ssBB π) to 0.584 (ssBC π) and, the dispersion estimates ranged from 0.867 (ssBA) to 0.958 (ssBRR). The results indicated that Bayesian Lasso was the most suitable model for genetic evaluation of milk yield by buffaloes, considering accuracy and dispersion as criteria.

Assessment of flow cytometric tools to characterize milk somatic cells in water buffalo

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Abstract

The aim of this Research Communication was to develop new flow cytometric tools for the fine identification and characterization of milk somatic cells in water buffalo (*Bubalus bubalis*). Four multicolor panels of antibodies were designed to identify different subsets of live leukocytes and epithelial cells in bulk milk samples. Panel 1, including the CD18/CD172a/CD14/CD16 markers and live/dead vitality dye, allowed us to identify total lymphocytes, polymorphonuclear neutrophils (PMN) and monocyte/macrophage subsets. Panel 2 (CD18/CD4/CD8/ δ chain/CD335 and live/dead dye) allowed us to identify T helper (CD4⁺), T cytotoxic (CD8⁺), $\gamma\delta$ lymphocytes and NK cells. Panel 3 (CD18/CD79a/CD21 and live/dead dye) allowed us to identify total and CD21⁺ B lymphocytes. Finally, with Panel 4 (CD18/MHC-I/pan Cytokeratin and live/dead dye) the epithelial cells were distinguished from leukocytes. In conclusion, we propose a fine characterization of live milk somatic cell (live

differential cell count (LDCC)) in buffalo species. In the future the determination of LDCC could be used to identify new markers for detecting early inflammatory states of the mammary gland or for monitoring the technological properties of milks of different somatic cell composition.

Prevalence of intramammary infection pathogens in dairy herds of the Northern Apennine mountains, Italy

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Abstract

This Research Communication presents a cross-sectional study to compare the prevalence of contagious, environmental, opportunistic and other intramammary infection pathogens in mountain dairy herds. In the Italian Apennine mountains, areas where dairy farming is thriving are interspersed among areas where only a few dairy herds remain. The disappearance of some dairy farms relates to the reduction of agricultural and veterinary services in a process that can jeopardize dairy herd profitability. Sixteen herds were screened for intramammary infection (IMI) pathogens. Antimicrobial susceptibility testing of mastitis pathogens was performed, and data on antimicrobial use was collected from the herd treatment registry. The prevalence of contagious IMI pathogens was significantly higher in areas where dairy farming is reducing, whereas environmental and opportunistic infections were more abundant in herds in thriving areas where farmers had a more consistent relationship with veterinarians. Antimicrobial resistance levels were low throughout all areas and did not relate to antimicrobial use, although it was significantly higher in areas where dairy herds were thriving.

Somatic cell count and presence of microbial pathogens in milk of goats in Slovakia

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Abstract

The objectives of the study were to determine somatic cell count (SCC) and evaluate the presence of pathogens (IMI – intramammary infection) in late lactation (LL), followed by the colostrum (CL), and the beginning of the next lactation (BL), as well as to assess the possible transmission of IMI from lactation to lactation. The study was performed on a dairy farm in northern Slovakia. A total of 489 half udder milk samples (242, 80 and 167 in LL, CL and BL, respectively) were collected. Pathogens were identified using MALDI-TOF MS and PathoProof

(the latter only in LL). SCC was determined only in LL and BL. Samples were divided according to SCC in four groups from lowest (SCC1 < 500×10³ cells mL⁻¹) to highest (SCC4 ≥ 2000×10³ cells mL⁻¹). SCC was higher in LL than in BL. The prevalence of pathogens identified using MALDI-TOF MS was 16.5, 38.8 and 12.6% in LL, CL and BL, respectively. Non-*aureus* staphylococci and mammaliicocci (NASM) were the most common isolated pathogens in goat milk and colostrum. *Staphylococcus (S.) caprae* and *S. epidermidis* species tended to cause persistent IMI in the next lactation. The identification of pathogens using PathoProof was higher than with MALDI-TOF MS. Of all the pathogens (n=262) identified using PathoProof, the most common were *Staphylococcus* spp. (86.7%) of which 65.8% exhibited the β -lactamase gene. Additionally, *Escherichia coli* (4.2%), *S. aureus* (2.7%), *Enterococcus* spp. (2.3%), *Streptococcus uberis* (1.9%), *Mycoplasma* spp., *Protetheca* spp. (0.8% each), *Arconabacterium pyogenes/Peptoniphilus indolicus* and yeast (0.4% each) were also detected using PathoProof. Better identification of pathogen presence in samples with high SCC could contribute to the discussion about SCC as an indicator of subclinical mastitis in goats.

An overview of dairy production in selected African and Asian countries: challenges and opportunities for sustainability

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Abstract

There is increasing demand for milk and dairy products and an associated increase in milk production in Asia and Africa, making them important emerging dairy markets for the future. To the best of our knowledge, there has been little effort to comprehensively review literature on dairy production in these regions despite the changing situation, growth and challenges that require sustainable solutions. Thus, the objective of this review was to present an overview and evaluation of the dairy industry in selected countries in Eastern Africa and Asia using recent literature. The countries were selected based on the potential of dairy production in the respective regions. It focused on two types of countries: those in East Africa, which are at different stages of intensification regarding the global production issue, and those in Asia, which have large dairy industries. Based on this, Ethiopia, Kenya and Tanzania were selected from eastern Africa, while India, Pakistan and China were selected from Asia. The review revealed that dairy production in Eastern Africa predominantly relies on small-scale production systems. Factors such as inadequate feed, disease prevalence, poor access to breeding and formal/organized market pose significant challenges to this region's dairy industry. However, recent efforts have focused on improving productivity through technology adoption, livestock breeding programmes and market development initiatives. In contrast, Asia showcases a diverse range of dairy production systems. Countries like India are known

for their large-scale dairy operations involving both indigenous and exotic dairy breeds. Additionally, cooperative models and public-private partnerships have contributed to the growth of the dairy sector in Asian countries. Nevertheless, challenges such as land/feed availability, environmental concern, and market competitiveness remain areas for improvement. While Eastern Africa aims to enhance small-scale farming systems through partly upgrading scale of production, innovation and market access, Asia seeks to bridge the gaps in productivity and sustainability.

Effect of bovine lactoferrin and lactoferrin-derived peptides on planktonic cells and abiotic surface biofilms of *Salmonella enterica*

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Mexico and the Netherlands

Abstract

Salmonella enterica is a Gram-negative bacterium responsible approximately for 155,000 deaths annually. *S. enterica* is one of the most important foodborne pathogens, affecting mainly people in developed countries. The human immune system produces antibacterial peptides and proteins like lactoferrin (LF). This work addresses the hypothesis that bovine lactoferrin (bLF) and its derivative peptides bLactoferricin17-30, bD-Lactoferricin17-30, bLactoferrampin265-284, bD-Lactoferrampin265-284 and bLF-chimera have antimicrobial activity on planktonic cells and pre-formed biofilms of *S. enterica*. Planktonic *Salmonella enterica* ATCC 14028 were treated with bLF and bLF-peptides for two hours, and bacterial viability was determined by counting colony-forming units/ml. In addition, *S. enterica* biofilms were pre-formed or established on an abiotic surface, and viability or disruption was assessed in the presence of bLF and bLF-peptides by counting colony-forming units/ml or using the live/dead viability kit. We observed that bLF and bLF-peptides were bactericidal against planktonic *S. enterica*, killing more than 80% of cultures after two hours of treatment. The bactericidal effect was concentration and time-dependent. In addition, bLF, bLFampin165-284, and bLF-chimera showed an anti-biofilm effect against *Salmonella* biofilms pre-formed during 8 and 12 hours on the abiotic surface, disorganizing more than 50% of the biofilms after 4 or 6 hours of treatment. We conclude that bLF and its peptides show antimicrobial activity against planktonic cells and pre-formed biofilms of *S. enterica* on abiotic surfaces and could potentially be a therapeutic solution to combat *Salmonella* infections.

Microbiological aspects in whey powder production: what is the relevance of enterotoxigenic *Staphylococcus aureus*?

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Abstract

Whey, a greenish-yellow liquid resulting from curd separation in cheese manufacturing, was historically considered economically insignificant in the dairy industry and often discarded into the environment without proper oversight. However, recognizing its high nutritional value, whey has become a valuable ingredient in the food industry. Unprocessed whey (raw material) is highly susceptible to contamination, as it can serve as a substrate for the multiplication of a range of microorganisms, including spoilage, spore forming, pathogenic and toxin producing bacteria, particularly if stored at inappropriate temperatures. *Staphylococcus aureus* is one of these potential pathogenic bacteria often associated to dairy, that can also persist in the environment through biofilm formation and, once reaching the food matrix, can grow and produce enterotoxins. During the processing of whey powder production, there are points where *S. aureus* might find its way into the final product. Here we demonstrate critical contamination steps, and we highlight the need for more research to assess the microbiological integrity of whey powder, especially in Brazil, where its production has been growing in recent years. Considering the increasing use of whey powder as an ingredient for various formulations, continuous surveillance for the presence of spoilage microbiota and potentially pathogens, including *S. aureus* and associated enterotoxins is indispensable to prevent food poisoning outbreaks.

Innovative thistle-curdled cheeses from the Mediterranean area: nutritional evaluation of some relevant compounds

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Abstract

Since ancient times, thistles have been used as clotting agents in the production of traditional cheeses, particularly in the Mediterranean area. In recent years, their use in cheesemaking has increased to satisfy the growing requests from vegetarian consumers. In this research paper, four different cheeses, typical of the Mediterranean area, were evaluated from a nutritional point of view: *Caciofiore* (from Italy) and *Torta del Casar* (from Spain), both typically produced using vegetable rennet, and *Queso de Murcia al vino* (from Spain) and *Feta*

(from Greece), traditionally produced using animal rennet. All the cheeses were manufactured according to their traditional cheesemaking procedures and used as controls. Experimental cheeses were produced using aqueous extracts obtained from flowers of either spontaneous or cultivated thistles indigenous to the Mediterranean area (respectively *Onopordum tauricum* for Caciofiore, and *Cynara humilis* for Torta del Casar, Queso de Murcia al vino, and Feta). All cheeses were characterized for fat-soluble and mineral compounds to assess their nutritional adequacy according to the recommended daily intake of each evaluated nutrient. All the cheeses were found to be a good source of vitamin A, calcium and phosphorus, with an optimal Ca/P molar ratio, except for Feta. By consuming the recommended serving (50 g) of the studied cheeses, the salt and cholesterol intake is, on average, 16.4% and 15.9%, respectively of recommended intake. The use of aqueous thistle extracts in cheesemaking appears to have no effect on the nutritional quality of the studied cheeses.

Fingerprinting Gir ghee (butter oil)

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India

Abstract

This research investigates the ghee/butter oil/anhydrous milk fat made from the Gir breed, examining its chemical and physical features. The study aims to understand the potential impact of consuming Gir ghee on blood cholesterol levels using the Wistar rat model. Ghee's distinctive flavour, processing techniques and breed of origin significantly influence its acceptance, which has gained widespread popularity due to its short-chain fatty acid composition, improved digestion and putative anti-cancer properties. Ghee is also a significant carrier of vital fatty acids and fat-soluble vitamins. Despite its health benefits, controversies surrounding its consumption have negatively impacted consumers' mindset. The study aims to provide a comprehensive understanding of the composition and properties of Gir ghee and its potential impact on cholesterol levels. The findings could have implications for the production and consumption of Gir ghee and contribute to existing knowledge on the relationship between ghee consumption and cholesterol.

Probiotic low-fat ice cream from goat milk: Characterization and resilience to simulated gastrointestinal conditions

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Abstract

We aimed to develop a new ice cream made from goat milk inoculated with the probiotic bacteria *Limosilactobacillus fermentum* CABA16. The physicochemical characteristics, meltdown behavior and sensory properties of ice cream produced with and without the probiotic bacteria were analysed. The ice cream with added *L. fermentum* was further evaluated for probiotic viability during frozen storage, and simulated gastrointestinal conditions. Results showed that the addition of *L. fermentum* CABA16 decreased the pH to 6.25 ($P < 0.05$), but had no effect on physicochemical properties such as overrun and melting behavior of ice cream samples. The viable probiotic count was 6.71 log CFU/g with survival rate of 90 % which was registered after 120 days of frozen storage. Considering the probiotic cell viability during gastrointestinal conditions, exposure to bile and pancreatin for six hours resulted in the decline of 3.6 log CFU/g cycles in ice cream samples previously stored at -18 °C for 120 days. Overall, the goat milk ice cream inoculated with *L. fermentum* received good sensory scores and satisfactory probiotic viability (6.7-7 log CFU/g) was maintained throughout the 120 days of frozen storage..