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COLLECTED ABSTRACTS

Editorial: Incorporating the automatic milking system into forage grazing management

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Australia

About 30 years ago, the first commercial automatic milking system (AMS) was installed and in operation in the Netherlands to reduce the human labour required for harvesting milk (de Koning, 2011). The AMS was then further developed and used worldwide to support dairy production, in particular in European, North American and Oceanian countries, with large herds. The AMS was developed mainly for indoor feeding systems, such as partial mixed ration (PMR) and total mixed ration (TMR) feeding systems (John et al., 2016). However, for countries like New Zealand and Australia, where milk production relies heavily on forage-based grazing systems to keep feed costs low, incorporating AMS is more challenging than in intensive feeding systems because cows must walk long distances from grazing paddocks to the milking units.

Apart from reducing labour costs, the improvement in cow traffic, productivity and profit from AMS-forage grazing systems are also key goals that dairy farmers strive to achieve (Taing, 2016). In recent years, some published work both in refereed publications (eg Lessire et al., 2020) and technical notes (eg https://futuredairy.com.au/publications/#automaticmilking) have highlighted the opportunities and challenges of using AMS in a forage grazing based dairy cow production system. Research in this space is vital to improve the understanding, and to support further development of AMS-forage grazing systems, with a major aim to optimise voluntary cow movement, reduce labour input and better utilise forage on the farm through rotational grazing systems. Further, more specific research questions are also of great interest to explore, such as what cow breed is suitable for AMS-forage grazing systems? Can genomic selection help to optimise cow suitability for AMS-forage grazing systems? How do grazing forage quality/quantity, forage allocation method, concentrate feeding and their interactions impact on cow traffic? How does changing environmental conditions impact on AMS-forage grazing systems? Does the AMS-forage grazing system produce less greenhouse gases than conventional milking systems?

Despite various production and animal-specific data being collected through the utilisation of monitoring technologies in conventional milking systems, the moden AMS automatically collects many production and animal-specific data in near real-time. This has a real potential to help producers to monitor, report, and validate production performance and in the future might enable carbon footprint calculation, which is an increasingly significant area to develop sustainable dairy production worldwide.

Novel SNPs and haplotypes identified in the *CD4* gene and their influence on deregressed MACE EBV indexes of milk-related traits in Simmental breed.

Francesco Napolitano, Francesco Grandoni, Giovanna De Matteis, Lorenzo Degano, Daniele Vicario and Luca Buttazzoni

Italy

Abstract

Cluster of differentiation 4 (CD4) is the accessory protein non-covalently bound to the T cell receptor that recognizes an invariant region of MHC class II on antigen presenting cells. Its cytoplasmic tail, physically associated with a protein tyrosine kinase, is important in the activation of helper/inducer T lymphocytes. In Bos taurus, CD4 gene is located on chromosome 5 from which two isoforms are transcribed, with a different number of amino acids due to splicing of exon 7 and variation in the reading frame. The aim of this study was to investigate the sequence of the entire CD4 gene in Simmental sires to evaluate the effects of genomic variants on the indexes of the bulls for milk, fat and protein yields, as well as somatic cell score. The associations among genomic variants and indexes were analysed using the Allele and GLM procedures of SAS 9.4. The analysis indicated that only four of the thirty-one identified SNPs influenced the considered traits. Identified variants insist on coding zones and intronic sequences, where we revealed the presence of sites for transcription factors. To evaluate the existence of haplotypic effects, combinations among the four genomic variants (SNP 3, SNP 8, SNP 11 and SNP 19) were investigated. Six different haplotypic alleles were identified, but only four of them were frequent enough to allow for an evaluation of any haplotypic effect (at least six copies in the examined sample): Hap1, Hap2, Hap3 and Hap6. The analysis of associations between the selected haplotypes in the CD4 gene with milk related indexes showed that bulls with Hap2 (T-A-C-C) had better indexes for milk and protein yields (P < 0.05), whereas the presence of the Hap1 haplotype (A-G-A-T) caused a significant decrease of the index for protein yield (P < 0.05). Frequencies of the two alleles Hap1 and Hap2 (9 and 36% respectively) make them of interest for their possible inclusion in breeding schemes and support the hypothesis of considering this gene as a candidate for the improvement of milk-related traits in the Simmental breed.

The need for national livestock surveillance in Pakistan

Muhammad Aamir Shahzad **Pakistan**

Abstract

Ranked amongst the top five milk-producing countries globally, the Pakistan dairy industry can help to overcome food shortage and hunger, alleviate poverty and positively impact economic growth. This influencing role could potentially be more significant while the COVID-19 pandemic severely affects humanity, challenges the economy and increases the risk of global food shortage. However, its large national population of dairy livestock contrasts with Pakistan's top-five ranking, indeed, four to five Pakistani cows produce milk equivalent to one dairy cow of countries with a well developed dairy industry. Low milk yield per cow negatively impacts the national production and compromises the development of an efficient processing sector, such that consumers are very often

forced to use adulterated milk sold by local "milkmen". As a consequence, whilst committed to alleviating global hunger, Pakistan imports in excess of half a million tons of milk and milk-based products annually. Many studies have identified unproductive, inefficient and imprecise management issues combined with poor genetics and imbalanced nutrition as the leading barriers to improvement in the Pakistani dairy livestock sector. At an individual level, lack of awareness, affordability issues, illiteracy and low ambition of a large percentile of dairy farmers creates additional significant barriers. To address low productivity and poor genetics, Pakistani corporate farms and wealthier individual farmers import genetically improved breeds to attain high milk yields. However, they are then faced with the challenge of managing such breeds to attain sustainable and persistent milk yields under Pakistani climatic conditions, often risking excessive culling even to the point of business liquidation. In developed dairy industries, automated sensor-based livestock management systems are now available to help monitor, compute, and optimize procedures in realtime and are proven to increase productivity and profitability. The term Precision Livestock Farming (PLF) is used to describe systems that monitor individual animals or groups of animals to overcome management deficienices and optimise productivity. My stance in this Opinion Paper is that adopting and utilizing such precision technologies may support Pakistan in raising its livestock resources toward greater productivity, thereby helping to overcome the global food shortage.

The effects of cow introductions on milk production and behaviour of the herd measured with sensors

Josje Scheurwater, Ruurd Jorritsma, Mirjam Nielen, Hans Heesterbeek, Jan van den Broek and Hilde Aardema

The Netherlands

Abstract

This research paper addresses the hypothesis that cow introductions in dairy herds affect milk production and behaviour of animals already in the herd. In dairy farms, cows are commonly regrouped or moved. Negative effects of regroupings on the introduced animals are reported in other studies. However, little is known about the effects on lactating cows in the herd. In this research a herd of 53 lactating dairy cows was divided into two groups in a cross-over design study. 25 cows were selected as *focal cows* for which continuous sensor data were collected. The treatment period consisted of replacing *non-focal cows* three times a week. Many potentially influencing factors were taken into account in the analysis. Replacement of cows in the treatment period indeed affected the focal animals. During the treatment period these cows showed increased walking and reduced rumination activity and produced less milk compared to the control period. Milk production per milking decreased in the treatment period up to 0.4 kg per milking on certain weekdays. Lying and standing behaviour were similar between the control and the treatment period. The current study suggests that cow introductions affect welfare and milk production of the cows already in the herd.

Growth rate and behaviour in permanently separated, daily separated or non-separated kids and the corresponding milk production of their mothers

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Sweden and Denmark

Abstract

We address the hypothesis that keeping kids and mothers together would have positive effects on the milk composition of the mother and the behaviour of the kids. Kids were either permanently separated (SEP), daily separated between 7.30-15h (DAY-SEP) or kept with mothers 24h/day (NON-SEP). The NON-SEP kids were only allowed to suckle one teat. All kids had similar growth rate throughout the study (lactation day 5 – 70). DAY-SEP kids spent 24 % of their time with their mother at both ages. NON-SEP spent only 15% of the time with their mothers at 2 weeks of age and this increased to 28% at 2 months of age. NON-SEP kids showed more hiding behaviour at 2 weeks and SEP were more active alone, at both 2 weeks and 2 months, compared to the other treatments. The mean available milk yield and fat concentration were higher in DAY-SEP goats (2420 g ± 119 g and $4.9 \pm 0.1\%$) compared with NON-SEP goats (2149 ± 79 g and $4.4 \pm 0.1\%$). There were no differences between DAY-SEP and NON-SEP goats in total protein, lactose, or casein concentrations. Based on these data it was estimated that 7.1 kg milk was needed to produce 1 kg semi-hard cheese in DAY-SEP goats and 7.5 kg in NON-SEP goats, respectively. When comparing milk yield and composition between udder halves, the milk yield was, as expected, higher from the machine milked teat than from the suckled one in the NON-SEP goats but there was no difference between right and left udder halves in DAY-SEP goats. Milk fat concentration varied between teats at morning and afternoon milkings in NON-SEP goats, but there was no difference in milk fat between udder-halves in DAY-SEP goats. In conclusion, the kid growth rate was similar in all treatments, however, an altered behaviour was seen in permanently separated kids (SEP). The results show that it is possible to have a high milk yield and fat concentration with one kid together with the dam.

A proposed structural approach to improve cow-claw health on Dutch dairy farms

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The Netherlands

Abstract

Despite extensive research leading to an improved understanding of the risk factors and pathogenesis of infectious and non-infectious disorders, claw health has not structurally improved in recent decades. Several studies have shown that claw disorders harm milk production, fertility and longevity of the dairy cows and job satisfaction of the farmer. This is enough reason to structurally improve claw health on dairy farms. The focus should be on a rapid curative intervention when lameness occurs and above all the prevention of claw problems. Most claw disorder diagnoses are nowadays made during regular claw trimming by the professional trimmer or the dairy farmer. Registration of the detected disorders during claw trimming is not always done consistently, so the estimated prevalence (number of cows with a claw disorder) is in most cases an underestimation of the real prevalence. The quality of these records often makes it difficult for consultants to formulate appropriate claw health advice. To be able to give good advice on claw health, insight into the

prevalence of the various hoof disorders on a farm is a key condition. However, good quality advice alone is not a guarantee for an improved claw health situation on a farm. Research has shown that in addition to high quality substantiated advice, the communication style between the consultant and the dairy farmer is essential for the interpretation and motivation of the dairy farmer to implement the advice. In this paper a 7-point plan is presented as a guidance for herd advisors who want to support dairy farmers to improve claw health.

Effects of milking, over-milking and vacuum levels on front and rear quarter teats in dairy cows
Theresa Vierbauch, Walter Peinhopf-Petz and Thomas Wittek
Austria

Abstract

Mechanical forces to the teat and vacuum during milking negatively affect teat condition and may result in increased mastitis risk. We compared vacuum levels during milking and over-milking as well as teat condition before and after milking between front and rear teats. We expected that the lower milk yield of the front quarters would result in a longer over-milking and higher vacuum levels in front teats, resulting in morphological differences. The study comprised 540 dairy cows in 41 Austrian dairy farms with conventional milking systems. Before and after milking teats were visually assessed (colour, swelling, rings, hyperkeratosis) and teat dimensions (length, diameter, wall thickness, teat canal length) were measured manually and ultrasonographically. Vacuum measurements were taken using a vacuum measurement device attached to the cluster (short milk tube, pulsation tube and mouth-piece chamber). These various measurements of front and rear teats were compared and a multivariable analysis with backward stepwise procedure was used for inclusion or exclusion from the model. Front teats showed a poorer teat condition and were overmilked for longer in comparison to the rear teats. However, during milking and over-milking the vacuum levels in the mouthpiece chamber were significantly higher at the rear teats. The changes in front teat morphology were only partially caused by milking, over-milking and vacuum levels, with approximately 70% of the variation due to other, undetermined variables. Milking, over-milking and vacuum levels had no or very limited impact on the morphological changes of the rear teats.

Negative effect of insulin-induced gene 2 on milk fat synthesis in buffalo mammary epithelial cells Xinyang Fan, Yongyun Zhang, Lihua Qiu and Yongwang Miao China

Abstract

Insulin-induced gene 2 (*INSIG2*) is a recently identified gene that is implicated in the regulation of cholesterol metabolism and lipogenesis in mammals. Although the data in goats emphasizes a role for *INSIG2* in milk fat synthesis, the regulatory mechanism in buffalo is not clear. In this study, we analyzed the protein abundance of *INSIG2* at peak lactation and dry-off period in buffalo mammary tissue. The results indicated that, relative to the peak lactation, the protein abundance of *INSIG2* in the dry-off period was higher. To determine the function of *INSIG2* in milk fat synthesis, *INSIG2* was overexpressed and knocked down by lentiviral transfection in buffalo mammary epithelial cells (BuMECs). The response to overexpressing *INSIG2* included down-regulation of *SREBP*, *PPARG*,

FASN, ELOVL6, SCD, APGAT6 and TIP47 coupled with a decrease in content of triacylglycerol (TAG). However, in response to knockdown of INSIG2, the significant increase in content of TAG along with marked up-regulation of SREBP, PPARG, FASN, ELOVL6, SCD, APGAT6 and TIP47 suggests that INSIG2 negatively affects milk fat synthesis in BuMECs. No significant difference in mRNA abundance of GPAM and DGAT2 in response to overexpression or interference of INSIG2 indicates that they might also be influenced by other regulatory factors. Taken together, our results provide strong support for the negative effect of INSIG2 on milk fat synthesis in BuMECs.

A potential treatment approach for subclinical mastitis in dairy cows: auriculotherapy of the auricular branch of the vagus nerve

Max Winkler, Sonja Franz, Thomas Wittek and Harald Pothmann **Austria**

Abstract

This research aims to test the hypothesis that neural therapy (NT) on the auricular branch of the vagus nerve (ABVN) in dairy cows diagnosed with subclinical mastitis (SCM) results in a reduction of the somatic cell count. Therapeutic options for SCM are mostly based on use of antibiotics and often lead to unsatisfactory results. An alternative therapy targeting the anti-inflammatory properties of the vagus nerve showing good efficacy, economic viability and without major side effects would be of considerable interest. Auriculotherapy (AT) was performed using three repeated infiltrations of 8.0 mg (0.4 mL) procaine hydrochloride (2%) at the location of the ear tag associated with the auricular acupuncture point (AAP) of the udder. Some 85 clinically healthy cows from nine dairy farms were sampled for evaluation of quarter somatic cell count (QSCC) on four days (d0, d2, d4 and d6). Quarters with a QSCC >100,000 cells/mL on d0 were included in the analysis. Over the study period, a total of 784 quarters were analysed, 385 control (CON) quarters from 40 cows and 399 treated (TRE) quarters from 45 cows. Results showed that AT of the ABNV resulted in a significant reduction of the QSCC after three treatments. The effect was independent of bacteriological culture results of the quarter milk samples. The bacteriological cure rate, however, was not influenced by AT. To opur knowledge this is the first report of AT reducing QSCC in dairy cows with SCM. Before AT can be regarded as an alternative therapeutic approach, further research should focus on possible long-term effects of AT on the reduction of SCC, any bacterial elimination and the neural pathways of AT in dairy cows with SCM.

Microscopic differential cell count and specific mastitis pathogens in cow milk from compostbedded pack barns and cubicle barns

Patricia Wagner, Kerstin Brügemann, Tong Yin, Petra Engel, Christina Weimann, Karen Schlez and Sven König

Germany

Abstract

Compost bedded pack barns (compost) as a new free walk housing system favorably influence udder health due to improved animal welfare and lying comfort. On the other hand, unfavorable effects on udder health are possible, due to the open bedded pack and the associated larger bacterial content in moisture. For in-depth farming system comparisons, the present study aimed to evaluate

the specific cell fractions and mastitis pathogens in milk from cows kept in compost and in conventional cubical barns (cubicle). For milk sample collection we used a repeated measurement data structure of 2,198 udder quarters from 537 Holstein cows kept in six herds (3 in compost and 3 in cubicle). Differential cell counting was conducted including lymphocytes, macrophages and polymorphonuclear leucocytes (PMN). Specific mastitis pathogens comprised major and minor pathogens. Mixed models were applied to infer environmental and cow associated effects on cell fractions and on prevalences for pathogen infections, with specific focus on system x lactation stage, system x milk yield and system x somatic cell count effects. The interaction between system and lactation stage showed significant differences (P < 0.01) between the systems. A significantly smaller number of bacteriologically positive quarters and lower prevalences for minor pathogens were detected in compost compared to cubicle. Least squares means for pathogen prevalences indicated a quite constant proportion of bacteriologically negative udder quarters across milk yield levels in compost, but a slight increase with increasing milk yield in cubicle. Cell fraction responses in both systems differed in relation to the overall bacteriological infection status and farming system particularities. In conclusion, different cell fractions and specific mastitis pathogens should be considered as an indicator for udder health in different production systems, taking into account cow associated factors (lactation stage, milk yield).

Comparative whey proteome analysis of Small-tailed Han and DairyMeade ovine milk

Urhan Bai, Xiaohu Su, Zhong Zheng, Liguo Zhang, Ying Ma, Yingjie Dou, Xiaoran Zhang, Guanghua Su, Ningcong Zhou, Guangpeng Li and Li Zhang

China

Abstract

We characterized the proteome profile of mid lactation Small-tailed Han (STH) and DairyMeade (DM) ovine milk in order to explore physiological variation and differences in milk traits between the two breeds. Methodology combined a tandem mass tag (TMT) proteomic approach with LC-MS/MS technology. A total of 656 proteins were identified in STH and DM ovine milk, of which 17and 29 proteins were significantly upregulated (P<0.05) in STH and DM, respectively. Immune-related proteins and disease-related proteins were highly expressed in STH milk, whereas S100A2 and AEBP1 were highly expressed in DM milk, which had beneficial effects on mammary gland development and milk yield. Our results provide a theoretical basis for future breeding of dairy sheep.

Case study on the dairy processing industries and their wastewater generation in Latvia

Basanti Ekka, Sandis Dejus and Talis Juhna

Latvia

Abstract

The objective of the research presented in this Research Communication was to access the environmental impact of the Latvian dairy industries. Site visits and interviews at Latvian dairy processing companies were done in order to collect site-specific data. This includes the turnover of the dairy industries, production, quality of water in various industrial processes, the flow and

capacity of the sewage including their characteristic, existing practices and measures for wastewater management. The results showed that dairy industries in Latvia generated in total approximately 2263 x 10³ m³ wastewater in the year 2019. The Latvian dairy effluents were characterized with high chemical oxygen demand (COD), biological oxygen demand (BOD) and total solids (TS). Few dairy plants had pre-treatment facilities for removal of contaminants, and many lacked onsite treatment technologies. Most facilities discharged dairy wastewater to municipal wastewater treatment plants. The current study gives insight into the Latvian dairy industries, their effluent management and pollution at Gulf of Riga due to wastewater discharge.

Innovative application of postbiotics, parabiotics and encapsulated *Lactobacillus plantarum* RM1 and *Lactobacillus paracasei* KC39 for detoxification of aflatoxin M1 in milk powder.

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Egypt

Abstract

This study aimed to evaluate aflatoxin M_1 (AFM₁) level in milk powder and infant milk formulae, in addition to applying innovative methods for AFM₁ & AFB₁ detoxification. Fifty random samples of milk powder and infant formulae (25 of each) were collected from the Egyptian markets for assessing AFM₁ level using ELISA technique. Bioactive components comprising cell free supernatants (postbiotic), acid-dead cells (parabiotic) and the encapsulated-cells of Lactobacillus plantarum RM1 and Lactobacillus paracasei KC39 were evaluated for their antifungal activity against toxigenic mold strains and their impact on AFB1 and AFM1 reduction in reconstituted milk powder. AFM1 concentration in unpacked milk powder was higher than that of packed samples and infant formulae, although these differences were not significant (P> 0.05). About 96.0, 29.4 and 25.0% of the tested infant formulae, unpacked, and packed milk powder were unacceptable in terms of the AFM₁ limit defined by Egyptian and European standards, while all samples were in accordance with the USA/FDA standard. All tested mycotoxigenic strains were sensitive to the different treatments of the probiotics with the highest sensitivity regarding Fusarium strain with L. paracasei KC39 compared to other genera. The degradation ratios of AFM1 using the bioactives of the L. paracasei KC39 were higher than that of L. plantarum RM1 bioactives. Additionally, KC39 parabiotic manifested the best AFB₁ reduction (60.56%). In conclusion, the positive and highly significant relationship (p<0.05) between these effective biocompounds mirrors their major detoxification role which gives a safe solution for AFs contamination issues in milk and milk products.

Changes in microbiological parameters, pH and titratable acidity during the refrigerated and room temperature storage of dahi prepared from the milk of Vechur cows: an indigenous cattle breed of Kerala

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Abstract

Vechur cow is an indigenous cattle breed of Kerala listed as a critical breed by FAO. This research communication is related to the hypothesis that the changes occurring in microbiological quality

parameters of Vechur cow milk dahi (VCMD) during storage will be superior to other milk and reflective of the traditional concepts of therapeutic properties attributed to Vechur milk. Microbiological quality of the VCMD stored at room (30 \pm 1° C) and refrigerated (4 \pm 1°C) temperatures in terms of total viable, coliform, yeast and mould and lactococcal counts is reported in this study, together with titratable acidity and pH. Results are compared with cross-bred cow milk dahi (CCMD) as control. On refrigerated storage, despite the comparable initial microbiological quality, VCMD exhibited significantly lower total viable, lactic acid bacteria, yeast and mold counts than CCMD, from the fifth day onwards for the first two parameters and the tenth day onwards for the last parameter. VCMD exhibited significantly higher pH values than CCMD from the fifth day onwards whereas the titratable acidity was significantly lower from the tenth day onwards. Though this study does not delineate the factors contributing towards the lower microbial population observed in VCMD, it provides an impetus to further researches for scientifically validating its traditionally-reported medicinal properties.

Foaming properties of camel and bovine sodium caseinates

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Tunisia and France

Abstract

In the present study, camel and bovine sodium caseinates (Na-cas) were extracted and different heat-treatments were performed (70, 80, 90 and 100°C for 30min). RP-HPLC profiles, foaming (foam capacity, FC and foam stability, FS) and physico-chemical properties (surface hydrophobicity, ζ -potential and interfacial tensionvalues) of the samples were evaluated and compared. The greatest foam was obtained with camel Na-cas in all heating temperatures (up to 130%) due to the higher β -casein content (~53.4% of total camel caseins, RP-HPLC results). Increasing heat-treatment temperature to 90°C and 100°C could significantly enhance the FC and FS values of both camel and bovine Na-cas. Good correlation was observed with the physico-chemical properties of bovine and camel Na-cas by raising the surface hydrophobicity and decreasing the electronegative charge and the interfacial tension values upon heating. These findings confirmed the denaturation and degradation of the caseins as proved by RP-HPLC analysis. This study concluded that the camel Na-cas has important foaming properties in agricultural and food industries.

Comparison of culture-dependent and culture-independent techniques in the detection of lactic acid bacteria biodiversity and dynamics throughout the ripening process: The case of Turkish artisanal Tulum cheese produced in the Anamur region

Talha Demirci, Aysun Oraç, Kübra Aktaş, Enes Dertli, İsmail Akyol and Nihat Akın **Turkey**

Abstract

Our objective was to analyse the diversity of the microbiota over 180 days of ripening of eight batches of artisanal goatskin Tulum cheeses by culture-dependent and culture-independent (PCR-DGGE) methods. V3 region of the bacterial 16S rRNA gene was amplified with the PCR after direct

DNA isolation from the cheese samples. Nine different species and five genera were determined by culturing, while 11 species were identified in the PCR-DGGE technique. This diversity revealed the uniqueness of artisanal cheese varieties. The dominant genera in all the cheese samples were composed of *Enterococcus* species. The culture-dependent method revealed five genera (*Enterococcus*, *Bacillus*, *Lactococcus*, *Lactobacillus*, *Sphingomonas*) while three genera (*Enterococcus*, *Streptococcus*, *Lactococcus*) were detected in the culture-independent method. It was concluded that combining the two methods is important for characterizing the whole microbiota of the Tulum cheese varieties produced in the Anamur region.

Lactose-free dulce de leche: compositional characterization, browning and texture profile

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Brazil

Abstract

Our objective was to elaborate lactose-free dulce de leche (DL) and evaluate the influence of the hydrolysis of this sugar on the attributes of the products. Fluid milk used was divided into two portions and, in one of them, enzymatic hydrolysis of lactose was carried through. Next, the homogenization of milk was performed at 20 Mpa. Four different treatments were studied. The final products were evaluated in relation to their composition and physical-chemical characteristics. The main results show that the homogenized lactose-free DL obtained a higher concentration of free 5-Hydroxymethylfurfural (HMF) (133.77 \pm 3.42 μ mol.L $^{-1}$). Consequently, browning was more intense due to Maillard Reaction. Texture parameters were higher (1611.00 \pm 598.78 g hardness and 19.52 \pm 2.46 g gumminess) when compared to the homogenized traditional product (28.45 \pm 1.16 μ mol.L $^{-1}$ free HMF, 437.17 \pm 279.3 g hardness, and 406.20 \pm 311.69 g gumminess). Lactose-free products are in high demand by consumers; however, the results of this work highlight the challenges to properly control the browning and the texture parameters of DL.

Influence of sucrose reduction on fouling during the production of dulce de leche

Erica F. Mauricio, Júlia D. A. Francisquini, Igor L. de Paula, José de C. C Cezarino Junior, Luiz F. C. de Oliveira, Rodrigo Stephani, Antônio F. De Carvalho and Ítalo T. Perrone

Brazil

Abstract

In this Research Communication we focus the food industry's broad tendency to decrease sugar content in food products onto dulce de leche (DL) and examine the influence of sucrose reduction on the detrimental deposits formed during the production process. The method used to identify the impact produced directly on the heat exchanger during the production of this product with low sucrose content required varying the quantity of sucrose in the milk. Different percentages of sucrose (20, 15, 10, 5 and 0 % w·w⁻¹) were submitted to the DL concentration process in a process simulator. After concentration, the quantification of the deposits formed in each was carried out and these deposits were characterized according to their composition. Methods such as Kjeldahl, Pregl-Dumas and SEM-EDS were used. Thus, the work highlights the need to change the product

manufacturing process due to changes in the formulation that directly impact the formation of deposits in the equipment used (fouling). This deposit changes significantly in relation to its quantity as well as in relation to the composition and chemical characteristics as the gradual reduction of the sucrose content in the production takes place. Therefore, these impacts must be considered in order to maintain better manufacturing and ensure efficient cleaning of equipment.

Developments in effective use of volatile organic compound analysis to assess flavour formation during cheese ripening

Mustafa Yavuz, Ceyda Kasavi and Ebru Toksoy Öner

Turkey

Abstract

In the burgeoning demand for optimization of cheese production, ascertaining cheese flavour formation during the cheese making process has been the focal point of determining cheese quality. In this research reflection, we have highlighted how valuable volatile organic compound (VOC) analysis has been in assessing contingent cheese flavour compounds arising from non-starter lactic acid bacteria (NSLAB) along with starter lactic acid bacteria (SLAB), and whether VOC analysis associated with other high-throughput data might help provide a better understanding the cheese flavour formation during cheese process. It is widely known that there is a keen interest to merge all omics data to find specific biomarkers and/or to assess aroma formation of cheese. Towards that end, results of VOC analysis have provided valuable insights into the cheese flavour profile. In this review, we are pinpointing the effective use of flavour compound analysis to perceive flavour-forming ability of microbial strains that are convenient for dairy production, intertwining microbiome and metabolome to unveil potential biomarkers that occur during cheese ripening. In doing so, we summarised the functionality and integration of aromatic compound analysis in cheese making and gave reflections on reconsidering what the role of flavour-based analysis might have in the future.

Effects of dietary iodine supplement on sheep milk and cheese

Veronica Carnicelli, Anna Rita Lizzi, Alessia Ponzi, Carla Luzi, Lisa Grotta, Francesca Bennato and Antonio Di Giulio

Italy

Abstract

The work reported in this paper addresses the iodine nutritional deficiency that still affects a large number of people. For this purpose, we analyzed the possibility to use, as iodine vehicle, a hard typical ewe cheese, called Canestrato d'Abruzzo, derived from milk of ewes fed with an iodine-fortified diet. Both in the milk and the cheese of these animals, the iodine level was higher than that measured in sheep with a normal diet. An increase in the lactoferrin and iron content was evident in the whey derived from milk of the iodine group. Furthermore, in derived cheese, the caseins seemed more efficiently transformed in small peptides making the product more digestible and, for this reason, particularly suitable for feeding the elderly. In conclusion, the dairy products obtained from ewes fed with iodine diet contain more bioactive compounds so that they represent a useful food to prevent iodine and iron deficiency in lamb and humans.