

COLLECTED ABSTRACTS

Editorial: Quality and choice: Aim high, don't muddle through!

Chris Knight

UK

The Journal of Dairy Research does not just aim to succeed, rather, it has success as an objective. If this sounds contradictory, it is because an objective is a tangible and definable outcome, whereas an aim is variously an action (to aim) or an object (the thing you are aiming at). As with much of the English language, there is muddle. Furthermore, aiming and missing does not mean that you did not aim! Has the Journal achieved success? For the second consecutive year our Impact Factor has increased, our community continues to grow and we have a very high rate of returning authors. Importantly, our submission rate has never been higher, whilst our Peer Review time has never been shorter. So yes, I would say that we have achieved our objectives and are succeeding. Are there things we could do better? Undoubtedly, but then that is the nature of success, it requires continuing improvement. Our next set of objectives include making Open Access publication more available without compromising our free-to-publish credentials, improving the services we offer to students and non-native English speaking researchers and increasing our collaboration with relevant international bodies such as the International Dairy Federation. Our overall objective is to combine quality (of research) and choice (of publication route). As part of that, I will include persuading our authors to have objectives rather than simply to aim, and if they insist on aiming, they must aim high.

Whatever happened to mastitis pathogenesis?

J Eric Hillerton

New Zealand

Abstract

We have learned a lot about infections of the mammary gland of dairy cows from experimental investigations of the pathogenesis of the various diseases. The understanding gained has contributed to huge successes in reducing the prevalence of infection in properly managed dairy herds. Now descriptive studies using DNA technologies reject previous concepts of mammary gland sterility by default. Bacteria, at least markers of genes, of many genera are reported even from absolutely healthy mammary glands. This may be a technical artefact. No direct evidence exists because experimental studies of infection are no longer fashionable. A regeneration of the lost arts in the pathogenesis of infection is essential to separate truth from conjecture and deal with coming challenges from rapidly changing farm systems and the reduction in access to antimicrobial drugs. In this Opinion Paper I shall argue for a return to experimental approaches that construct hypotheses, and then test them, in intramammary disease research.

Streptococcus spp. from bulk-tank milk and milking machine teatcups on small ruminant farms, and factors potentially associated with their isolation

Dimitris C. Chatzopoulos, Daphne T. Lianou, Charalambia K. Michael, Dimitris A. Gougoulis, Vasia S. Mavrogianni, Natalia G.C. Vasileiou, Angeliki I. Katsafadou, Antonis P. Politis, Nikos G. Kordalis, Eleni I. Katsarou, Katerina S. Ioannidi, Efthimia Petinaki and George C. Fthenakis

Greece

Abstract

The objectives of this work were (a) to determine the presence of streptococci in samples from small ruminant dairy farms (bulk-tank milk and, where possible, teatcup swabs), (b) to investigate the potential adverse effects of streptococci on milk quality and (c) to investigate the importance of some husbandry factors for the isolation of streptococci. Bulk-tank milk samples and teatcups swab samples were examined bacteriologically for the presence of streptococci. Somatic cell counting and milk composition measurements were also performed. The husbandry factors present in each farm were assessed for potential associations with the isolation of streptococci. Streptococci were isolated from milk samples from 31.4% of sheep and 17.4% of goat farms and from 4.8% of sheep and 5.9% of goat teatcups. Streptococci were isolated more frequently from the upper part than the lower part of teatcups: 5.0% *versus* 1.9%. Most isolates (57.9%) were identified as *Streptococcus uberis*. Most isolates (68.4%) were slime-producing; slime-production was more frequent among isolates from teatcups (83.3%) than from bulk-tank milk (55.0%). Somatic cell counts and milk composition did not differ between farms in which streptococci were or were not isolated. Machine-milking was associated with the isolation of streptococci from bulk-tank milk samples. The initial stage of the milking period (first two months) was found to be associated with the isolation of streptococci from milking machine teatcups in sheep farms only.

Modeling cow somatic cell count using sensor data as input to generalized additive models

Dorota Anglart, Charlotte Hallén-Sandgren, Patrik Waldmann, Martin Wiedemann and Ulf Emanuelson

Sweden and Germany

Abstract

This research paper presents a study investigating if sensor data from an automatic milking rotary could be used to model cow somatic cell count (CMSCC). CMSCC is valuable for udder health monitoring and individual cow udder health surveillance could be improved by predicting CMSCC between routine samplings. Data regularly recorded in the automatic milking rotary, in one German dairy herd, were collected for analysis. The cows (Holstein-Friesian, n=372) were milked twice daily and sampled once weekly in afternoon milkings for 8 weeks for CMSCC. From the potential independent variables, including quarter conductivity, milk flow, blood in milk, kick-offs, not milked quarters and incomplete milkings, new variables that combined quarter data were created. Past period records, i.e. lags, of up to seven days before the actual CMSCC sampling event were added in the dataset to investigate if they were of use in modelling the cell count. Univariable generalized additive models (GAM) were used to screen the data to select potential independent variables. Furthermore, several multivariable GAM were fitted in order to compare the importance of the potential independent variables and to explore how the model performance would be affected by

using data from various number of days before the CMSCC sampling event. The result of the model selection showed that the best explanation of CMSCC was provided by the model incorporating all significant variables from the variable screening for the seven preceding days, including the day of the CMSCC sampling event. However, using data from only three days before the CMSCC sampling event is suggested to be sufficient to model CMSCC. Variables combining conductivity quarter data, together with quarter conductivity, are suggested to be important in describing CMSCC. We conclude that CMSCC can be modeled with a high degree of explanation using the information routinely recorded by the milking robot.

Antimicrobial resistance profile of non-aureus *Staphylococci* isolates from buffalo, goat and sheep mastitis in the Northeast region of Brazil

André de Souza Santos, Débora Costa Viegas de Lima, Atzel Candido Acosta Abad, Pollyanne Raysa Fernandes de Oliveira, José Givanildo da Silva, Guilherme Santana de Moura, Amanda Thaís Ferreira Silva, Vinícius da Silva Amorim, Mateus Matiuuzzi da Costa and Rinaldo Aparecido Mota

Brazil

Abstract

The study described in this Research Communication investigated the genotypic and phenotypic profiles of resistance to beta-lactams and other antimicrobials in non-aureus *Staphylococci* (NAS) isolated from buffalo, goat and sheep mastitis in the Northeast region of Brazil. A total of 190 isolates were analyzed and 42.3%, 43.9% and 23.6% of them were positive for *blaZ* gene in buffalo, goat and sheep, respectively. Regarding the animal groups, in goats, amoxicillin was the antimicrobial with highest resistance index (72.7%), followed by penicillin G in buffaloes (51.9%) and ampicillin in sheep (43.1%). With regard to multiple antimicrobial resistance, 30.8% of NAS isolates from buffalo milk samples, 25.8% from goats and 25.0% from sheep presented multidrug-resistance. In the minimum inhibitory concentration (MIC) technique, amoxicillin MIC₅₀ and MIC₉₀ were 64 and 128 ug/mL, respectively, among isolates of the three animal species. In conclusion, high rates of resistance to beta-lactams are presented among NAS isolated from mastitis cases in buffaloes, goats and sheep in Northeast region of Brazil. These results provide an alert to animal and human health researchers, suggesting that the frequency of NAS needs to be reduced because they carry resistance genes which might increase the existing levels of antimicrobial resistance

Timing of entry of *Streptococcus uberis* into the mammary gland of the dairy cow.

J Eric Hillerton

New Zealand

Abstract

Streptococcus uberis do not colonise the teat canal and appear to invade the mammary gland of the dairy cow by direct entry through the canal. When they enter the mammary gland, and the early resulting processes, are unclear. Experimental infusions of the lactating mammary gland have been made to determine outcomes of infection, mastitis and disease. Infusion of 500 cfu bacteria was made immediately after milking (8 and 16 h intermilking interval) and 1, 4 or 12 h prior to milking. A mastitis resulted from all infusions, probably in response to the skim milk carrier. Infusions post

milking resulted in clinical mastitis in more than half of the quarters, whereas infusion 1 h pre milking created no clinical mastitis. Infusion 4 or 12 h pre milking resulted in the most severe reactions, with all quarters developing moderate to severe clinical mastitis. This was more rapid with the 4 h pre milking group. The results demonstrate that the initial inflammatory response caused by an invasion of the mammary gland is not necessarily protective against establishment of a pathogen, and that especially the response to invasion in the intermilking interval is often insufficient to prevent infection and/or disease.

Chronic subclinical mastitis reduces milk and components yield at the cow level

Larissa Martins, Melina Melo Barcelos, Roger I. Cue, Kevin L. Anderson, Marcos Veiga dos Santos and Juliano Leonel Gonçalves

Brazil, Canada and USA

Abstract

We evaluated the effects of chronic subclinical mastitis (CSM) caused by different types of pathogens on milk yield and milk components at the cow level. A total of 388 Holstein cows had milk yield measured and were milk sampled three times at intervals of two weeks for determination of SCC and milk composition, and microbiological culture was performed. Cows were considered healthy if all three samples of SCC were $\leq 200,000$ cells/mL and had culture-negative at the third milk sampling. Cows with one result of SCC $> 200,000$ cells/mL were considered to suffer non-chronic subclinical mastitis whereas cows with at least 2 out of 3 results of SCC $> 200,000$ cells/mL had CSM. These latter cows were further sorted according to culture results into chronic negative-culture or chronic positive-culture. This resulted in four udder health statuses: healthy, non-chronic, chronicNC or chronicPC. The milk and components yields were evaluated according to the udder health status and by pathogen using a linear mixed effects model. A total of 134 out of 388 cows (34.5%) were chronicPC, 57 cows (14.7%) were chronicNC, 78 cows (20.1%) were non-chronic and 119 cows (30.7%) were considered healthy, which resulted in a grand total of 1,164 cow records included in the statistical model. The healthy cows produced more milk than each of the other groups (+2.1 to +5.7 kg/cow.day) and produced higher milk component yields than the chronicPC cows. The healthy cows produced more milk than cows with chronicPC caused by minor (+5.2 kg/cow.day) and major pathogens (+7.1 kg/cow.day) and losses varied from 5.8 to 11.8 kg/cow.day depending on the pathogen causing chronicPC mastitis. Chronic positive-culture cows had a reduction of at least 24.5% of milk yield and 22.4% of total solids yield.

Detection of clinical bovine mastitis caused by *Mycoplasma bovis* in Brazil

Nathália Brancato Junqueira, Anelise Salina, Gabriela Capriogli Oliveira, Elena Mettifogo, Sâmea Fernandes Joaquim, Felipe Freitas Guimarães, Felipe Morales Dalanezi and Helio Langoni

Brazil

Abstract

The work reported in this research communication investigated the occurrence of *Mycoplasma bovis* (*M. bovis*) in milk samples from cows with clinical mastitis on dairy farms from seven Brazilian states. We hypothesized that *M. bovis* was present in bovine clinical mastitis milk in Brazil. A total

of 561 milk samples were cultured on Hayflick agar and incubated in a microaerophilic atmosphere at 5% CO₂. Polymerase chain reaction (PCR) was performed for the detection of *Mycoplasma* spp. and *Mycoplasma bovis* in milk samples. *Mycoplasma* spp. were isolated in 2% of the milk samples, and *Mycoplasma bovis* was verified in 3% of the milk samples by PCR. The results showed that *Mycoplasma bovis* is involved in clinical mastitis in Brazilian dairy herds. We emphasize the need for further studies to investigate the infection by this agent in clinical mastitis cases, particularly in Brazil, due to the lack of knowledge about its prevalence.

Antimicrobial activity of polypyrrole nanoparticles and aqueous extract of *Moringa oleifera* against *Staphylococcus* spp. carriers of multi-drug efflux system genes isolated from Brazilian dairy farms

José Givanildo da Silva, Mariana de Barros, Nataly Diniz de Lima Santos, Patrícia Maria Guedes Paiva, Thiago Henrique Napoleão, Maria José de Sena, Mateus Matiuzzi da Costa, Helinando Pequeno de Oliveira, Maria Aparecida Scatamburlo Moreira and Rinaldo Aparecido Mota

Brazil

Abstract

Our objectives were to identify genes of the multi-drug efflux system and to evaluate the antimicrobial activities of polypyrrole nanoparticles (PPy-NPs) and aqueous extract of *Moringa oleifera* against *Staphylococcus* spp. isolated from dairy farms in Northeast Brazil. Initially, 162 *Staphylococcus* spp. isolates were subjected to *in vitro* antimicrobial sensitivity tests. Of these, 35 presented antimicrobial multi-drug resistance phenotypes. These 35 isolates were then referred for the detection of *norA*, *norB*, *norC*, *msrA*, *mgrA*, *tet-38*, and *ImrS* genes, all of which feature in multi-drug efflux systems. In the isolates carrying the genes, the minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) of PPy-NPs and *Moringa oleifera* aqueous extract were determined. In the molecular analysis of the 35 isolates *norA*, *norC*, *tet-38*, and *msrA* genes were detected and for the other genes *norB*, *ImrS* and *mgrA* there was no amplification. Antimicrobial activity was verified of PPy-NPs and aqueous extract *Moringa oleifera* in *Staphylococcus* spp. carrying multi-drug efflux system genes. We concluded that there are multi-drug efflux system genes present in the *Staphylococcus* spp. from this agricultural environment. Aqueous extract of *Moringa oleifera* and PPy-NPs both showed bactericidal activity against the *Staphylococcus* isolates tested.

Effect of heat stress on udder health of dairy cows

Md Rezaul Hai Rakib, Man Zhou, Siyu Xu, Yang Liu, Muhammad Asfandyar Khan, Bo Han and Jian Gao

China

Abstract

This short review presents an overview of the effects of heat stress on dairy cattle udder health and discusses existing heat stress mitigation strategies for a better understanding and identification of appropriate abatement plans for future stress management. Due to high ambient temperatures with high relative humidity in summer, dairy cows respond by changes of physical, biochemical and

biological pathways to neutralize heat stress resulting in decreased production performance and poorer immunity resulting in an increased incidence of intramammary infections (IMI) and a higher somatic cell count (SCC). In vitro studies on bovine polymorphonuclear cells (PMN) suggested that heat stress reduces the phagocytosis capacity and oxidative burst of PMN and alters the expression of apoptotic genes and miRNA which, together with having a negative effect on the immune system, may explain the increased susceptibility to IMI. Although there are limited data regarding the incidence rate of clinical mastitis in many countries or regions, knowledge of SCC at the cow or bulk tank level helps encourage farmers to improve herd health and to develop strategies for infection prevention and cure. Therefore, more research into bulk tank SCC and clinical mastitis rates is needed to explain the effect of heat stress on dairy cow udder health and functions that could be influenced by abatement plans.

Invited Review: Ruminal epithelium: a checkpoint for cattle health

Lisa Baaske, Gotthold Gäbel and Franziska Dengler

Germany

Abstract

The reticulorumen, as the main fermentation site of ruminants, delivers energy in the form of short-chain fatty acids (SCFA) for both the animal as well as the ruminal wall. By absorbing these SCFA, the ruminal epithelium plays a major role in the maintenance of intraruminal and intraepithelial acid-base homeostasis as well as the balance of osmolarity. It takes up SCFA via several pathways which additionally lead to either a reduction of protons in the ruminal lumen or the secretion of bicarbonate, ultimately buffering the ruminal content effectively. Nutrition of the epithelium itself is achieved by catabolism of the SCFA, especially butyrate. Catabolism of SCFA also helps to maintain a concentration gradient across the epithelium to ensure efficient SCFA uptake and stability of the epithelial osmolarity. Furthermore, the ruminal epithelium forms a tight barrier against pathogens, endotoxins or biogenic amines, which may emerge from ruminal microorganisms and feed. Under physiological conditions, it reduces toxin uptake to a minimum. Moreover, the epithelium seems to have the ability to degrade biogenic amines like histamine. Nonetheless, in high performance production animals like dairy cattle, the reticulorumen is confronted with large amounts of rapidly fermentable carbohydrates. This may push the epithelium to its limits, even though it possesses a great capacity to adapt to varying feeding conditions. If the epithelial limit is exceeded, increasing amounts of SCFA lead to an acidotic imbalance that provokes epithelial damage and thereby elevates the entrance of pathogens and other potentially harmful substances into the animal's body. Hence, the ruminal epithelium lays the foundation for the animal's health, and in order to ensure longevity and high performance of ruminant farm animals, it should never be overburdened.

Genetic analysis of persistency indices of milk yield in Jersey crossbred cattle

Subrata Koloi and Ajoy Mandal

India

Abstract

The study reported in this Research Communication was conducted to estimate genetic parameters for different lactation persistency indices and their association with reproductive traits in Jersey crossbred cattle. Data on lactation traits (part lactation yields and 305-days milk yield) comprising all lactations as well as reproductive traits viz. calving interval, conception rate and gestation length of 378 Jersey crossbred cattle, maintained at National Dairy Research Institute, West Bengal, India, were collected over a period of 35 years (1982-2016). Five lactation persistency indices of animals (P_{21} , P_{31} , P_{32} , P_4 and P_5) were calculated using ratio method. A total of six different animal models, ignoring or including maternal genetic or permanent environmental effects, were fitted for all persistency traits. The best model was chosen after testing the improvement of the log-likelihood values. The estimates of direct heritability were low in magnitude and ranged from 0.02 to 0.14 for the studied traits under the best fitted animal model. The permanent maternal environmental (c^2) effects of different lactation persistency indices accounted for 2-9% of the total phenotypic variance in this study. Estimated genetic correlations of lactation persistency indices with all studied reproductive traits were low to moderate and negative (-0.11 to -0.68), except for calving interval. Phenotypic correlations of lactation persistency measures with studied reproductive traits were low (0.01 to 0.15). The low heritability estimates of all the persistency indices indicate some limited scope of genetic improvement of lactation persistency of animals through selection under the prevailing management conditions.

Effect of feeding hay vs. silages of various types to dairy cows on feed intake, milk composition and coagulation properties

Elisa Manzocchi, Werner Hengartner, Michael Kreuzer and Katrin Giller
Switzerland

Abstract

This research paper addresses the hypotheses (1) that milk produced from hay-fed cows differs from that of silage-fed cows and (2) that silage type has an important impact, too. Four diets differing in forage type but with equal estimated milk production potential and a forage:concentrate ratio of 0.85:0.15 were compared regarding their effect on feed intake, milk yield and milk properties. The forages tested were hay, grass silage, conventional short-chopped and long-chopped maize silage subjected to a novel processing technology (Shredlage®). Twenty-four dairy cows were fed two of the four diets in two consecutive runs in an incomplete (4×2) Latin-square design ($n = 12$ per diet). Each experimental period lasted 22 days, with 12 days of adaptation and 10 days of sampling. During sampling, feed intake and milk yield were recorded daily, milk composition and coagulation properties were determined four times. The composition of the diet ingredients was analysed weekly. Data were analysed with a mixed model considering feed, period and their interaction as fixed effects. Stage of lactation, milk yield and milk composition from the pre-experimental period were used as covariates in the model. Dry matter intake was lower with the long-chopped processed maize silage compared to the other three groups. There were some diet differences in intakes of net energy for lactation and absorbable protein in the duodenum, but this did not result in changes in milk yield. The milk fat content was higher with the grassland-based diets compared to the maize silage diets. No treatment effect on milk acidity and rennet coagulation properties was observed. In conclusion, there were no indications for specific physico-chemical properties of milk from a hay-

based diet, and maize processing technology was not of large effect either. Future investigations should focus on sensory differentiation of the milk produced with different forages.

Predicting milk yield in Pelibuey ewes from the udder volume measurement with a simple method

Roger Iván Espinosa-Mendoza, Darwin Nicolas Arcos-Álvarez, Ricardo Alfonso Garcia-Herrera, Gamaliel Antonio-Molina, Ricardo Vicente-Pérez, Ulises Macias-Cruz, Manuel González Ronquillo, Augusto C Lizarazo Chaparro and Alfonso J Chay-Canul

Mexico

Abstract

In this research communication we describe the creation of an equation for the prediction of milk yield (MY) from udder volume (UV). A total of 280 measurements were collected between 5 and 15 d postpartum (pp) from 36 multiparous Pelibuey ewes. Study variables were measured between 2 and 9 weeks pp and MY was measured by manual milking, UV prior to and following milking was measured using the technique of making moulds from aluminium foil. The MY ranged from 0.09 to 0.83 kg/d, meanwhile UV prior and following milking ranged from 155 to 1940 and 90 to 1520 cm³, respectively. Measurements of UV had a moderate to high ($P < 0.01$; $0.58 \leq r \leq 0.78$) correlation with MY. The UV prior to milking was the best prediction model for MY, which explained 62 % of the variation in MY. This equation presented moderate precision ($r^2 = 0.61$) and high accuracy (bias correction factor = 0.94), confirming a good reproducibility index (concordance correlation coefficient = 0.73). Modeling efficiency (MEF = 0.59) showed moderate concordance between observed and predicted values. In conclusion, MY in lactating Pelibuey ewes could be predicted in a moderate way using the predictor variable UV measured with the technique of moulds made with aluminium foil.

Effects of exogenous C18 unsaturated fatty acids on milk lipid synthesis in bovine mammary epithelial cells

Hang Zhang, Ni Dan, Changjin Ao, Sizhen Wang, Khas-Erdene and Mohammed Umair Ashraf

China

Abstract

We determined the effects of a combination of C18 unsaturated fatty acids (C18-UFAs) consisting of oleic, linoleic, and linolenic acids on milk lipogenesis in bovine mammary epithelial cells (BMECs). By orthogonal experiments to determine cellular triacylglycerol (TAG) accumulation, a combination of 200 $\mu\text{mol/L}$ C18:1, 50 $\mu\text{mol/L}$ C18:2, and 2 $\mu\text{mol/L}$ C18:3 was selected as C18-UFAs combination treatment, and culture in medium containing fatty acid-free bovine serum albumin was used as the control. The expression of genes related to milk lipid synthesis and intracellular FA composition was measured. The results showed that cytosolic TAG formation was higher under C18-UFAs treatment than under control treatment. The mRNA expression of acetyl-CoA carboxylase- α (*ACACA*), fatty acid synthase (*FASN*), and peroxisome proliferator-activated receptor gamma (*PPARG*) did not differ between treatments. The abundance of stearoyl-CoA desaturase (*SCD*) and acyl-CoA synthetase long-chain family member 1 (*ACSL1*) was higher, whereas that of sterol regulatory element binding transcription factor 1 (*SREBF-1*) was lower after C18-UFAs treatment compared to control

treatment. The C16:0 and SFA content was decreased following C18-UFA treatment compared to control treatment, while the *cis*-9 C18:1 and UFA content was increased. In conclusion, C18-UFAs could stimulate triglyceride accumulation, increase the cellular UFA concentration, and regulate lipogenic genes in BMECs.

Effect of *INSIG1* on the milk fat synthesis of buffalo mammary epithelial cells

Xinyang Fan, Lihua Qiu, Xiaohong Teng, Yongyun Zhang and Yongwang Miao

China

Abstract

We hypothesized that insulin-induced gene 1 (*INSIG1*) affects milk fat synthesis in buffalo. For this reason, the protein abundance of *INSIG1* in the mammary tissue of buffalo during the peak period of lactation and dry-off period was evaluated. The results showed that the expression of *INSIG1* at the peak of lactation was lower than that in the dry-off period. To explore the role of *INSIG1* in milk fat synthesis, the buffalo mammary epithelial cells (BMECs) were isolated and purified from buffalo mammary tissue, and *INSIG1* gene were overexpressed and knocked down by constructing the recombinant lentivirus vector of *INSIG1* gene and transfecting into BMECs. Results revealed that *INSIG1* overexpression decreased the expression of *INSIG2*, *SREBP*, *PPARG*, *SCD*, *GPAM*, *DGAT2* and *AGPAT6*, which led to reduction of triglycerides (TAG) content in the cell. In contrast, knockdown of *INSIG1* had a positive effect on mRNA expression of the above genes. Overall, the data provide strong support for a key role of *INSIG1* in the regulation of milk fat synthesis in BMECs.

Colostrum from primiparous Holstein cows shows higher antioxidant activity than colostrum of multiparous ones

Débora B. Moretti, Caroline B. Santos, Severino M. Alencar and Raul Machado-Neto

Brazil

Abstract

Antioxidant components of colostrum prevent oxidative cell damage caused by free radicals that could harm the calf's development. The relationship of antioxidant potential of colostrum with parity is not well defined and could enlighten the importance of these components for the neonate and for the protection of the intestinal epithelium. The purpose of this work was to determine the antioxidant potential of colostrum from primiparous and multiparous Holstein cows in a commercial dairy farm. Samples from the first milk secretion from primiparous (first lactation, n=8) and multiparous (second and third lactations, n=8) Holstein cows were collected after birth of calves for determination of immune and antioxidant factors. The cows sampled in this study were vaccinated during pregnancy in order to improve colostrum quality. Colostrum from primiparous cows showed higher values of ceruloplasmin activity, oxygen radical absorbance capacity (ORAC) and transferrin saturation index (TSI) than colostrum from multiparous cows ($P<0.05$). The total iron binding capacity (TIBC) and transferrin concentration in the colostrum of primiparous cows showed a non-significant numerical decrease ($P=0.06$) in relation to the value in the colostrum of multiparous cows. Concentration of proteins, immunoglobulin G, and activity of lactoperoxidase, lysozyme, glutathione peroxidase and catalase, in turn, did not differ ($P>0.05$). Metabolic differences between

primiparous and multiparous cows may have affected the antioxidative status of colostrum, since ORAC values were twice higher in first lactation cows. Lower values of transferrin and TIBC and higher TSI in colostrum from primiparous cows suggests a relationship between lower iron stock and higher antioxidant activity. Thus, this work indicates an important role of the antioxidant potential of colostrum for neonates from first-lactation cows. Additionally, the iron stock may be directly related to the higher antioxidant potential of the colostrum from primiparous cows, and further investigations are required.

Metataxonomics contributes to unravel the microbiota of a Brazilian dairy

Diego Araújo Frazilio, Otávio Guilherme Gonçalves de Almeida, Carlos Augusto Fernandes de Oliveira, Sarah Hwa In Lee, Carlos Humberto Corassin, Virgínia Farias Alves and Elaine Cristina Pereira De Martinis

Brazil

Abstract

For this research communication, 90 samples of a Brazilian dairy were combined into four groups (raw material, final product, food-contact and non-food contact surfaces) and analysed by metataxonomics based on 16S rRNA gene sequencing. The results showed high alpha-diversity indexes for final product and non-food contact surfaces but, overall, beta-diversity indexes were low. The samples were separated in two main clusters, and the core microbiota was composed by *Macrococcus*, *Alkaliphilus*, *Vagococcus*, *Lactobacillus*, *Marinilactibacillus*, *Streptococcus*, *Lysinibacillus*, *Staphylococcus*, *Clostridium*, *Halomonas*, *Lactococcus*, *Enterococcus*, *Bacillus* and *Psychrobacter*. These results highlight that rare taxa occur in dairies, and this may aid the development of strategies for food protection.

Production of sialic acid rich glycopeptide from bovine κ -casein glycomacropeptide by hydrolyzing with papain

Takuo Nakano and Mirko Betti

Canada

Abstract

Bovine κ -casein glycomacropeptide (GMP) is a sialic acid containing glycopeptide having many biological activities. The study described in this research communication was undertaken to determine whether sialic acid rich glycopeptide can be produced from GMP by proteinase treatment. A sample of GMP was hydrolyzed with papain, and the obtained hydrolysate was chromatographed on a column of diethylaminoethyl-Sephacel to obtain a glycopeptide fraction (GPF). This product accounted for average 48.1% dry weight of GMP or 81.1% total recovered sialic acid from GMP. The content of sialic acid (expressed as % dry weight) was 1.7 times higher in GPF (22.6) than in unhydrolyzed GMP (13.4). Major differences in amino acid composition between GPF and GMP were found in the contents (mol%) of: lysine (< 1 and 4.5, respectively), serine (20.3 and 10.3, approximately twice higher in GPF), asparagine/aspartic acid and isoleucine. The contents of the last two amino acids were approximately twice lower in GPF. On gel filtration chromatography with Sephacryl S-100, GMP was eluted as a single peak with elution volume similar to that of dimeric

β -lactoglobulin (36.6 kDa) whereas GPF was eluted in two peaks both with elution volumes greater than that of α -lactalbumin (14.2 kDa). These peak fractions containing high (fraction I) and low (fraction II) molecular size glycopeptides gave different sialic acid to peptide ratio, which was 1.7 times higher in fraction I than in fraction II. Results of size exclusion HPLC on Superdex-75 were consistent with those of gel filtration chromatography. On cellulose acetate electrophoresis, the mobility of GPF relative to that of GMP as 1.0 was found to average 1.2, suggesting a higher negative charge density in GPF than in GMP. It was concluded that papain digestion of GMP is an efficient method to produce glycopeptide with high sialic acid content.

Identification of *Pseudomonas jessenii* and *Pseudomonas gessardii* as the most proteolytic *Pseudomonas* isolates in Iranian raw milk and their impact on stability of sterilized milk during storage

Mehdi Zarei, Hooriyeh Mohammadpour, Darioush Gharibi and Mahdi Pourmahdi Borujeni
Iran

Abstract

Identification of the most proteolytic *Pseudomonas* strains that can produce heat-resistant proteases and contribute to the Ultra High Temperature (UHT) milk destabilization is of great interest. In the present study, among the 146 *Pseudomonas* isolates that encoded the *aprX* gene, five isolates with the highest proteolytic activity were selected and identified based on 16S rRNA, *rpoD* and *gyrB* gene sequences data. The identification results were confirmed by phylogenetic analysis based on multilocus sequence analysis and identified the representative isolates as *P. jessenii* (two isolates) and *P. gessardii* (three isolates). Casein zymography demonstrated the ability of these species to produce heat-resistant enzymes, AprX, with molecular mass of about 48 kDa during storage at 7 °C for 72 h. In sterilized milk samples, the residual activity of AprX caused a considerable enhancement in the degree of protein hydrolysis, non-protein nitrogen and non-casein nitrogen contents of the samples during a two-month storage. This enhancement was slightly higher in samples containing enzyme produced by *P. jessenii* compared to *P. gessardii* ones, resulting in earlier onset of sterilized milk destabilization. Hence, this study revealed that *P. jessenii* and *P. gessardii* can play a considerable role in deterioration of Iranian commercial long-life milk.

Optimization of spray drying process in microencapsulated cream powder production

Ahsen Burcin Himmetagaoglu, Serap Berktaş, Mustafa Cam and Zafer Erbay
Turkey

Abstract

In this Research Communication we describe the optimisation of spray drying conditions in the production of microencapsulated cream powder. Oil-in-water emulsions were prepared using maltodextrin (18 DE) and sodium caseinate as wall materials (with the total wall material per total solid content ratio of 30%) and then converted into powder by spray drying. Response surface methodology was used to optimize the factors of spray drying system i.e. inlet drying temperature, feed flow rate, and aspiration rate, where the levels were in the range of 150-190 °C, 9-30 mL/min, and 50-100%, respectively. Our objective was to perform spray drying with the highest drying yield

and to obtain a microencapsulated cream powder with the highest bulk density, the shortest wetting time, and the lowest surface fat content. The calculated and validated optimum conditions for the spray drying process were found to be 162.8 °C for inlet drying temperature, 11.51 mL/min for feed flow rate, and 72.8% for aspiration rate. At these optimum conditions, drying yield, bulk density, wettability, and surface fat content values were 36.37%, 269.9 kg/m³, 115.2 s, and 26.2%, respectively.

Effect of fermentation time and acid casein concentration as nitrogen source on microbial rennet production

Héctor A Fileto-Pérez, Luis G. Montoya-Ayón, Esther Soto-García, Jesús B. Páez-Lerma, Nicolás O Soto-Cruz, Blanca E. García-Caballero and José G. Rutiaga-Quiñones

Mexico

Abstract

We evaluated the effects of fermentation time and acid casein content on the microbial rennet obtained by solid-state fermentation using wheat bran as the carbon source. The experiments used two fermentation times (72 and 96 h), while acid casein content was 1.5, 2.0, 2.5, and 3.0 g. Rennet strength from eight enzymatic extracts was measured using pasteurized whole milk. Rennet strength of samples from 72 h of fermentation showed an increase when acid casein content increased. The rennet strength increased at 96 h of fermentation with increasing amount of casein (up to 2.5 g), and then decreased with the largest addition (3.0 g) of casein. Coagulation time for the sample with highest rennet strength was 420 s.

The influence of adaptive stresses on the survival of spray-dried *Lactococcus lactis* cells

Débora C Cnossen, Ramila Cristiane Rodrigues, Evandro Martins, José de Castro Cezarino Junior and Antônio Fernandes de Carvalho

Brazil

Abstract

The research described in this technical research communication examines the hypothesis that sublethal stress conditions can improve the survival of *Lactococcus lactis* subsp. *lactis* during drying and subsequent storage. After drying, the *L. lactis* that had adapted to acid or osmotic stresses did not differ statistically in terms of cell viability loss compared to the control samples tested (~0.38 log cycles). However, the cells that had adapted to oxidative conditions demonstrated a cell viability loss of only 0.01 log cycles. After 45 days of storage at temperatures of 4 and 25 °C, the final *L. lactis* sample populations were shown to be higher (112.5%) when they had been submitted to sublethal conditions of oxidative stress. When the cell samples were exposed to acid stress conditions, they exhibited a viability loss (0.82 log cycles) that was statistically different from the control sample (0.58 log cycles) after 45 days. Osmotic stress conditions did not demonstrate any influence over cell survival rates. Thus, submitting cells to oxidative stress conditions prior to storage has been shown to be a potential strategy for producing dehydrated cultures of *L. lactis* strains that are less sensitive to oxygen exposure.