

COLLECTED ABSTRACTS

Editorial: Ninety years young

Christopher H Knight

Denmark

My very first attempts at exploiting the wonders of lactation were an abject failure, or so my mother has informed me. Despite that (or maybe partly because of it?), I have retained a fascination with the topic throughout my upbringing and then career. As a biological process, the production of milk is arguably the most undervalued attribute of the vertebrate class Mammalia; the basis of nomenclature but constituting only a small paragraph or two in physiology textbooks. As nutrition for the neonate, milk is unsurpassed and almost certainly always will be: Kevin Nicholas' fascinating account of marsupial lactation and the role it plays in the development of the altricial joey is not only a joy to read but also points to huge potential for improved prognosis in premature human birth (Nicholas, 2019). As nutrition for the general population, milk (from dairy animals) has come to be regarded as something akin to Jekyll and Hyde. I shall not enter into that debate here, but suffice to say that mankind has exploited dairy animals for many centuries in order to sustain and grow the species; milk and dairy products have been a major player in our success and could play a significant part in further sustaining both our expanding human population and our global environment. The Journal of Dairy Research has played a key role in achievements to date and will continue to make a crucial contribution to those still to come.

Biomarkers of fitness and welfare in dairy cattle: healthy productivity

Maya Zachut, Marcela Šperanda, André M. de Almeida, Gianfranco Gabai, Ali Mobasher and Lorenzo E. Hernandez-Castellano

Israel, Croatia, Portugal, Italy, Lithuania, Finland, UK and Denmark

Abstract

Milk production intensification has led to several unwanted aspects, such as sustainability issues and environmental pollution. Among these, increased milk outputs that have been achieved over the last 70 years have led to several health and pathophysiological conditions in high yielding dairy animals, including metabolic diseases that were uncommon in the past. Increased occurrence of diverse metabolic diseases in cattle and other domestic animals is a key feature of domestication that not only affects the animals' health and productivity, but also may have important and adverse health impacts on human consumers through the elevated use of drugs and antibiotics. These aspects will influence economical and ethical aspects in the near future. Therefore, finding and establishing proper biomarkers for early detection of metabolic diseases is of great interest. In the present review, recent work on the discovery of fitness, stress and welfare biomarkers in dairy cows is presented, focusing in particular on possible biomarkers of energy balance and oxidative stress in plasma and milk, and biomarkers of production-related diseases and decreased fertility.

This is a companion article to our recent review of biomarkers related to the stress response to environmental perturbations in dairy animals (Almeida et al., 2019).

Long term dietary supplementation with microalgae increases plasma docosahexaenoic acid in milk and plasma but does not affect plasma 13, 14-dihydro-15-keto PGF_{2α} concentration in dairy cows

Bethan E Till, James A Huntington, Kirsty E Kliem, Jules Taylor-Pickard, and Liam A Sinclair
UK and Ireland

Abstract

The aims of the study were to determine the long-term effects of dietary supplementation with microalgae (SCIM) on milk and blood fatty acid (FA) composition and reproductive hormones in early lactation dairy cows. Sixty Holstein-Friesian dairy cows (30 per treatment) were unsupplemented (Control) or supplemented with 100 g of SCIM (*Schizochytrium imancinum* sp) per cow per day from 25 ± 0.5 days post-partum for 98 days. Intake and milk yield were recorded daily, with milk samples collected at weeks 0, 1, 2, 4, 8 and 14, and blood samples collected from 12 representative pairs per treatment at weeks 0, 2, 4, 8, and 14 for subsequent analysis of FA, β-hydroxybutyrate, non-esterified fatty acids and glucose. At 33 ± 0.9 days postpartum the oestrus cycle of 24 cows (12 per treatment) were synchronised and plasma 13,14-dihydro-15-keto PGF_{2α} (PGFM) concentrations determined following an oxytocin challenge. Data were analysed by repeated measures analysis of variance. There was no effect of treatment on dry matter intake, milk yield or milk fat content, with mean values across treatments of 22.1 and 40.6 kg/d, and 37.2 g/kg respectively. Milk fat concentration of C22:6 n-3 increased rapidly in cows receiving SCIM, reaching a maximum of 0.38 g/100 g FA by week 14. Similarly, blood concentration of C22:6 n-3 increased to 1.6 g/100 g FA by week 14 in cows fed SCIM. There was no effect of treatment on plasma metabolites, but plasma glucose was lower in cows fed SCIM compared to the Control at week 2, and higher in weeks 4 and 8. There was no effect of treatment on peak plasma PGFM concentration or area under the curve. It is concluded that feeding SCIM rapidly increases blood and milk concentrations of C22:6 n-3 which are maintained over time, but does not improve plasma PGFM in dairy cows.

Genome-wide association study for buffalo mammary gland morphology

Jun Li, Jiajia Liu, Shenhe Liu, Giuseppe Campanile, Angela Salzano, Bianca Gasparri, Graham Plastow, Chunyan Zhang, Zhiquan Wang, Aixin Liang and Liguang Yang
China, Italy and Canada

Abstract

This Research Communication describes a genome-wide association study for Italian buffalo mammary gland morphology. Three single nucleotide polymorphisms (AX-85117983, AX-8509475 and AX-85117518) were identified to be significantly associated with buffalo anterior teat length, posterior teat length and distance between anterior and posterior teat, respectively. Two significant signals for buffalo mammary gland morphology were observed in two genomic regions on the chromosome 10, and chromosome 20. One of the regions located on the chromosome 10

has the most likely candidate genes ACTC1 and GJD2, both of which have putative roles in the regulation of mammary gland development. This study provides new insights into the genetic variants of buffalo mammary gland morphology and may be beneficial for understanding of the genetic regulation of mammary growth.

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

Dinesh Bhattarai, Rahim Dad, Tesfay Worku, Sutong Xu, Farman Ullah, Min Zhang, Xianwei Liang, Tingxian Den, Mingxia Fan and Shujun Zhang

China

Abstract

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

Effects of *FABP4* variation on milk fatty-acid composition for dairy cattle grazed on pasture in late lactation

Yunhai Li, Huitong Zhou, Long Cheng, Miriam Hodge, Jenny Zhao, Rosy Tung, Grant Edwards & Jonathan Hickford

Australia and New Zealand

Abstract

This research communication describes associations between variation in the fatty acid binding protein 4 gene (*FABP4*) and milk fat composition in New Zealand (NZ) Holstein-Friesian × Jersey (HF×J)-cross dairy cows. After correcting for the effect of the amino acid substitution p.K232A in diacylglycerol O-acyltransferase 1 (DGAT1), which is associated with variation in many milk fatty acid (FA) component levels, the effect of *FABP4* c.328A/G on milk FA levels was typically small. For the five genotypes analysed, the AB cows produced more medium-chain fatty acids (MCFA) than CC cows ($P < 0.05$), and more C14:0 FA than AA and AC cows ($P < 0.05$). The AA and AC cows produced less C22:0 FA ($P < 0.01$) than the BC cows, and the AC cows produced more C24:0 FA ($P < 0.05$) than was produced by the BC cows. Cows of genotype CC produce more long-chain fatty

acids (LCFA), than cows of genotype *BC* ($P < 0.05$).

Autoregressive repeatability model for genetic evaluation of longitudinal reproductive traits in dairy cattle

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Brazil and Portugal

Abstract

We aimed to evaluate the efficiency of the autoregressive repeatability model (AR) for genetic evaluation of longitudinal reproductive traits in Portuguese Holstein cattle and compare the results with those from conventional repeatability model (REP). The data set comprised records taken during the first four calving orders, corresponding to a total of 416, 766, 872 and 766 thousand records for interval between calving to first service, days open, calving interval and daughter pregnancy rate, respectively. Both models included fixed (month and age classes associated to each calving order) and random (herd-year-season, animal and permanent environmental) effects. For AR model, a first-order autoregressive (co)variance structure was fitted for the herd-year-season and permanent environmental effects. The AR outperformed the REP model, with lower Akaike Information Criteria, lower Mean Square Error and Akaike Weights close to unity. Rank correlations between estimated breeding values (EBV) with AR and REP models ranged from 0.95 to 0.97 for all studied reproductive traits, when the total bulls were considered. When considering only the top-100 selected bulls, the rank correlation ranged from 0.72 to 0.88. These results indicate that the re-ranking observed at the top level will provide more opportunities for selecting the best bulls. The EBV reliabilities provided by AR model was larger for all traits, but the magnitudes of the annual genetic progress were similar between two models. Overall, the proposed AR model was suitable for genetic evaluations of longitudinal reproductive traits in dairy cattle, outperforming the REP model.

On-farm use of a water hardness test kit to assess total blood calcium level in dairy cattle

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Italy

Abstract

In this Research Communication we report the measurement of total blood calcium concentration with a water hardness test kit (WHTK) in dairy cattle and compare the results to a reference method. The study was carried out on 107 Holstein Friesian cows from three commercial dairy farms in Sardinia (Italy). Blood samples were collected ≤ 7 days from calving and total serum calcium concentration was determined using a biochemical analyser and a WHTK. The relationship between the laboratory results and the WHTK results was investigated using Spearman's rank correlation test and simple linear regression was determined. Sensitivity, specificity, negative and positive predictive values, intra and inter-assay coefficient of variation were also calculated. The test values were highly correlated with the laboratory values ($R^2 = 0.72$, $P < 0.001$). Sensitivity and specificity were respectively 88% and 83% for the WHTK and intra and inter-assay coefficients of

variation were 7.3% and 11.3% respectively. The WHTK was identified as a potential on-farm tool for monitoring early postpartum Ca concentrations at herd level.

Ketotic cows display a different serum nonesterified fatty acid composition

Lei Liu, Taiyu Shen, Wei Yang, Hongjiang Yu, Sansi Gao, Baoyin Huang and Chuang Xu
China

Abstract

The experiments reported in this research communication aimed to compare the serum nonesterified fatty acid (NEFA) composition in ketotic cows and healthy cows during the perinatal period. NEFAs play significant roles in etiology and pathology of ketosis. We hypothesized that ketotic cows will display a different serum NEFA composition compared to healthy controls, and fatty acid related indicators for ketosis prediction can be screened. Pre-partum healthy cows were recruited, and blood samples were collected on -7 d, 3 d, 7 d, 14 d and 21 d postpartum. Cows were further divided into a healthy control group (C group, n=6) and a ketosis group (K group, n=6) if blood beta-hydroxybutyric acid levels exceeded 1.2 mM during the experiment. NEFA composition was then analyzed by means of Gas Chromatography-Mass Spectrometer (GC-MS). Only C12:0% was significantly higher in C group than K group on 7 d pre-partum ($P<0.05$), when the cows were not diagnosed with ketosis. Five fatty acids displayed statistical differences in composition between C and K group ($P<0.05$), namely C12:0, C16:0, C17:0, C18:1n9 and C22:1n9. Saturates%, unsaturates%, mono-unsaturates% and saturates/unsaturates were also different between C and K group ($P<0.05$). Of note, C18:1n9/C12:0 and C18:1n9/C22:1n9 in K group were significantly higher than those in controls on 7 d pre-partum ($P<0.05$). It is suggested that the ratios show potential as indicators for prediction of ketosis.

Cooling Management Effects on Dry Matter Intake, Metabolic Hormones Levels and welfare Parameters in Dairy Cows during Heat Stress

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Israel

Abstract

This research paper addresses the hypothesis that intensive cooling management during the summer improves the secretion of metabolic hormones in dairy cows. To test this hypothesis, we characterized the effect of different cooling managements on the different ghrelin isoforms and leptin secretion of 20 Israeli-Holstein dairy cows during 5 weeks during heat stress. The cows were divided into two groups: one was exposed to 5 cooling sessions per day (5CS) and the other to 8 cooling sessions per day (8CS). Blood was collected and leptin and ghrelin isoforms level were radioimmunoassayed. Analysis of the interaction between coolings and the week of the experiment showed that the 8CS group consumed more food and produced more milk, although neither difference was statistically significant. In addition, the 8CS group exhibited higher blood levels of acyl-ghrelin and leptin as compared to the 5CS group. Conversely, the blood levels of total ghrelin were lower in the cows exposed to 8CS as compared to cows from the 5CS treatment.

Furthermore, a significant correlation was found only between total ghrelin levels and the weeks, but not with other parameters examined. We further compared digestibility as well as stress parameters between the groups. We found that the 8CS group cows ruminated and lay down more hours during a day and simultaneously had better activity time. No significant difference was detected between groups in milk yield and digestibility parameters. Our results suggest that intensive cooling management during the hot season influences the levels of metabolic hormones in the circulation and helps to mitigate the detrimental effect of heat stress on dairy cow welfare and production.

Supplementing conjugated and non-conjugated L-methionine and acetate alters expression patterns of CSN2, proteins and metabolites related to protein synthesis in bovine mammary cells

Seungwoo Jeon, Jay Ronel Conejos, Jungeun Kim, Minjeong Kim, Jeongeun Lee, Baekseok Lee, Jinseung Park, Junok Moon, Jaesung Lee and Honggu Lee

Korea

Abstract

The experiments reported in this research paper aimed to determine the effect of supplementing different forms of L-methionine (L-Met) and acetate on protein synthesis in immortalized bovine mammary epithelial cell line (MAC-T Cell). Treatments were Control, L-Met, conjugated L-Met and acetate (CMA), and non-conjugated L-Met and Acetate (NMA). Protein synthesis mechanism was determined by omics method. NMA group had the highest protein content in the media and CSN2 mRNA expression levels ($P < 0.05$). The number of upregulated and downregulated proteins observed were 39 and 77 in L-Met group, 62 and 80 in CMA group and 50 and 81 in NMA group from 448 proteins, respectively ($P < 0.05$). L-Met, NMA and CMA treatments stimulated pathways related to protein and energy metabolism ($P < 0.05$). Metabolomic analysis also revealed that L-Met, CMA and NMA treatments resulted in increases of several metabolites ($P < 0.05$). In conclusion, NMA treatment increased protein concentration and expression level of CSN2 mRNA in MAC-T cells compared to control as well as L-Met and CMA treatments through increased expression of milk protein synthesis-related genes and production of the proteins and metabolites involved in energy and protein synthesis pathways.

An endocrine hypothesis to explain obesity-related lactation insufficiency in breastfeeding mothers

Christopher H Knight

Denmark

Abstract

In this Research Reflection I shall develop and validate the hypothesis that lactation insufficiency in obese breastfeeding mothers has an endocrine explanation. I shall not present data, but I shall review pertinent literature to show that obesity is associated with a partial or sometimes complete failure to initiate and maintain lactation, and critically examine the belief that this is due to psychosocial factors, a failure of prolactin secretion or both. Since progesterone is inhibitory to lactogenesis and oestrogens are inhibitory to milk secretion, I shall then explore the possibility that these steroids are linked to lactation failure, through sequestration of progesterone and aromatization of oestrogen in mammary adipose tissue. I shall conclude by describing experimental approaches in animal models that could be used to test this hypothesis.

Dairy producers in the Southeast United States are concerned with cow care and welfare

Amanda Lee, Susan Schexnayder, Liesel Schneider, Stephen Oliver, Gina Pighetti, Christina Petersson-Wolfe, Jeffrey Bewley, Stephanie Ward and Peter Krawczel

USA

Abstract

This Research Communication addresses the hypothesis that Southeast dairy producers' self-reported bulk tank somatic cell count (BTSCC) was associated with producers' response to three statements (1) "a troublesome thing about mastitis is the worries it causes me," (2) "a troublesome thing about mastitis is that cows suffer," and (3) "my broad goals include taking good care of my cows and heifers." Surveys were mailed to producers in Georgia, Kentucky, Mississippi, North Carolina, South Carolina, Tennessee, and Virginia (29% response rate, N =596; final analysis N = 574), as part of a larger survey to assess Southeastern dairy producers' opinions related to BTSCC. Surveys contained 34 binomial (n = 9), Likert scale (n =7), and descriptive (n = 18) statements targeted at producer self-assessment of herd records, management practices, and BTSCC. Statements 1 and 2 were assessed on a 5-point Likert scale from "strongly disagree" to "strongly agree." Statement 3 was assessed on a 5-point Likert scale from "very unimportant" to "very important." Reported mean BTSCC for all participants was 254,500 cells/mL. Separate univariable logistic regressions using generalized linear mixed models (SAS 9.4, Cary, NC, USA) with a random effect of farm, were performed to determine if BTSCC was associated with probability for a producer's response to statements. If BTSCC was significant, forward manual addition was performed until no additional variables were significant ($P \leq 0.05$), but included BTSCC, regardless of significance. Bulk tank somatic cell count was associated with "a troublesome thing about mastitis is the worries it causes me," but not with Statements 2 or 3. This demonstrates that > 75% of Southeastern dairy producers are concerned with animal care and cow suffering, regardless of BTSCC. Understanding Southeast producers' emphasis on cow care is necessary to create targeted management tools for herds with elevated BTSCC.

Risk factors of *S. aureus* intramammary infection in pre partum dairy heifers under grazing conditions and molecular characterisation of isolates from heifers and cows

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Argentina

Abstract

The aims of the research reported here were to identify potential risk factors associated with the presence of *Staphylococcus aureus* intramammary infection (IMI) in pre partum dairy heifers on 17 dairy farms from three provinces of Argentina and to characterise, at molecular level, isolates from those heifers and lactating cows from two selected herds. A total of 1,474 heifers and 4,878 lactating cows were studied. The prevalence of *Staphylococcus aureus* IMI in the heifers, heifers at quarter level and lactating cow mammary quarters was 14.41, 4.82, and 14.65%, respectively. Univariate analysis showed the key variables associated with *S. aureus* IMI presence in the heifers were: *S. aureus* IMI prevalence in cows of the lactating herd, the time calves stayed with their dam

after birth, the calf rearing system, the place of rearing (own farm or other dairy farm) and fly control on the farm. None of the variables included in the multivariable analysis was associated with the presence of *S. aureus* IMI in the pre partum heifers, probably due to low variability among management practices used by the farms for rearing the heifer calves. At the molecular level, *S. aureus* isolates were grouped into three main PFGE clusters and several genotypes within the clusters. Isolates from mammary secretion of pre partum heifers and milk of lactating cows comprised different PFGE clusters in both herds, although two exceptions occurred. The absence of gene *FnBPB*, which codifies for a virulence factor protein involved in cell invasion by *S. aureus*, was significantly more frequent in pre partum heifer secretion isolates than in isolates from lactating cow milk. These results suggest that, under these management conditions, isolates from mammary secretions of pre partum heifers do not originate from the milk of lactating cows, but rather other sources to which the heifer is exposed.

ACAA2 and FASN polymorphisms affect the fatty acid profile of Chios sheep milk

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Cyprus and UK

Abstract

The objective of the research reported in this research communication was the identification and association of single nucleotide polymorphisms (SNP) in the ovine *DGAT1*, *FASN*, *SCD1* and *ACAA2* genes with milk fat percentage and fatty acid (FA) content. Three consecutive monthly milk samplings were obtained from a total of 429 purebred Chios ewes during mid-lactation. Genotypic data were jointly analyzed with 1,184 fat content and 37,718 FA percentage records using mixed models. The 3' untranslated region (UTR) of the *DGAT1* gene and the 5' and 3'UTRs of the *SCD1* gene appeared to be monomorphic. The *FASN* g.14777C>T SNP on exon 31 was associated with C13:0 and the *ACAA2* g.2982T>C SNP on the 3'UTR was associated with C9:0, C11:0, C12:1 *cis*-9, C13:0 and the ω 6/ ω 3 index, while fat percentage was not affected by the identified SNPs. The results could be useful for breeding programs aiming to improve the quality and nutritional value of ovine milk.

Impact of industrial cream heat treatments on the protein composition of the milk fat globule membrane

Steffen F. Hansen, Bjørn Petrat-Melin, Jan T. Rasmussen, Lotte B. Larsen and Lars Wiking
Denmark

Abstract

The impact of cream processing on milk fat globule membrane (MFGM) was assessed in an industrial setting for the first time. Three creams and their derived MFGM fractions from different stages of the pasteurisation procedure at a butter dairy were investigated and compared to a native control as well as a commercial MFGM fraction. The extent of cross-linking of serum proteins to MFGM proteins increased progressively with each consecutive pasteurisation step. Unresolved high molecular weight aggregates were found to consist of both indigenous MFGM proteins and β -lactoglobulin as well as α _{s1}- and β -casein. With regards to fat globule stability and

in terms of resistance towards coalescence and flocculation after cream washing, single-pasteurized cream exhibited reduced sensitivity to cream washing compared to non- and double-pasteurized creams. Inactivation of the agglutination mechanism and the increased presence of non-MFGM proteins may determine this balance between stable and non-stable fat globules.

Evaluation of *Mycobacterium smegmatis* as indicator of the efficacy of high hydrostatic pressure and ultra- high pressure homogenization treatments for pasteurization-like purposes in milk

Rita M. Velázquez-Estrada, Tomás J. López-Pedemonte, María Manuela Hernández-Herrero and Artur Xavier Roig-Sagués

Mexico, Uruguay and Spain

Abstract

The objectives of this study were: to assess the efficiency of high hydrostatic pressure or ultra-high pressure homogenization against *Mycobacterium smegmatis* in milk and to discuss whether *M. smegmatis* can be considered a suitable surrogate for other *Mycobacterium* spp. in high pressure inactivation trials using milk. Three strains of this specie (CECT 3017, 3020 and 3032) were independently inoculated into both skimmed (0.2% fat) and whole milk (3.4 % fat) at an approximate load of 6.5 Log CFU/ml and submitted to HHP treatments at 300, 400 or 500 MPa for 10 minutes at 6 °C and 20 °C. Evolution of the surviving cells of the inoculated strains was evaluated analysing milk immediately after the treatments and after 5 and 8 days of storage at 6 °C. HHP treatments at 300 MPa were seldom efficient at inactivating *M. smegmatis* strains, but lethality increased with pressure applied in all cases. Generation of sub-lethal injured cells was observed only after 400 MPa treatments since inactivation at 500 MPa was shown to be complete. Significant differences were not observed due to either temperature of treatment or fat content of milk, except for strain CECT3032, which was shown to be the most sensitive to HHP treatments. Milk inoculated with strain CECT3017 was submitted to ultra-high pressure homogenization (UHPH) treatments at 200, 300 and 400 MPa. Maximum reductions were obtained after 300 and 400 MPa treatments, although less than 3.50 Log CFU/ml were inactivated. UHPH did not cause significant number of injured cells. Surviving *M. smegmatis* cells were also able to increase counts in milk during the subsequent cold storage at 6 °C. The usefulness of this species as a marker for pressure-based processing seems limited since it showed greater sensitivity than some pathogenic species including other *Mycobacteria* reported in previous studies.

Comparative experiments of electrical conductivity from whey protein concentrates conventional film and nanofibril film

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China

Abstract

We compared the electrical conductivity from two different aggregates of whey protein concentrates (WPC) film: conventional amorphous aggregation at natural pH (pH 6.5) and amyloid fibrils at a low pH (pH 2.0) far away from the isoelectric point. The two types of film fabricated by these solutions with different aggregate structures showed large variations in electrical

conductivity and other properties. The WPC fibril film (pH 2.0) exhibited higher electrical conductivity than that of the conventional WPC film (pH 6.5), improved mechanical properties and oil resistance, due to varying morphology, higher surface hydrophobicity and more (absolute value) surface charge of film-forming solutions. The evidence from this study suggests that fibrilized WPC with high-ordered and β -sheets-rich structures fabricated high electrical conductivity film, which broadens the potential application of fibrils as functional bio-nanomaterials.

Technological properties of indigenous *Lactococcus lactis* strains isolated from Lait caillé, a spontaneous fermented milk from Burkina Faso

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Burkina Faso and Denmark

Abstract

The experiments reported in this research paper aimed to determine the technological properties of indigenous *Lactococcus lactis* strains isolated from Lait caillé, a spontaneous fermented milk, from the perspective of starter culture development. Fermentations were conducted to determine the acidification patterns. Theropy character, growth in 0.04 g/ml NaCl and citrate metabolism were additionally tested. Furthermore, the rheological properties of samples from selected strains and the impact of cold storage were evaluated. Based on the rate of acidification, the indigenous strains were divided into 2 groups depending on their fermentation time, i.e. 10-13 h (fast acidifier), and up to 72 h (slow acidifier), respectively. The physiological tests suggested that most of these strains produced exopolysaccharides but none could ferment citrate. The flow properties of the samples inoculated by the fast acidifier strains showed a time-dependant shear thinning behaviour, while their viscoelastic properties corresponded structurally to those of weak gels. Cold storage decreased the viscosity and CFU counts for most of the indigenous strains tested. This study is a step towards the definition of starter cultures for African spontaneous fermented milks such as Lait caillé.

***Penicillium commune* affects textural properties and water distribution of hard and extra-hard cheeses**

Miguel Jurado and Carlos Javier Vicente

Spain

Abstract

We analysed the effects of growth of *Penicillium commune*, one of the most frequent fungal species associated with cheese, on the water diffusion and texture of hard and extra-hard cheeses. A total of 36 hard cheese blocks and 36 extra-hard cheese blocks were manufactured, salted at different levels (0.5, 1.25 and 2% w/w), and assigned to different treatments (control and inoculated). Cheese texture was analysed using a penetration needle probe at 2 and 5 weeks after ripening. Firmness, defined as the maximum force detected in the penetration probe, was higher in both hard and extra-hard inoculated cheese blocks compared with the control. In addition, the

presence of fungal growth on cheese rind increased the total work of penetration (a measure of resistance to probe penetration), but only in extra-hard cheeses, suggesting that the moisture of cheese might be affecting the growth capacities and performance of *P. commune*. The change in textural properties of cheeses was linked to desiccation of the upper 0.5-cm rind layer mediated by *P. commune*.

A comparative study of extraction techniques for maximum recovery of β -galactosidase from the yogurt bacterium *Lactobacillus delbrueckii ssp. bulgaricus*

Rabin Gyawali, Ayowole Oyeniran, Tahl Zimmerman, Sulaiman O. Aljaloud, Albert Krastanov, and Salam A. Ibrahim

USA, Saudi Arabia and Bulgaria

Abstract

The study reported in this Research Communication evaluates the chemical (solvents) and mechanical (sonication, bead-beater) extraction methods to determine the maximum recovery of β -galactosidase from *L. bulgaricus* spp. Among all extraction techniques, sonication-assisted extraction yielded the highest amounts of enzyme activity (between 1892-2156 Miller Units) in cell-free extract (supernatant). Interestingly, solvent extracted enzyme activities were found to be very low (between 83-153 Miller Units) in supernatant. SDS-polyacrylamide gel electrophoresis and the total protein determination showed that mechanical methods can completely lyse the cells. Our results thus demonstrated that the mechanical extraction method of sonication is the best one for recovering the maximum amount of lactase from *L. bulgaricus* strains.

Isolation of κ -casein glycomacropeptide from bovine whey fraction using food grade anion exchange resin and chitin as an adsorbent

Takuo Nakano* and Mirko Betti

Canada

Abstract

Bovine κ -casein glycomacropeptide (GMP) found in cheese whey is a sialylated phosphorylated peptide which is thought to be a potential ingredient for functional food as well as dietetic food. This study was undertaken to determine whether high purity GMP can be isolated from soluble whey fraction (SWF) using column chromatography on food grade anion exchange resin and chitin as an adsorbent. Samples of commercially available anion exchange resin (resin A, resin B and resin C) and those of chitin (chitin A, chitin B and chitin C) were examined in this experiment. The GMP fraction obtained from each column was analyzed for amino acid composition which reflects the purity of the peptide. Major findings for commercial anion exchange resin were that: 1) the proportion of GMP monitored as sialic acid in total recovered sialic acid was similar among the three samples of resin accounting for average 78% of recovered sialic acid; 2) the GMP fraction from resin A or resin B contained undetectable level of contaminating amino acids including phenylalanine, histidine, arginine and tyrosine; 3) the GMP fraction from resin C contained small amounts (< 1 mol%) of contaminating amino acids, arginine, phenylalanine and tyrosine; and 4) the GMP binding capacity expressed as mg/100 mg dry weight of resin was more than 2.5 times

higher in resin C (average 22.9) than in resin A or resin B with no difference between resin A and resin B averaging 8.7. Results obtained for chitin A, chitin B and chitin C were in general similar to those found with resin A and resin B. Since chitin has a remarkable GMP binding capacity averaging 8.6 mg/100 mg dry weight of chitin, it may be a useful adsorbent for whey fractionation. Further research is needed to develop an efficient inexpensive method to purify GMP.

Effect of fermented whey with a probiotic bacterium on gut immune system

Gisela García, María Emilia Agosto, Lilia Cavaglieri and Cecilia Dogi

Argentina

Abstract

The aim of the work presented in this Research Communication was to evaluate the effect of fermented whey (FW) with *L. rhamnosus* RC007 in a mice model. BALB/c mice were divided into three groups: control group: animals received orally 0.1 ml of phosphate buffered saline (PBS); FW group: animals received orally 0.1 ml of FW; whey (W) group: animals received orally 0.1 ml of W without fermentation with probiotic bacterium. After 10 days mice were sacrificed. Small intestines were collected for determination of IL-10; IL-6, TNF α , goblet cells and intraepithelial lymphocytes. Increases of all the cytokines assayed were observed in mice that received FW compared to control and W group. The ratio between the anti and pro-inflammatory cytokines (IL-10/TNF α) increased in the group of mice that received FW. The number of goblet cells and intraepithelial lymphocytes were also increased in animals that received FW. The results showed that FW with *L. rhamnosus* RC007 was able to stimulate and to modulate mouse immune system. Whey fermented by this probiotic bacterium is an interesting alternative for development of a new food additive for pig production, taking advantage of the beneficial properties of probiotic bacterium and the nutritional properties of whey.

Book review: Microbiology and Technology of Fermented Foods

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USA

The second edition of Microbiology and Technology of Fermented Foods edited by Robert W Hutkins was recently published by Wiley Blackwell (Hutkins, 2019). As a research faculty in food science, I work with undergraduate assistants in food microbiology. It is critical to provide these students with a valuable and updated reference that helps them to understand the basic concepts of fermentation technology. Most of the current textbook content and references on the topic of fermentation are highly technical with a complex content presentation style that necessitates advanced knowledge of food microbiology. As an instructor in food microbiology, I too have often found the topic of food fermentation to be somewhat frustrating to teach. Making this course content interesting and relevant has always been a challenge, especially with regard to students who are coming from a non-food science background. In addition, I have noticed that within the food microbiology curriculum, the topic of fermentation seems to receive less attention than food safety and pathogens or probiotics.

While many food science programs offer courses in microbiology and fermented foods, no recently published texts exist that fully address the subject. Food fermentation professionals and researchers have also lacked a single book that covers the latest advances in biotechnology, bioprocessing, and a foundation in microbial genetics, physiology, and taxonomy.

The first edition of *Microbiology and Technology of Fermented Foods* was published in 2006 with 473 pages consisting of 12 chapters of comprehensive information related to fermentation and the technology of fermented food products. Recently, a second edition was published with a total of 15 chapters. In the preface to the second edition, the author clearly states that the updated edition is intended to serve multiple purposes. For example, the second edition is written primarily at a level suitable for use as a textbook for an upper division or graduate course. However, the book can also serve as a general reference for researchers and scientists in the field of food fermentation.

Letter to the Editor: Controlling the spread of Bovine Digital Dermatitis

Gareth J Staton, Amy Gillespie, Nicholas J Evans, Roger Blowey and Stuart D Carter

UK

To the Editor,

Bovine digital dermatitis (BDD) is a major infectious cause of lameness in both beef and dairy cattle worldwide, with significant welfare and economic implications. Pathogenic spirochetes belonging to the genus *Treponema* are highly associated with the BDD lesion and are considered essential to its aetiology. BDD transmission routes have yet to be fully defined, although transmission via unsterilized foot trimming equipment, and in particular, trimming blades, is supported by epidemiological data: Wells *et al.* (1999) demonstrated that a failure to clean trimming blades between cows was associated with a high (>5%) herd incidence of BDD (Odds Ratio 1.9). Recent research undertaken by our group has demonstrated that blades used to trim BDD-symptomatic feet readily become contaminated with the BDD-associated treponeme DNA and cultivatable cells (Sullivan *et al.*, 2014). Moreover, we have shown that under aerobic conditions, treponeme viability on foot trimming blades is maintained for up to two hours (Gillespie *et al.*, 2019), which may facilitate both intra- and inter-herd transmission. To mitigate the risk of BDD transmission via this route, disinfection of the foot trimming blades should be considered.

Previously, an *in vitro* evaluation of several footbath disinfectants against a BDD treponeme isolate (*Treponema phagedenis*-like) revealed that the minimum inhibitory concentrations and minimum bactericidal concentrations remained below working disinfectant concentrations (Hartshorn *et al.*, 2013). In addition, this activity persisted despite up to 20% manure contamination, implying that effective concentrations could be achieved practically on farm. Recently, we investigated the disinfection efficacy of popular disinfectants against BDD-associated treponemes on foot trimming blades *in vitro* and demonstrated that a 20 second contact with 1% FAM[®]30, 2% Virkon[®] or 2% sodium hypochlorite rendered treponemes non-viable (Gillespie *et al.*, 2019), effectively eliminating the potential for transmission.

With these data, we have developed a standardised blade disinfection protocol which we recommend as part of a holistic approach to BDD infection control. The disinfection protocol, to be applied during foot trimming, is available online at: <https://ahdb.org.uk/reducing-spread-of-DD>