Journal of Dairy Research Vol 88 (3) August 2021

COLLECTED ABSTRACTS

Editorial: Strategizing food: stick, carrot but not nearly enough dairy?

Chris Knight

UK

The editorial will be available online at www.journalofdairyresearch.org/editorials.html

AGPAT3 gene polymorphisms are associated with milk production traits in Chinese Holstein cows Xiaomei Sun, Yan Liang, Qisong Gao, Jiahe Guo, Cheng Tang, Kerong Shi, Zhangping Yang and Yongjiang Mao

China

Abstract

The current study reports the identification of previously undiscovered single nucleotide polymorphisms (SNPs) in the bovine *AGPAT3* gene and further investigates their associations with milk production traits. Our results demonstrate that the major allele C of the SNP g.12264 C>T is positively correlated with test-day milk yield, protein percentage and 305-day milk yield. Importantly, *in silico* analysis showed that the C/T transition at this locus gives rise to two new transcription factor binding sites (TFBS), E2F1 and Nkx3-2. Polymorphism g.18658 G>A was the only SNP associated with milk urea nitrogen (MUN) with the G allele related to an increase in milk urea nitrogen as well as fat percentage. The GG genotype of SNP g.28731 A>G was associated with the highest fat and protein percentage and lowest 305-day milk yield and somatic cell score (SCS). The association between *AGPAT3* locus and milk production traits could be utilized in marker-assisted selection for the genetic improvement of milk production traits and, probably in conjunction with other traits, for selection to improve fitness of dairy cattle.

Comparison of metabolic, oxidative and inflammatory status of Simmental x Holstein crossbred with parental breeds during the peripartal and early lactation periods

Giovanna De Matteis, Maria Carmela Scatà, Gennaro Catillo, Francesco Grandoni, Emanuela Rossi, David Meo Zilio, Alessandra Crisà, Vincenzo Lopreiato, Erminio Trevisi and Vittoria Lucia Barile **Italy**

Abstract

The aim of the research reported in this paper was to evaluate plasma concentrations of energy, oxidative and inflammatory biomarkers of Simmental (sire) x Holstein (dam) crossbred cows, in comparison with the two parental breeds during the peripartal and early lactation periods and to estimate the effects of heterosis for these traits. Thirty-three animals, managed under the same

conditions, 8 Simmental (SI), 9 Holstein (HO) and 16 crossbred (CR) cows were enrolled in this study. Glucose, non-esterified fatty acids (NEFA), β-hydroxybutyrate (BHB), total bilirubin, aspartate aminotransferase (AST), alanine aminotransferase (ALT), alkaline phosphatase (ALP), creatine kinase (CK), total protein, albumin, creatinine and urea were determined in blood sampled at six different time points (30±3 and 15±3 days before the expected calving date, at calving and 15, 30 and 60 days after calving). Furthermore, derived reactive oxygen metabolites (d-ROMs), biological antioxidant potential (BAP), interleukin-6 (IL-6), haptoglobin (Hp) and serum amyloid A protein (SAA) were determined to evaluate inflammatory and oxidative status. Results showed that the CR group had significantly lower average values of glucose and NEFA when compared to HO group; significantly lower values of urea than SI group and significantly higher values of creatinine than HO. Furthermore, CR cows showed the lowest average value of d-ROMs with respect to SI and HO parental breeds. Finally, the average value of haptoglobin was significantly lower in CR and HO groups, when compared to SI group. As for the heterosis we found the highest (positive) percentage for CK (98%) and BAP (47%) and the lowest (negative) percentage for OSi (-75%) and d-ROMs (-39%). A negative percentage was also found for the glucose (-11%) and NEFA (-20%) toward the Simmental parental breed. Our results suggest a different response among the three genetic groups during the peripartal and early lactation periods. In particular, CR and SI cows seem more adaptable regarding energy metabolism and oxidative status. Heterosis led to a positive effect on those parameters in Simmental (sire) x Holstein (dam) crossbred cows F1 population (50% Simmental and 50% Holstein).

Untargeted lipidomics of ovine milk to analyse the influence of different diet regimens

Cristina Manis, Margherita Addis, Maria Sitzia, Paola Scano, Viviana Garau, Andrea Cabiddu, Marco Caredda, Antonio Pirisi, Antonio Pulina, Pierpaolo Roggero and Pierluigi Caboni **Italy**

Abstract

In this work we report a lipidomics approach to study the effects of two diet systems on the composition of ovine milk. Milk from two groups of Sarda sheep grazing on 40% (P40) and 60% (P60) of pasture were analyzed by a UHPLC-QTOF-MS analytical platform and data submitted to multivariate statistical analysis. Pairwise partial least square discriminant analysis of the lipid profile of the data was carried out to classify samples and to find discriminant lipids. The two dietary groups were characterized by differences in triacylglycerols, phosphocholines and phosphatidylethanolamines levels. Discriminants of the P40 group were TG and PC containing in their backbone saturated medium chain FA thus suggesting greater de novo fatty synthesis in the mammary gland. On the other hand, the P60 group was characterized by TG and PC formed by unsaturated long chain FA originating from the diet or from lipid mobilization.

Determination of factors affecting milk yield, composition and udder morphometry of Hair and cross-bred dairy goats in a semi-intensive system

Hakan Erduran and Birol Dag

Turkey

Abstract

In this Research Communication we report milk yield, milk composition and udder morphometry of Hair, Alpine \times Hair F_1 (AHF₁), and Saanen \times Hair F_1 (SHF₁) cross-bred goat genotypes managed in a semi-intensive system. The SHF₁ genotype had sighificantly higher lactation milk yield, fat yield, protein yield, and electrical conductivity than other genotypes, whilst AHF₁ was intermediate. The milk fat, protein, lactose, solids-non-fat and total solids contents as well as pH and density of the Hair goat milk were significantly higher than the corresponding values of the cross-bred genotypes. The highest correlation amongst udder characteristics and production was between lactation milk yield and udder volume (P < 0.01; r = from 0.63 to 0.77). The results of this study suggest that crossbreeding can have a positive effect on the milk production characteristics of local goats, thereby reducing the pressure on the ecosystem, and suggest that udder measurements, especially volume, can be a helpful tool for estimating milk yield.

Motivations and attitudes of Brazilian dairy farmers regarding the use of automated behaviour recording and analysis systems

Aline C. Vieira, Vivian Fischer, Maria Eugênia A. Canozzi, Lisiane S. Garcia and Jessica Tatiana Morales-Piñeyrúa

Brazil and Uruguay

Abstract

In this Research Communication we investigate the motivations of Brazilian dairy farmers to adopt automated behaviour recording and analysis systems (ABRS) and their attitudes towards the alerts that are issued. Thirty-eight farmers participated in the study distributed into two groups, ABRS users (USERS, n=16) and non-users (NON-USERS, n=22). In the USERS group 16 farmers accepted being interviewed, answering a semi-structured interview conducted by telephone, and the answers were transcribed and codified. In the NON-USERS group, 22 farmers answered an online questionnaire. Descriptive analysis was applied to coded answers. Most farmers were young individuals under 40 years of age, with undergraduate or graduate degrees and having recently started their productive activities, after a family succession process. Herd size varied with an overall average of approximately 100 cows. Oestrus detection and cow's health monitoring were the main reasons given to invest in this technology, and cost was the most important factor that prevented farmers from purchasing ABRS. All farmers in USERS affirmed that they observed the target cows after receiving a health or an oestrus alert. Farmers believed that they were able to intervene in the evolution of the animals' health status, as the alerts gave a window of three to four days before the onset of clinical signs of diseases, anticipating the start of the treatment. The alerts issued by the monitoring systems helped farmers to reduce the number of cows to be observed and to identify pre-clinically sick and oestrous animals more easily. Difficulties in illness detection and lack of definite protocols impaired the decision making process and early treatment, albeit farmers believed ABRS improved the farm's routine and reproductive rates.

Classification of environmental factors potentially motivating for dairy cows to access shade

Matheus Deniz, Karolini Tenffen de Sousa, Isabelle Cordova Gomes, Marcos Martinez do Vale and João Ricardo Dittrich

Brazil

Abstract

The aim of this Research Communication was to apply the data mining technique to classify which environmental factors have the potential to motivate dairy cows to access natural shade. We defined two different areas at the silvopastoral system: shaded and sunny. Environmental factors and the frequency that dairy cows used each area were measured during four days, for 8h each day. The shaded areas were the most used by dairy cows and presented the lowest mean values of all environmental factors. Solar radiation was the environmental factors with most potential to classify the dairy cow's decision to access shaded areas. Data mining is a machine learning technique with great potential to characterize the influence of the thermal environment in the cows' decision at the pasture.

Oxytocin and cortisol release during suckling, hand-milking and machine milking in camels

Marwa Brahmi, Moufida Atigui, Ihmen Hammadi, Jacques Portanguen, Mohamed Hammadi and Pierre-Guy Marnet

Tunisia and France

Abstract

This research paper addresses the hypothesis that oxytocin (OT) could be released during suckling and during milking with and without the presence of a calf and that this release could be regulated by maternal behaviour. Plasma concentration patterns of OT and cortisol (CORT) were measured in six Tunisian dromedary camels during 2 suckling episodes, 2 manual milking episodes with calves beside the mother and 2 machine milking episodes without calves present. Various patterns of OT release were observed between each camel including specific two peak release patterns. Higher plasma OT concentrations were found during the suckling and hand-milking episodes with simultaneous suckling of calves, than during the machine milking episodes without calves. Exclusive mechanical milking episodes also evoked significant mean OT release, although greatly reduced compared to suckling and hand milking. The low basal levels and classical CORT release patterns suggested non-stressful management practices were used and there were very limited differences in udder stimulation between managements. The OT release induced by exclusive suckling and suckling together with hand-milking gives a reference point for what a good milk ejection stimulation is in camels. The important and specific reduction of OT release during machine milking without the calf present could be a physiological consequence of the maternal behaviour (selectivity for the own young) and to a lesser extent explained by a lower stimulation by machine milking.

Going further post-RNA-seq: *In silico* functional analyses revealing candidate genes and regulatory elements related to mastitis in dairy cattle

Hyago Passe Pereira, Lucas Lima Verardo, Mayara Morena Del Cambre Amaral Weller, Ana Paula Sbardella, Danísio Prado Munari, Raquel Morais de Paiva Daibert, Wanessa Araújo Carvalho, Marco Antonio Machado and Marta Fonseca Martins

Brazil

Abstract

This study aimed to obtain a better understanding of the regulatory genes and molecules involved in the development of mastitis. For this purpose, the transcription factors (TF) and MicroRNAs (miRNA) related to differentially expressed genes previously found in extracorporeal udders infected with *Streptococcus agalactiae* were investigated. The Gene-TF network highlighted *LOC515333, SAA3, CD14, NFKBIA, APOC2* and *LOC100335608* and genes that encode the most representative transcription factors *STAT3, PPARG, EGR1* and *NFKB1* for infected udders. In addition, it was possible to highlight, through the analysis of the gene-miRNA network, genes that could be post-transcriptionally regulated by miRNAs, such as the relationship between the *CCL5* gene and the miRNA bta-miR-363. Overall, our data demonstrated genes and regulatory elements (TF and miRNA) that can play an important role in mastitis resistance. The results provide new insights into the first functional pathways and the network of genes that orchestrate the innate immune responses to infection by *Streptococcus agalactiae*. Our results will increase the general knowledge about the gene networks, transcription factors and miRNAs involved in fighting intramammary infection and maintaining tissue during infection and thus enable a better understanding of the pathophysiology of mastitis.

Intracellular *Staphylococcus aureus* Inhibits Autophagy of Bovine Mammary Epithelial Cells through Activating $p38\alpha$

Run Wang, Wen Zhang, Lumei Wang, Na Geng, Xiaozhou Wang, Meihua Zhang, Jianzhu Liu, Yongxia Liu and Bo Han

China

Abstract

Staphylococcus aureus is a common pathogen of bovine mastitis which can induce autophagy and inhibit autophagy flux, resulting in intracellular survival and persistent infection. The aim of the current study was to investigate the role of p38α in the autophagy induced by intracellular *S. aureus* in bovine mammary epithelial cells. An intracellular infection model of MAC-T cells was constructed, and activation of p38α was examined after *S. aureus* invasion. Through activating/inhibiting p38α by anisomycin/SB203580, the autophagosomes, LC3 and p62 level were analyzed by immunofluorescence and western blot. To further study the detailed mechanism of p38α, phosphorylation of ULK1ser757 was also detected. The results showed that intracellular *S. aureus* activated p38α, and the activation developed in a time-dependent manner. Inhibition of p38α promoted intracellular *S. aureus*-induced autophagy flow, up-regulated the ratio of LC3 II/I, reduced the level of p62 and inhibited the phosphorylation of ULK1ser757, whereas the above results were reversed after activation of p38α. The current study indicated that intracellular *S. aureus* can inhibit autophagy flow by activating p38α in bovine mammary epithelial cells.

Identification of bovine mastitis pathogens using MALDI-TOF mass spectrometry in Brazil

Thais Cristina de Assis Oliveira, Maria Aparecida Vasconcelos Paiva Brito, Marcia GiambiagideMarval, Nívea Maria Vicentini and Carla Christine Lange

Brazil

Abstract

In this Research Communication we evaluate the use of matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) to identify 380 bacteria isolated from cases of bovine mastitis in Brazil. MALDI-TOF MS identifications were compared to previous identifications by biochemical tests and 16S rRNA sequencing. MALDI-TOF MS achieved a typeability of 95.5%. The accuracy of MALDI-TOF MS for the identification of *Staphylococcus* isolates was 93.2%. The agreement between MALDI-TOF MS and biochemical identification of *Streptococcus agalactiae* was 96%, however, the agreement between these techniques for identifying other catalase-negative, Gram-positive cocci was lower. Agreement in identifying Gram-negative bacteria at the genus level was 90.5%. Our findings corroborate that MALDI-TOF MS is an accurate, rapid and simple technique for identifying bovine mastitis pathogens. The availability of this methodology in some research institutions would represent a significant step toward increasing the diagnosis and epidemiological studies of bovine mastitis and other animal infectious diseases in Brazil.

Extensive countrywide field investigation of somatic cell counts and total bacterial counts in bulk tank raw milk in goat herds in Greece

Daphne T. Lianou, Charalambia K. Michael, Natalia G.C. Vasileiou, Efthimia Petinaki, Peter J. Cripps, Katerina Tsilipounidaki, Angeliki I. Katsafadou, Antonis P. Politis, Nikos G. Kordalis, Katerina S. Ioannidi, Dimitris A. Gougoulis, Constantina Trikalinou, Denise C. Orfanou, Ilektra A. Fragkou, Dimitra V. Liagka, Athina Tzora, Marzia Albenzio, Vasia S. Mavrogianni, Mariangela C. Caroprese and George C. Fthenakis

Greece, UK and Italy

Abstract

Dairy goat farming is an important sector of the agricultural industry in Greece, with an annual total milk production exceeding 450,000l and accounting for over 25% of all goat milk produced in the European Union; this milk is used mainly for cheese production. Despite the importance of goat milk for the agricultural sector in Greece, no systematic countrywide investigations in the bulk-tank milk of goats in Greece have been reported. Objectives were to investigate somatic cell counts (SCC) and total bacterial counts (TBC) in raw bulk-tank milk of goat herds in Greece, study factors influencing SCC and TBC therein and evaluate their possible associations with milk content. Throughout Greece, 119 dairy goat herds were visited for milk sampling for somatic cell counting, microbiological examination and composition measurement. Geometric mean SCC and TBC were 0.838×10⁶ cells mL⁻¹ and 581×10³ cfu mL⁻¹, respectively. Multivariable analyses revealed annual frequency of checkups of milking system and total milk quantity per goat (among 53 variables) to be significant for increased TBC. Negative correlation of SCC with total protein was found; mean total protein content in the bulk-tank milk in herds with SCC >0.75×10⁶ cells mL⁻¹ was 5.1% lower and in herds with SCC >1.5×10⁶ cells mL⁻¹, it was 7.8% lower.

Occurrence and etiology of subclinical mastitis in water buffalo in Bangladesh

Shuvo Singha, Carl David Ericsson, Salma Chowdhury, Sanjib Chandra Nath, Ovirup Bhushan Paul, Md. Ahasanul Hoque, Sofia Boqvist, Ylva Persson and Md. Mizanur Rahman

Italy, Bangladesh and Sweden

Abstract

Subclinical mastitis (SCM) in water buffalo is a production disease associated with decreased milk yield and impaired milk quality and safety. Water buffalo is an important livestock species in Bangladesh, but information about the occurrence and etiology of SCM in this species is scarce. A cross-sectional study was conducted as part of the Udder Health Bangladesh Programme to i) determine the occurrence of SCM and bulk milk somatic cell count (SCC) in water buffalo in Bangladesh, ii) identify pathogens causing SCM and iii) evaluate penicillin resistance in isolated staphylococci strains. Sixteen buffalo farms in the Bagerhat and Noakhali regions of Bangladesh were selected for study and a bulk milk sample was collected from each farm. In addition, 299 udder quarter milk samples were collected from 76 animals. The bulk milk samples were assessed by direct SCC and the quarter milk samples by California mastitis test (CMT). The occurrence of SCM calculated at quarter and animal level was 42.5% and 81.6%, respectively. Milk samples from 108 CMT-positive quarters in 48 animals and 38 randomly selected CMT-negative quarters in 24 animals were investigated using bacteriological culture. Estimated mean bulk milk SCC was 195,000 cells/mL milk (range 47,000-587,000 cells/mL milk). On culture, estimated quarter-level intramammary infection (IMI) was 40.4%. The identity of isolated bacteria was confirmed by MALDI-TOF mass spectrometry. Non-aureus staphylococci (NAS) were the most common pathogens (24.7%) and, among 36 NAS tested, 36.1% were resistant to penicillin. Thus there was high occurrence of SCM on the study farms, with relatively high penicillin resistance in NAS. Further studies are needed to identify underlying risk factors and develop an udder health control strategy for water buffalo in Bangladesh.

Variations in the levels of acute phase proteins and lactoferrin in serum and milk during bovine subclinical mastitis

Aarsha Raj, Vinodkumar Kulangara, Tresamol P Vareed, Deepa P Melepat, Latha Chattothayil and Sunanda Chullipparambil

India

Abstract

Variations in the levels of acute phase proteins and lactoferrin in serum and milk for diagnosis of subclinical mastitis in dairy cows are described in this research paper. Milking animals from two organized dairy farms in Kerala, India, were screened by California Mastitis Test (CMT), Electrical Conductivity test (EC) and Somatic Cell Count (SCC) test to identify animals affected with sub clinical mastitis (SCM). The concentrations of acute phase proteins (APP) Haptoglobin (Hp), C- reactive protein (CRP), Albumin, Lactoferrin (Lf) and α - 1 acid glycoprotein (AGP) in milk and Hp, Albumin, Serum Amyloid A (SAA) and CRP in the serum of 40 normal cows and 40 cows affected with sub clinical mastitis were assessed. Solid phase ELISA was employed for assessment of all parameters except the albumin levels, for which spectrophotometry was used. The values of Hp in milk; and SAA, AGP and Lf in serum, were significantly elevated in the group with sub clinical mastitis. Such variations were found to be independent of the specific bacterial organism causing the disease. These results show that significant variations exist in the levels of acute phase proteins Hp, AGP and Lf in milk, and SAA in serum of animals affected with subclinical bovine mastitis that are not affected by specific bacterial etiology.

Milk metabolites, proteins and oxidative stress markers in dairy cows suffering from Staphylococcus aureus subclinical mastitis with or without spontaneous cure

Nooroldin Tabatabaee, Mohammad Heidarpour and Babak Khoramian Iran

Abstract

Our objective was to evaluate relationships between milk components (acute phase proteins, enzymes, metabolic parameters and oxidative indices) and the spontaneous cure outcome of *Staphylococcus aureus* subclinical mastitis in dairy cows. The values of haptoglobin, serum amyloid A (SAA), malondialdehyde (MDA), total antioxidant capacity, milk urea nitrogen (MUN), lactate dehydrogenase (LDH), alkaline phosphatase (ALP), electrolytes (Cl and K), total protein, albumin, α -lactalbumin, β -lactoglobulin, and immunoglobulin were measured in milk samples of *S. aureus* subclinical mastitis cows with spontaneous cure (n= 23), *S. aureus* subclinical mastitis cows without spontaneous cure (n= 29) and healthy cows (n=23). The comparison of measured parameters revealed that subclinical mastitis cows with spontaneous cure had lower ALP and haptoglobin concentrations both at diagnosis and after cure (p<0.05). In contrast, total antioxidant capacity and MDA concentration in subclinical mastitis cows without spontaneous cure significantly increased with time (p<0.05). We can suggest that elevated haptoglobin concentration and higher ALP activity indicative of enhanced oxidative stress could potentially serve as early diagnostic indicators of chronic disease and the persistence of *S. aureus* subclinical mastitis in dairy cows.

The relationship of bovine milk somatic cell count to neutrophil level in samples of cow's milk Zlatina Chengolova, Yavor Ivanov and Galina Grigorova Bulgaria

Abstract

This research communication describes the application of a fluorescent automatic cell counter Lactoscan SCC for simultaneous determination of somatic cell count and neutrophils in bovine milk. The obtained results were compared with results obtained by a flow cytometer and a light microscope. The Pearson correlations between the methods were calculated. A comparison between the main characteristics of the three kinds of analysis was made - the assay duration and the intra-assay precision. A relation between the SCC and neutrophil cells was observed in 55 milk samples. The obtained results confirm that the simultaneous determination of SCC and neutrophil analysis are necessary and support the early diagnosis of mastitis, the timely treatment of the animal and the avoidance of major economic losses.

Neutrophil and CD4⁺ milk cell count related to natural incidence of mastitis in Jersey cattle Zlatina Chengolova, Milka Atanasova and Tzonka Godjevargova Bulgaria

Abstract

This Research Communication describes the relation between somatic cells and microbial content in milk from Jersey cattle. Milk samples were classified in groups: healthy, dirty and mastitic (from *Staphylococcus spp., Escherichia coli, Coliforms*). The somatic cells in each of those groups were

analysed by two methods – flow cytometric and automatic fluorescent cell counting. Those methods were compared. Total somatic cell count (SCC), neutrophil count, and lymphocytes with cluster of differentiation 4 (CD4 $^+$ cells) were determined. There was a positive relationship between microbes and somatic cells. It was noticed that the neutrophil count was generally increased together with SCC, whilst the CD4 $^+$ cell count was higher in healthy milk samples (about 8%) compared to mastitic ones (about 3%). Lower number of CD4 $^+$ cells (from 1 to 4%) was determined in samples positive for *Staphylococcus spp.* but with lower SCC (from 2.7 to 4.0 × 10 5 cells/ml). Also, the number of CD4 $^+$ cells in *Staphylococcus spp.*-positive samples increased (to 4.8%) together with higher SCC, somehting that was not observed in the other mastitic samples. Knowledge of those relations could be useful for veterinary medical tests in the initial phase of inflammation.

Risk factors for poor colostrum quality and failure of passive transfer in Scottish dairy calves Alexandra Haggerty, Colin Mason, Kathryn Ellis and Katharine Denholm UK

Abstract

Failure of passive transfer (FPT) has health, welfare and economic implications for calves. Immunoglobulin G (IgG) concentration of 370 dairy calf serum samples from 38 Scottish dairy farms was measured via radial immunodiffusion (RID) to determine FPT prevalence. IgG concentration, total bacteria count (TBC) and total coliform count (TCC) of 252 colostrum samples were also measured. A questionnaire was completed at farm enrolment to investigate risk factors for FPT and poor colostrum quality at farm-level. Multivariable mixed effect logistic and linear regressions were carried out to determine significant risk factors for FPT and colostrum quality. Prevalence of FPT at calf level was determined to be 14.05 %. Of 252 colostrum samples, 111 (44.05%) failed to meet Brix thresholds for colostrum quality. Of these 28 and 38 samples also exceeded TBC and TCC thresholds, respectively. Increased time between parturition and colostrum harvesting was numerically (nonsignificantly) associated with a colostrum Brix result <22%, and increased time spent in a bucket prior to feeding or storing was significantly associated with high TBC (≥100,000cfu/ml and also ≥10,000cfu/ml). High TBC values in colostrum were significantly associated with lower serum IgG concentrations. This study highlights associations between colostrum quality and FPT in dairy calves as well as potential risk factors for reduced colostrum quality; recommending some simple steps producers can take to maximise colostrum quality on farm.

Physical properties of UHT light cream: Impact of the high-pressure homogenization and addition of hydrocolloids

Virgínia Nardy Paiva, Lucas de Souza Soares, Rodrigo Stephani, Álvaro Augusto Pereira Silva, Antônio Fernandes de Carvalho, Isis Rodrigues Toledo Renhe and Ítalo Tuler Perrone

Brazil

Abstract

The beneficial effects of a healthy diet on the quality of life have prompted the food industry to develop low-fat variants, but fat content directly affects the physicochemical and sensory properties of food products. The utilization of high-pressure homogenization (HP) and incorporation of

hydrocolloids have been suggested as strategies to improve the physical stability and rheological properties of light cream. Thus, this study aims to analyze the associated effect of high-pressure homogenization (80 MPa) and three different hydrocolloids: microcrystalline cellulose, locust bean gum and xanthan gum, on emulsion stability and rheological properties of ultra-high-temperature (UHT) light cream (ULC) with a 15% w/w fat content. The stability of ULC was determined by the ζ potential of oil droplets and emulsion stability percentage. Rheological characterization was based on flow behavior tests and dynamic oscillatory measurements, which were carried out in a rheometer. Results showed that the high-pressure homogenization process did not influence the emulsion stability of the treatments. Moreover, the hydrocolloids added to systems present weak interactions with milk proteins since all ULC showed macroscopical phase separation. The samples presented the same rheological behavior and were classified as pseudoplastic fluids (n < 1). ULC treated at 80 MPa was significantly (p \leq 0.05) more consistent than the treatments at 20 MPa. All ULC showed a predominant elastic behavior (G' > G"), and a remarkable increase in both G' and G" at 80 MPa. The results presented in this study highlight the potential of HP for altering some rheological characteristics of UHT light cream, for example, to increase its consistency. These results are important for the dairy industry and ingredient suppliers, in the standardization of UHT light cream and/or to develop low-fat products.

Effects of microbial transglutaminase levels on donkey cheese production

Angela Gabriella D'Alessandro, Giovanni Martemucci and Michele Faccia **Italy**

Abstract

Microbial transglutaminase (MTGase) is an enzyme widely used in the dairy sector to improve the functional properties of protein-based products via the formation of a network between protein molecules. The aim of this study involving cheese from the milk of donkeys was to evaluate the effects of treatment with MTGase at the concentrations of 0 (control), 5, 8 and 10 Ug⁻¹ milk protein on the cheese-making process parameters, as well as the physical and chemical characteristics of the resulting cheese. MTGase influenced the time of gel formation from rennet addition (P<0.05), with a delay at the two highest concentrations, accompanied by a lower (P<0.01) pH of cheese and the lowest (P<0.01) loss in cheese weight at 24 h of storage. The highest gel viscosity (P<0.01) was observed at the highest concentration of the enzyme, reaching the value of 70 mPa·sec after 60 min. The chemical composition and color of the cheeses were not significantly affected by the inclusion of MTGase, regardless of the enzyme concentration. These findings may be of relevance in adapting the cheese-making process and might help in the design of new dairy products from donkey milk.

Fermented foods and probiotics: An approach to lactose intolerance

Salam A. Ibrahim, Rabin Gyawali, Saddam S. Awaisheh, Raphael D. Ayivi, Roberta C. Silva, Kiran Subedi, Sulaiman O. Aljaloud Shahida Anusha Siddiqui and Albert Krastanov

USA, Jordan, Saudi Arabia, Germany and Bulgaria

Abstract

The aim of this review was to present various topics related to lactose intolerance with special attention given to the role of fermented foods and probiotics in alleviating gastrointestinal

symptoms. Lactose intolerance is a common digestive problem in which the human body is unable to digest lactose, known as milk sugar. Lactose intolerance can either be hereditary or a consequence of intestinal diseases. Recent work has demonstrated that fermented dairy products and probiotics can modify the metabolic activities of colonic microbiota and may alleviate the symptoms of lactose intolerance. We suggest that, lactose free dairy products could be recommended as alternatives for the alleviation of lactose intolerance and for the promotion of human health and wellness.