

Virtually absent

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Genomic prediction and genetic correlations estimated for milk production and fatty acid traits in Walloon Holstein cattle using random regression models

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Abstract

The aims of this study were to: 1) estimate genetic correlation for milk production traits (milk, fat and protein yields and fat and protein contents) and fatty acids (FA: C16:0, C18:1 *cis*-9, LCFA, SFA, and UFA) over days in milk, 2) investigate the performance of genomic predictions using single-step GBLUP (ssGBLUP) based on random regression models (RRM), and 3) identify the optimal scaling and weighting factors to be used in the construction of the H matrix. A total of 302,684 test-day records of 63,875 first lactation Walloon Holstein cows were used. Positive genetic correlations were found between milk yield and fat and protein yield (r_g from 0.46 to 0.85) and between fat yield and milk FA (r_g from 0.17 to 0.47). On the other hand, negative correlations were estimated between fat and protein contents (r_g from -0.22 to -0.59), between milk yield and milk FA (r_g from -0.22 to -0.62), and between protein yield and milk FA (r_g from -0.11 to -0.19). The selection for high fat content increases milk FA throughout lactation (r_g from 0.61 to 0.98). The test-day ssGBLUP approach showed considerably higher prediction reliability than the parent average for all milk production and FA traits, even when no scaling and weighting factors were used in the H matrix. The highest validation reliabilities (r^2 from 0.09 to 0.38) and less biased predictions (b_1 from 0.76 to 0.92) were obtained using the optimal parameters (i.e., $\omega = 0.7$ and $\alpha = 0.6$) for the genomic evaluation of milk production traits. For milk FA, the optimal parameters were $\omega = 0.6$ and $\alpha = 0.6$. However, biased predictions were still observed (b_1 from 0.32 to 0.81). The findings suggest that using ssGBLUP based on RRM is feasible for the genomic prediction of daily milk production and FA traits in Walloon Holstein dairy cattle.

Potential response from selection schemes based on progeny testing and genomic selection for the Chilean dairy cattle under pastoral systems: a deterministic simulation

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Chile and New Zealand

Abstract

Recently a selection index called Valor Económico Lechero (VEL) was developed for Chilean dairy cattle under pasture. However, a specific selection scheme has not yet been implemented. This study aimed to estimate genetic progress from selection on the VEL selection index based on selection schemes using progeny testing (PT) and genomic selection (GS). Under a PT-scheme, estimated genetic progress was 41.50, 3.44, and 2.33 kg/year for milk, fat, and protein yield, respectively. The realised genetic gain takes eight-year after the PT-scheme implementation, which may be a disincentive for implementing a PT-scheme, suggesting that importing frozen semen of proven bulls could be a preferred alternative. In this case, an option may be to conduct the genetic evaluation of those bulls using their progeny in Chile for the traits included in VEL selection index. In the case of implementing a specific selection scheme, compared to PT, a more profitable alternative might be the implementation of a GS-scheme, that would result in a faster genetic gain in the aggregate breeding value or merit for all the traits included in the selection objective (0.323-0.371 vs 0.194 σ_g /year).

Effect of inclusion of bakery by-products in the dairy cow's diet on milk fatty acid composition

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Abstract

Bakery by-products (BP), rich in fats and sugars, are unconventional feed sources for cows whose effects on milk fat composition have not yet been evaluated. This research paper aimed to assess the effects of dietary BP inclusion rate and feeding period on the milk fatty acid composition. Twenty-four Simmental cows were fed a diet without BP (CON) for 1 week. Then they either continued with the CON diet or switched to one of the BP diets (with 15% or 30% BP in diet dry matter) for 3 weeks. Milk samples were taken before diet change and three times during BP feeding and analysed for fatty acid composition. Data showed that increasing BP content in the diet increased total fatty acid intake, especially of 18:1 n9. In the milk fat, the percentages of total monounsaturated fatty acids especially of the 18:1 origin linearly increased with increasing dietary BP level. The percentage of fatty acids de novo synthesized in the mammary gland (the sum of 4:0 – 14:0) remained similar among diets (32-34% of total fatty acids). The 16:0 percentage dropped from 32.5 to 29.6% and from 33.6 to 28.3% for 15% and 30% BP, respectively. Only 30% BP elevated the percentage of conjugated linoleic acids

(CLA: by 59%) compared with CON throughout the 3 weeks. Proportions of 18:2 n6 and 18:3 n3 and the n6:n3 ratio were unaffected by BP and feeding time. BP feeding improved all those estimated health indices of the milk fat that are suggested to be related to coronary health. In summary, the inclusion of BP in dairy rations beneficially shifted the milk fatty acid profile to more 18:1 fatty acids at the expense of 16:0. At a 30% inclusion rate, BP feeding showed an additional benefit of increased CLA content in milk fat.

Effects of supplementary inulin on ewes milk composition and rumen fermentation parameters

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Abstract

This experiment aimed to investigate the effects of inulin supplementation on milk production and composition, feed intake, nutrient digestibility and rumen fermentation parameters in lactating ewes. The experimental treatments were 1) control group (basal diet), 2) basal diet plus 2% inulin (w/w) and 3) basal diet plus 4% inulin (w/w). The experiment was carried out for 21 days in a fully randomized design involving eighteen Ghezel ewes. Production and composition (percentages of fat, protein, lactose and fat-free solids and fatty acid profiles) of milk were measured. Faeces were collected in the last three days of the experiment to determine digestibility. On the last day of the experiment, rumen fluid samples were taken from the esophagus 3 hours after feeding and fermentation parameters (pH, ammonia nitrogen (N-NH₃), volatile fatty acids (VFA) and protozoal population) were examined. Daily milk production was not significantly affected by inulin supplementation, but the fat and protein content of the milk was increased whilst urea nitrogen (MUN) and unsaturated fatty acids were decreased (P<0.05). The dry matter (DM) intake results showed that there was no significant difference between different diets. The highest digestibility of DM and NDF belonged to the inulin fed group (P<0.05). Inulin consumption numerically increased the pH of the rumen fluid of the animals and significantly decreased the rumen N-NH₃ value (P<0.05). Inulin supplementation also significantly increased total VFA, acetate, and butyrate levels (P<0.05). In general, it can be concluded that inulin supplementation can improve rumen fermentation, DM and NDF digestibility, as well as compositional aspects of the ewe's milk production.

Associating changes in the bacterial community of rumen and faeces and milk fatty acid profiles in dairy cows fed high-starch or starch and oil-supplemented diets

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Abstract

The experiment reported in this research paper aimed to evaluate the effects of high-starch or starch and oil-supplemented diets on rumen and faecal bacteria, and explore links between the structure of bacterial communities and milk fatty acid (FA) profiles. We used four Holstein dairy cows in a 4 x 4 Latin square design. Cows were fed a diet rich in cereals (high-starch diet with 23% starch content on dry matter (DM) basis), a diet supplemented with saturated FA from Ca salts of palm oil + 18% DM starch, a diet with high content of monounsaturated FA (from extruded rapeseeds) + 18 % DM starch or a diet rich in polyunsaturated FA (from extruded sunflower seeds) + 17% DM starch. At the end of each experimental period, cows were sampled for rumen and faecal contents, which were used for DNA extraction and amplicon sequencing. Partial least squares (PLS) regression analysis highlighted diet-related changes in both rumen and faecal bacterial structures. Sparse PLS discriminant analysis was further employed to identify biologically relevant operational taxonomical units (OTUs) driving these differences. Our results show that *Butyrivibrio* discriminated the high-starch diet and linked positively with higher concentrations of milk odd- and branched-chain FA. YS2-related OTUs were key taxa distinguishing diets supplemented with Ca salts of palm oil or sunflower seeds and correlated positively with linoleic acid in milk. Similarly, diets modulated faecal bacterial composition. However, correlations between changes in faecal and rumen bacteria were poor. With this work, we demonstrated that high-starch or lipid-supplemented diets affect rumen and faecal bacterial community structure, and these changes could have a knock-on effect on milk FA profiles.

Antimicrobial (ESBL) resistance genes in faecal *E. coli* of calves fed waste milk with antimicrobial residues

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Portugal

Abstract

This research paper aimed to evaluate the association between feeding waste milk to calves and the occurrence of antimicrobial multi-resistance by extended spectrum β -lactamase (ESBL) enzymes through determining their production by *E. coli* isolates from 32 dairy farms. Among β -lactamase enzymes, ESBL provide resistance to a wide variety of β -lactam antimicrobials including penicillin and 2nd, 3rd and 4th generation cephalosporins. Feeding

waste milk to calves has been observed to lead to increased antimicrobial resistance in faecal isolates of calves. In each farm included in this study, faecal samples were collected from the rectum of five healthy calves in the first month of life and pooled into a single container. Five isolates from each pool were selected and confirmed to be *E. coli* by amplification of the 16S rRNA gene. ESBL production was confirmed phenotypically on 148 isolates from 31 farms by use of the double-disk synergy test. Genotypic confirmation of ESBL production was performed by PCR for the genes blaCTX-M-1, -2, -8, -9 and blaCMY-2. A questionnaire was also performed and a mixed logistic regression model was used to identify risk factors for the occurrence of antimicrobial resistance. A negative binomial regression model was also used, in order to assess whether there was any association between certain farm management practices and the number of ESBL-producing *E. coli* isolates from each farm. Phenotypic confirmation of ESBL production was obtained on 40 *E. coli* isolates from 15 farms (48.4%), whereas genotypic confirmation was obtained on 55 isolates from 20 farms (64.5%). The use of three or more different intramammary antimicrobials to treat mastitis within the previous year significantly impacted the number of ESBL-producing *E. coli* isolates; on farms that did so, there were more isolates in which ESBL-producing *E. coli* was present, when compared to farms that had used less formulations within the same time span.

Associations between cow-level parameters and heart rate variability as a marker of the physiological stress response in dairy cows

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Abstract

To maintain and enhance cow productivity and welfare, it is important that we can accurately assess and understand how cows respond to the physiological demands of gestation and lactation. Several methods have been developed for assessing the physiological responses to stressors and for detecting distress in cattle. Heart rate (HR) variability (HRV) is a non-invasive measure of autonomic nervous system activity and consequently a component of the physiological response to stress. In cattle, HRV has been successfully used to measure autonomic responses to a variety of health conditions and management procedures. The objectives of this study were to determine whether, among commercial Holstein Friesian cows and across farms, relationships exist between cow-level factors, HR and HRV. HRV parameters were compared with production records for 170 randomly selected, Holstein-Friesian-cows on 3 commercial dairy farms. Production data included parity, days in milk (DIM), milk yield, somatic cell count (SCC), % butterfat and protein, body condition score (BCS) and genetic indices. Fixed-effect, multivariable linear regression models were constructed to examine the association between cow-level variables and HRV parameters. Statistically significant relationships were found between HR and farm, temperature and BCS, and between HRV parameters and farm, rectal temperature, BCS, DIM, and percentage butterfat.

Given the significant association between farms and several of the indices measured, it is recommended that care must be taken in the interpretation of HRV studies that are conducted on animals from a single farm. The current study indicated that within clinically normal dairy cattle HRV differed with the percentage of butterfat and BCS. Based on the relationships reported previously between HRV and stress in dairy cattle these results suggest that stress may be increased early in lactation, in cows with BCS <2.75 that are producing a high percentage of butterfat milk. Future work could focus on the physiological mechanisms through which these factors and their interactions alter HRV and how such physiological stress may be managed within a commercial farm setting.

Udder health of dairy cows with an extended voluntary waiting period from calving until the first insemination

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the Netherlands

Abstract

This study aimed to evaluate the effect of an extended voluntary waiting period (VWP) on SCC, SCC elevations and clinical mastitis incidence during the complete lactation and the first 6 weeks of the next lactation. Holstein-Friesian dairy cows (N=154) were blocked for parity, expected milk yield, calving season and breeding value for persistency and were randomly distributed across 3 VWP (50, 125, or 200 days: VWP-50, VWP-125, VWP-200). Cows were monitored from calving until 6 weeks into the next lactation, or until culling. An elevation of SCC in milk was defined as SCC in milk $\geq 200,000$ cells/mL after two previous weeks with SCC <200,000 cells/mL. Over the complete lactation, extending the VWP did not affect SCC elevations and the occurrence of clinical mastitis per lactation or per cow per year. There was no clear effect of VWP length on SCC in the complete lactation, except that multiparous cows in VWP-125 had a higher SCC compared with multiparous cows in VWP-50. Dry-off antibiotic usage per cow per year was lower in VWP-200 compared with VWP-50 for multiparous cows. In the first 6 weeks of the next lactation, cows in VWP-200 had a higher SCC compared with cows in VWP-50, with no effect of VWP on the number of elevations of SCC or the occurrence of clinical mastitis. Extending the VWP may therefore be used to reduce the frequency of transition periods and the associated use of dry-cow antibiotics, with limited impact on udder health, and a similar occurrence of SCC elevations and clinical mastitis per year.

The teat cup detachment level affects milking performance in an automatic milking system with teat cleaning and milking in the same teat cup

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Abstract

The goal of the present study was to determine the best quarter milk flow for teat cup detachment depending on lactational stage and milking interval to optimise the milking process in automatic milking systems (AMS). Milking characteristics and post-milking teat condition were recorded in an AMS with all actions from teat cleaning to post-milking teat dipping occurring in the same teat cup and liner (GEA DairyRobot R9500). In 24 dairy cows, 12 in early (< 80 DIM) and 12 in late lactation (> 180 DIM), 294 milkings were recorded during 12 consecutive days. Teat cup detachment was set at a quarter milk flow of 50, 87.5 or 125 g/min. Voluntary milking intervals varied similarly in cows in early (6.1 - 14.8 h) and late lactation (6.3 - 15.7 h). Total milk yield, milk production per h and average milk flow were higher in early than in late lactation cows. Total milk yield per milking did not differ between detachment levels. The mean milking time was reduced by up to 1.5 min at the highest compared to the lowest detachment level mainly in early lactation cows ($P < 0.05$). However, no significant effect of the detachment level on milking time was observed at milking intervals >10 h. Average milk flow was higher at milking intervals >10 h than ≤ 10 h ($P < 0.05$). In the early lactation cows (only) the average milk flow increased with higher detachment levels ($P < 0.05$). Teat condition did not differ among detachment settings or milking intervals. In conclusion, teat cup detachment up to 125 g/min reduces milking time in both early and late lactation without a loss of milk yield or affecting the teat condition. Combined with a higher average milk flow through avoiding too short milking intervals, the total milking time and hence stall occupancy can be optimized by early teat cup detachment.

The effect of various automatic cluster removal switch-point settings on milking and overmilking duration and total, peak and overmilking claw vacuum in dairy cows

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Abstract

This research communication describes the effect of three automatic cluster removal (ACR) switch-point settings on machine-on time, overmilking duration, and the mean, peak-flow and overmilking vacuums. The objective was to reduce the overmilking and milking time, attaining a lower mean claw vacuum during overmilking. In a randomised experiment, 25 cows were subjected to three ACR switch-point settings at flow rates of 0.840 kg/min, 0.630 kg/min and 0.504 kg/min each for 15 morning-milkings. Pre-milking preparations and cow comfort were observed and evaluated, showing evidence that the switch-point setting of

0.840 kg/ml denoted the least proportion of behavioural problems ($1.1\% \pm 0.6$) compared to the settings at 0.640 kg/ml ($16.0\% \pm 2.2$) and 0.504 kg/ml ($9.4\% \pm 1.7$). A VaDia device (Biocontrol) determined the machine-on time and vacuum levels at the claw, mouthpiece and pulsator chamber. The machine-on time varied from 290 ± 72.8 (mean \pm SD) to 289 ± 64.4 and 303 ± 66.3 for the 0.840, 0.630 and 0.504 kg/min settings, respectively. Overmilking was shortened by 29.3% and 26.4% and the claw vacuum during overmilking was reduced by 3.7 kPa and 4.3 kPa when using the 0.840 kg/min switch-point setting, compared to the others. An increased cluster-removal milk flow threshold reduced both overmilking and vacuum level during overmilking, lowering the risk of teat damage. Adapting ACR switch-point settings offers a valuable opportunity to increase parlour efficiency and cow comfort in dairy herds.

Triacylglycerol fingerprint of sow milks during different lactation stages and from different breeds

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China

Abstract

Sow milk fats not only provide energy but also essential nutrients for piglets. Thus, feeding strategies must be aligned with fat composition, especially triacylglycerols (TAGs) and their isomers. The triacylglycerol (TAG) profiles of sow milk fats from five typical breeds (Landrace \times Large White, Landrace, Large White, Duroc, Pietrain) and two lactation stages (colostrum and milk) were systematically studied. A total of 45 major TAG species were identified using ultra-performance liquid chromatography coupled with quadrupole time-of-flight mass spectrometry. The most abundant TAG was oleic acid-palmitic acid-linoleic acid (O-P-L) (13.92% and 12.03% in colostrum and milk, respectively), which was not significantly different in colostrum among all breeds. TAG composition of sow milk was affected mainly by the lactation stage rather than sow breed. Furthermore, TAG compositions of sow milk fats were similar to those of human milk fats, but significant differences were observed between commercial piglet formulas and sow milk. Therefore, the results will contribute to the optimization of piglet formulas to improve the growth and wellness of piglets, as well as potentially providing a basis for food usage as a new source of nutrients for human infants in future.

Determination of N-acetylneuraminic and N-glycolylneuraminic acids in unprocessed milk of four cattle breeds

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Abstract

This research communication reports concentrations of two sialic acids (SA), N-acetylneuraminic (Neu5Ac) and N-glycolylneuraminic (Neu5Gc), in fresh milk from different cow breeds throughout lactation. According to published studies, the two SA types found in animal-derived products have diverse and conflicting effects on human health, but SA content is not routinely analysed in individual milk cows samples. We measured the content of Neu5Ac and Neu5Gc in milk from Holstein Friesian (HO), Simmental (SM), Simmental x Holstein crossbred (SMxHO), and Podolica (POD) cows at 60 and 120 days following calving. HO, SM and SMxHO were reared in an intensive production while POD were raised in an extensive system. Results showed that total Neu5Ac was overall thirty times more abundant than Neu5Gc, and their concentrations were higher at 120 days than at 60 days ($P < 0.001$). Neu5Gc values were greater in HO, SM, and SM x HO than in POD ($P < 0.001$), while HO had a higher Neu5Ac value than the other three breeds ($P < 0.001$). These findings shed light on the differences in SA content among cow breeds and lay the groundwork for future research to select animals that produce milk with desirable characteristics for human health.

The impact of pasture and non-pasture diets on the sensory and volatile properties of whole milk powder

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Abstract

This study evaluated the impact of three distinct diets; perennial ryegrass (GRS), perennial ryegrass/white clover (CLV) and total mixed ration (TMR), on the sensory properties and volatile profile of whole milk powder (WMP). The samples were evaluated using a hedonic sensory acceptance test ($n = 99$ consumers) and by optimized descriptive profiling (ODP) using trained assessors ($n = 33$). Volatile profiling was achieved by gas chromatography mass spectrometry using three different extraction techniques; headspace solid phase micro-extraction, thermal desorption and high capacity sorptive extraction. Significant differences were evident in both sensory perception and the volatile profiles of the WMP based on the diet, with WMP from GRS and CLV more similar than WMP from TMR. Consumers scored WMP from CLV diets highest for overall acceptability, flavour and quality, and WMP from TMR diets highest for cooked flavour and aftertaste. ODP analysis found that WMP from TMR diets

had greater caramelised flavour, sweet aroma and sweet taste, and that WMP from GRS diets had greater cooked aroma and cooked flavour, with WMP derived from CLV diets having greater scores for liking of colour and creamy aroma. Sixty four VOCs were identified, twenty six were found to vary significantly based on diet and seventeen of these were derived from fatty acids; lactones, alcohols, aldehydes, ketones and esters. The abundance of δ -decalactone and δ -dodecalactone was very high in WMP derived from CLV and GRS diets as was γ -dodecalactone derived from a TMR diet. These lactones appeared to also influence sweet, creamy, and caramelised attributes in the resultant WMP samples. The differences in these VOC derived from lipids due to diet are likely further exacerbated by the thermal treatments used in WMP manufacture.

Nitrogen source: an effective component for the growth and viability of *Lactobacillus delbrueckii* subsp. *Bulgaricus*

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Abstract

In this study, we developed and optimized a growth media by evaluating various nitrogen sources for the cultivation of *Lactobacillus bulgaricus*, a probiotic and an important dairy starter culture. We modified the composition of deMan, Rogosa and Sharpe (MRS) culture media and substituted the nitrogen content with alternative nitrogen sources X-Seed KAT, X-Seed Carbo Max and X-Seed Nucleo Max in various blends of 5g/L and 10g/L respectively. Results showed that bacterial growth was significantly higher when the nitrogen source blend KCMAX (10/10) was used. The optical density (OD_{610nm}) of the *Lactobacillus bulgaricus* strains were higher (1.34 and 1.79) in the KCMAX (10/10) medium than in the MRS medium (0.89 and 1.42) ($P < 0.05$). There was no significant difference in the bacterial counts for both the MRS medium and the KCMAX (10/10) medium, and all bacterial counts were estimated at 8 Log CFU/ml. The buffering capacity of KCMAX (10/10) was also tested and supplemented with L-histidine and was significantly different ($P < 0.05$) than that of the MRS control medium. Calcium supplemented in the KCMAX (10/10) also served as a cryoprotectant for the cells during freezing and freeze-drying. Bacterial counts of the recovered calcium-treated freeze-dried cells were statistically significant ($P < 0.05$). We hypothesized that alternative nitrogen sources such as selected yeast extracts from the X-Seed brand of complex nitrogen sources could efficiently support the viability of *Lb. bulgaricus*. Our results thus suggested the growth of *Lb. bulgaricus* was efficiently supported by the X-Seed KAT, X-Seed Nucleo Max and X-Seed Carbo Max nitrogen sources. Consequently, these alternative nitrogen sources could potentially be recommended for dairy starter culture fermentations.

A simple and fast triplex-PCR for the identification of milk's animal origin in Halloumi cheese and yoghurt

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Abstract

In this research communication we describe a straightforward triplex-PCR protocol able to differentiate the origin of milk from three closely related species (goat, sheep and cow) in Halloumi, a cheese with Protected Designation of Origin (PDO) and yogurts. Halloumi must contain at least 51% sheep or goat milk, therefore, the fraudulent adulteration of this cheese with excess of cow milk must be routinely tested. The assay employs one universal forward primer and three species-specific reverse primers giving rise to 287 bp (cow), 313 bp (goat), and 336 bp (sheep) amplicons, under the same amplification conditions. This protocol when used to test a small number of Cyprus commercial products correctly detected mislabeling in Halloumi (2 out of 6 samples were adulterated) and yogurt brands (1 out of 4 was adulterated). The suggested protocol is a reliable tool for identifying the origin of milk in halloumi cheeses and yogurts and can be used in any laboratory equipped with a thermocycler and an agarose gel electrophoresis apparatus.

Effects of pH, stirring rate, reaction time, and sequential ultrafiltration of whey protein solution on recovery and purification of glycomacropptides

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Abstract

This study was designed to show the changes in glycolmacropptides (GMPs) of whey protein solution (WPS) due to different pretreatments before and after ultrafiltration (UF). The two variants (A&B) of GMPs available in WPS are useful compounds for nutritional management of phenylketonuria and ulcerative-colitis diseases provided they have a low content of phenylalanine (Phe). WPS with 10% concentration was prepared, acidified (adjusted to pH=3.0), and passed through a PES (polyethersulfone) membrane in the 1st-stage of ultrafiltration (UF-1). Then the resulting permeate was neutralized and went through the 2nd-stage of ultrafiltration (UF-2) under similar conditions. Four experiments of TRT-CON, CON-TRT, TRT-TRT, and CON-CON were used with different pretreatments, where TRT was a mixing-treatment of 30 min at 150 RPM applied either after acidification of WPS or after neutralization of first permeate and before UF-2 process. While the concentration and purity of the combined GMPs in UF-2 retentate in TRT-TRT respectively were > 95.6 and 99.5%, its Phe became <10 ppm among the experiments. Highly glycolyzed polymers of GMPs (MW= 45-50kDa) were formed in the TRT-TRT experiment and went through the pore sizes of PES

membrane of UF-1 easily because of their flexible structure. However, they remained in the UF-2 retentate, due to the formation of bulky polymers. Since the TRT-TRT experiment had the highest reversible and irreversible resistances for passing and remaining the PES-membranes respectively in the UF-1 and UF-2 among the four experiments, its fouling index was significantly less than in other treatments.

Possibilities of using the continuous type of UV light on the surface of lor (whey) cheese: Impacts on mould growth, oxidative stability, sensory and colour attributes during storage

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Abstract

This research paper addresses the hypothesis that the optimum doses of a continuous type of ultraviolet (UV) light applied to the surface of lor (whey) cheese needs to be identified to maximize mould inactivation and shelf life while minimizing quality deterioration. Therefore, the mould inactivation, protein and lipid oxidation products, sensory and colour attributes of lor cheese subjected to different doses of UV light (1.617, 4.018, and 36.832 kJ/m²) in a continuous type of UV system were evaluated. UV treated samples presented mould counts lower than those of untreated ones. UV treatment at more than 4.018 kJ/m² allowed around 0.7–2.7 log reductions on mould growth during storage. The increase in UV light dose caused significant increases in primary and secondary lipid oxidation products. In particular, the highest doses applied to the surface of cheese samples had the highest values of protein carbonyls, as well as lipid oxidation products. Strong positive correlations were recorded between lipid and protein oxidation markers. Exposure to the highest doses of UV light increased foreign flavour perception, probably due to the oxidative reactions. The results indicated that the application of UV light to the lor cheese surface allowed delaying mould growth during storage but extreme doses could induce lipid and protein oxidation reactions, leading to quality deterioration.