

Feed intake, milk composition and cheese making properties in Girgentana grazing goats with different genotype at α_{s1} -casein and κ -casein

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ABSTRACT

Milk ability for cheese manufacturing depends on both animals utilization of dietary nutrients and genetic polymorphism of caseins. It is well known that strong alleles associated with high content of α_{s1} -casein increase cheese-making properties of goat milk, whereas there is little information about the effect of genetic variants of κ -casein. The aim of this experiment was to investigate the effect of some composite α_{s1} -casein and κ -casein genotypes in changing feeding behaviour at pasture and milk yield and properties of Girgentana goats. Forty goats were genotyped at α_{s1} , α_{s2} , β and κ -casein loci using specific PRC protocols at DNA level and IEF technique at milk protein level. Twelve goats, differing only for α_{s1} and κ -casein genotype and averaging 136±5 days in milk and 38±6 kg of live weight, were selected and divided equally into 3 groups according to their genotype: WA, with weak alleles (FF) for α_{s1} -casein and A^{IEF} for κ -casein; SA, with strong alleles (AA) for α_{s1} -casein and A^{IEF} for κ -casein; SB, with strong alleles (AA) for α_{s1} -casein and B^{IEF} for κ -casein. No goats with weak alleles for α_{s1} -casein and B^{IEF} for κ -casein were found. Over a 5 weeks period in spring, goats were allowed to graze daily an Italian ryegrass and berseem clover mixture, and supplied with 500g/d of barley. Measurements, sampling and analyses of individual milk and forage selected by goats were performed weekly. Forage intake of goats at pasture was assessed by *n*-alkane technique. Data were analysed by MIXED procedure of SAS 9.1.3, using a model with genotype as fixed effect and goat as random effect. The genotype did not influence the goats intake of DM (1180, 1137, 1250 g/d DM for WA, SA, SB), net energy, crude protein and NDF, and milk yield (994, 1104, 1130 g/d for WA, SA, SB). Milk casein increased passing from WA to SA and SB genotypes (2.66, 2.93, 3.33%; P<0.01), similarly to casein/fat ratio (0.66, 0.74, 0.79%; P<0.05). The genotype associated with high α_{s1} -casein was responsible of a reduction in whey protein (0.71, 0.49, 0.55% for WA, SA, SB; P<0.01) and an increase in the casein N/TN ratio (71, 79, 80 for WA, SA, SB; P<0.001). The values of casein N/N intake ratio (109, 143, 158g/kg for WA, SA, SB; P<0.001) indicate an effect of strong alleles of α_{s1} -casein in improving the efficiency of dietary N utilization for milk casein synthesis. Milk from WA genotype showed higher pH (6.70, 6.63, 6.58; P<0.05) and lower titratable acidity (3.15, 3.55, 3.76°SH/50ml; P<0.05) than SB milk, with intermediate values for SA genotype. Clotting time (*r*) (10.7, 10.5, 9.3min for WA, SA, SB; P<0.05) and curd firming time (*k*₂₀) (1.56, 1.56, 1.24min for WA, SA, SB; P<0.001) were lower in milk from goats with B^{IEF} for κ -casein than in milk from goats with A^{IEF}, regardless of α_{s1} -casein alleles. Curd firmness (*a*₃₀) was improved by strong alleles than weak alleles of α_{s1} -casein, and more by B^{IEF} than A^{IEF} for κ -casein (41.8, 51.1, 59.8 mm for WA, SA, SB; P<0.001). These first results suggest that the strong alleles of α_{s1} -casein could act at metabolic level by increasing the efficiency of dietary nitrogen utilization and, consequently, the milk casein synthesis, and evidence the additional role of B^{IEF} alleles of κ -casein in increasing casein content and improving coagulation properties of goats milk, but require further investigations to be confirmed.

Milk coagulation ability map of Veneto Region

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ABSTRACT

Aims of this study were to define a milk coagulation ability map and to estimate effects of geographic area on milk quality and technological traits. The Veneto region is a heterogeneous geographic area, with plain, hill and mountain areas, located in northeast part of Italy. In this region milk is traditionally processed by dairy cooperatives to produce high value PDO cheeses. Since geographical conformation of this area, dairy cattle herds are more varied in terms of size, breed, feeding, and management practises influencing milk quality and technological traits. Data on biweekly herd milk composition (fat and protein percentages, somatic cell and bacterial count) and total monthly milk yield were collected, from January to December 2007, in dairy farms associated with 4 dairy cooperatives. A total of 13,646 records belonging to 1,210 dairy farms were available. Data of milk coagulation properties (MCP) of herd milk samples (n=966) were collected from June to December 2008. For all herds, address was recorded and geocoded (latitude and longitude) by using Google Earth® service and a G.I.S. software applications (ESRI, ArcGIS 9.2®) in order to display data on Veneto Region map. Data were analysed by using SAS package. Results showed that geographic areas influenced milk quality and MCP traits. Latitude is positively correlated, more than longitude, with high fat and protein percentage, low somatic cell score, low log bacterial, and favourable MCP. Dairy farms located in mountain area seem to produce milk more suitable to be processed into cheese. Dairy cooperatives are interesting to know these information for defining milk for cheese production and milk for fresh consumption, in order to improve efficiency of dairy-chain.

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In silico analysis of caseinophosphopeptides in ruminants

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ABSTRACT

Milk proteins are the main source of bioactive peptides with different functions. These milk activities are hidden in the native proteins and require the proteolytic cleavage to become extrinsic. The biopeptides generated from milk protein digestion show a wide range of activities. On the basis of the effects induced in the organism, biopeptides can be classified in the following categories: opioid-agonist, opioid-antagonist, antihypertensive, antithrombotic, immunomodulatory, antimicrobial, and mineral carrier peptides. These last peptides, also called caseinophosphopeptides (CPPs), possess the ability to bind and solubilise minerals, such as Ca²⁺. Consumption of high concentrations of Ca²⁺ in early life contributes to the development of maximal bone density, which in turn can prevent osteoporosis in later life. Furthermore, a positive correlation was found between Ca²⁺ intake and the prevention of hypertension. The high bioavailability of Ca²⁺ from milk and dairy products has, in part, been attributed to the production of CPPs with different levels of phosphorylation. The studies on the biological effect of different CPPs were carried out mainly in the bovine species, without taking genetic polymorphism into account. The biological activity of peptides released from milk protein digestion may be affected by amino acid exchanges or deletions resulting from gene mutations, as well as by post-translational changes. The aim of this work was to carry out an *in silico* analysis of the CPPs in order to detect differences in the amino acid sequence linked to the species (bovine, caprine, and ovine) and the genetic variants. Three, 2, and 3 CPPs, respectively carried by α_{s1} -casein (*CSN1S1*), β -casein (*CSN2*), and α_{s2} -casein (*CSN1S2*), were analysed. The biological effects of these peptides, or fragments of them, are known from literature. A total of 29 differences were detected when comparing the bovine, caprine, and ovine species as well as the genetic variants within each specie. The differences detected involved amino acid exchanges or deletions, and the occurrence of not phosphorylated serine. Small ruminants differ from the bovine species for 8 (goat) and 5 CPPs (sheep). Differences among genetic variants were found for bovine *CSN1S1*F*, *E*, and *H*; *CSN2*A⁴*, *C*, *D*, *E*, and *H¹*; *CSN1S2*B*, *C*, and *D*; caprine *CSN1S1*F*, and *M*; *CSN1S2*B*, and *F*; ovine *CSN1S1*D*. Potential changes in the biological function of the different CPPs need to be evaluated by further studies.

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Prediction of milk coagulation properties in herd milk sample using Mid-Infrared Spectroscopy

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ABSTRACT

This study investigated the application of mid-infrared spectroscopy (MIR) for the determination of milk coagulation properties (MCP) in herd milk samples. MCP is measured as a combination of milk coagulation time (RCT, min) and curd firmness (a_{30}). Currently, assessment of MCP can be performed through milk coagulation meters but routine direct assessment is not feasible. MIR may be a possible alternative technique for the assessment of MCP. Measurements of MCP (527 herd milk samples) were carried out using a computerized renneting meter and MIR spectra were collected over the spectral range of 4,000 to 900 cm^{-1} . Models were developed by partial least squares regression using untreated spectra and using random cross-validation (number of segment 30 and samples per segment 18). The mean values of RCT and a_{30} were 19.22min (SD 3.68min) and 25.30mm (SD 8.03mm), respectively. The root mean square errors of cross-validation for the models were 2.48 min for RCT and 5.57 mm for a_{30} . The models could discriminate between high and low values of RCT ($R^2=0.55$) and a_{30} ($R^2=0.52$), although the models require further development to improve their accuracy before their application in dairy industry.

Microbiological characteristics of Trentingrana cheese after nine months of ripening

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ABSTRACT

Trentingrana cheese is a hard cooked cheese subjected to a long ripening period (up to 2 years), similarly to Grana Padano cheese. It is produced in the Trentino region (Alpine area located in the North part of Italy). It is a cheese made from partially skimmed raw cow's milk curdled by commercial rennet with the addition of whey daily produced at the dairy factory, thus containing a high microbial biodiversity. The aim of this study was to describe the lactic acid bacterial (LAB) at 9 months, which represents the clue-time for the ripening of this cheese, as well as understand its role in cheese ripening. The diversity of dominant LAB population in nine-month ripened Grana Trentino cheese was investigated by a culture-dependent approach including randomly amplified polymorphic DNA-polymerase chain reaction (RAPD-PCR) and denaturing gradient gel electrophoresis (DGGE). For each nine-month ripened cheese we took one sample closed to the smear surface of the cheese dish, one in the core of the section and another one in the middle between the first two sampling. For each sampled area the cultivable bacteria were enumerated on different agar media. About 300 LAB strains were isolated and subjected to RAPD-PCR in order to perform a grouping. Some strains for each biotype were tested for protease production, acidification, salt resistance, diacetyl and ammonia production from arginine. LAB population was estimated at high numbers (about 10^6 CFU·g⁻¹) at nine months of ripening. In the external (smear surface) and internal (core) zones of Grana Trentino cheeses, different trends in microbial counts and species distribution were observed. The most wide spread species were *Lactobacillus paracasei* and *Lactobacillus rhamnosus*.

Relationship between milkability traits recorded with flowmeters and udder type traits in Italian Holstein Friesian cows

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ABSTRACT

The Lactocorder® is an instrument that measures the milk flow rate, yield and duration of milking. Its use is extensively introduced by several breeders associations in Italy and it allows to collect detailed information on milking. The aim of this study was to investigate the relationships between milkability, udder health traits (electric conductivity and Somatic Cell Score (SCS)) and udder type traits (udder depth, fore udder attachment, rear udder width, rear udder height, udder ligament teat thickness and teat placement). The study was carried out in 137 Italian Holstein-Friesian dairy herds in Lombardia (Italy) and the data set consisted of 3,292 milk flow curves of the whole udder. Statistical analyses were performed using the CORR and GLM procedures of the statistical program SAS (SAS, Inst. Inc., Cary, N.C.). **Only first lactation records** were used to relate the udder conformation to the milkability traits.

Close to one-third (32%) of milk flow curves were classified as bimodal. Lactation number, peak flow and premilking operations influenced most of the flow traits. All Pearson correlation coefficients and ANOVA analyses between milk flow characteristics and udder traits were rather low, albeit significant, as they obtained from a large number of milk flow curves. Correlations between the duration of the whole milking and type traits were negative for udder depth (-0.09), fore udder attachment (-0.03) and udder ligament (-0.03), and positive for rear udder width (0.09) and teat thickness (0.08). Correlations between the maximum of milk flow and type traits were negative only for teat thickness (-0.05) and positive for udder depth (0.05), fore udder attachment (0.05), rear udder attachment (0.07) and udder ligament (0.03). Only the udder depth was associated with the duration of the plateau phase (-0.07) but almost all udder traits with the exception of fore attachment and teat placement were positively related with the duration of the main milking phase. Also the correlations between conductivity and the udder depth (-0.03) and between conductivity and the ligament (-0.05) were low but negative. This would indicate that **udders not too deep** and with strong ligaments are more resistant to disease, as the enhancement of electrical conductivity is related to an inflammation of the udder. **Milking speed seemed to be fairly associated with traits related to mastitis susceptibility** (udder depth, fore udder attachment, udder ligament and teat thickness), similarly to the unfavorable association reported in literature.

The associations resulting between udder depth, milk flow traits and electrical conductivity would suggest that deep udders are more productive. But also, for the same association, it seems that a limited development of the udder would have a positive effect on health status and milking speed.

The results of this study confirm that the analysis of milk flow curves plays an important role in suggesting a correct milking routine to respect the cow physiology improving also the udder health.

Characterization of Pecorino Siciliano in relation to the production area

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ABSTRACT

Samples of Pecorino Siciliano produced across Sicily were collected at 4 different ages (0, 60, 120 and 140d). About 300 samples representing 7 production areas, which differs for climatic and botanical composition of forages were analyzed for pH, dry matter, fat, nitrogen, soluble protein, free fatty acids and salt content. Ground samples were also scanned in diffuse reflectance on a near infrared spectrophotometer (Nirflex N-500, Buchi, Milano) between 1000 and 2500nm. Chemical analysis were subjected to a two way analysis (Statistica 8.0) and were also used to discriminate samples for the different production areas using the General Discriminant Analysis of Statistica. Spectral data were used to develop prediction models and also to discriminate area of production using partial least square discriminate analysis. The age had the largest effect and was significant ($P<0.05$) for all the chemical characteristics considered. Area of production was significant ($P<0.05$) only for pH, dry matter and fat content. Considering all the samples the discriminate analysis on average classified correctly only 33% of the samples. When considering only the samples at the oldest age the classification improved (48%) but was not satisfactory. Using spectral data also did not improve correct classification of area of production.

Fatty acid profile of milk fat in goat supplemented with iodized salt

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ABSTRACT

Iodine is an essential nutrient of the human and animal diet which is needed for the synthesis of the thyroid hormones. These hormones play an important role in the regulation of fat metabolism. In fact, increased thyroid hormone levels stimulate fat mobilization, leading to increased concentrations of plasma triglyceride (Nikkila and Kekki, 1972) and enhanced oxidation of fatty acids in many tissues. Recently, Bauman *et al.* (2006) showed the involvement of a protein called spot 14, highly responsive to thyroid hormones, in the regulation of the mammary synthesis of milk fat. However, the effects of Iodine supplementation on plasma and milk fatty acid profile in dairy animals has not been elucidated yet. The aim of this study was to evaluate if the fatty acid (FA) profile of milk changes in goats supplemented with Iodine. Thirty crossbreed dairy goats were divided into 3 groups were used and supplemented with 0 (group 0), 450 (group 1), or 900 (group 2) µg of KI/day per head. Each dose of KI (76.5% of Iodine) was orally administered in water every day for 8 weeks. Milk yield was recorded and milk samples were collected every two weeks. A total of 120 milk samples were analyzed by gas chromatography (GC). Milk yield was not influenced by treatments. Milk fat content was the highest ($P < 0.01$) in group 1 (4.65%) compared to group 0 (4.15%) and group 2 (4.17%). Iodine treatments did not influence milk fatty acid profile except for the content of some short-chain fatty acids. In particular, only the contents of C8:0 FA (2.22, 2.24 and 2.12 in groups 0, 1 and 2, respectively; $P < 0.01$) and C10:0 (9.74, 9.49 and 9.02 in groups 0, 1 and 2, respectively; $P < 0.01$) decreased due to supplementation with the highest dose of KI. In conclusion, in this study Iodine supplementation did not show substantial effects on goat's milk FA profile, probably due to the low doses of KI used. Nevertheless, the observed decrease of some short-chain fatty acids, which are synthesized *ex-novo* by the mammary gland, in goats supplemented with the highest KI dose tested is compatible with a potential involvement of Iodine or thyroid hormones in the regulation of fat synthesis in the mammary gland.

Effect of ripening time on lipid composition of 'Caciocavallo' cheese obtained from Podolian cattle Genetic Type. Preliminary results

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ABSTRACT

The Genetic Type (GT) 'Podolica' was originated from the *Bos taurus primigenius*, present in Italy 2 million years ago; it is diffused now only in Central Southern Italy and it is primarily raised by 'transhumant' system. The milk produced results particularly interesting in order to individuate fatty acid profile that safeguards the consumer's health. Endogenous and exogenous factors so contribute to determine, quantitative and qualitative variations of lipids. This study intends to underline the possible relationship between fatty acid content and the ripening time. The study was carried out on 30 'Caciocavallo' cheeses related to three different cheese making time (March, April and May) and ripened at 1, 3, 6, 9 and 12 months. The lipid fraction was extracted according to the method of Folch and subsequently submitted to transesterification. The FAMES (fatty acid methyl esters) were analyzed by Fisons HR-Mega2 GC/FID equipped with SPB2560 (100m x 0,25 id) column. The fatty acid profile interested the fatty acids distinguished, for molecular weight, in short (C4-C6), medium (C8-C12) and long (C14-C24) chain and, for saturation level, in saturated and unsaturated fatty acids [including conjugated linoleic acid isomers (CLA)]. The results were expressed as percentage of the dry matter. All the percentage values are converted into arcsin. The percentage incidence of the fatty acids changes in relation to the ripening period: (i) for the short chain fatty acids, related to the cheese making of March and May, a decreasing linear function ($P < 0.05$) was observed and a polynomial function of third order ($P < 0.001$) for the cheese making of April was found; (ii) for the medium and long chain saturated fatty acids and total long chain fatty acids were found a polynomial function of third order ($P < 0.001$) for all three cheese making; (iii) for the saturated fatty acids were found a function like that estimated for the medium and long chain fatty acids; (iv) for the unsaturated fatty acids were found an increasing linear function ($P = 0.05 \div 0.001$) for March and May cheese making and a polynomial function of third order ($P < 0.001$) for the cheese making of April; (v) for the CLA was found an increasing linear function ($P < 0.001$), for the cheese making of March, a polynomial function of third order ($P < 0.001$) for the cheese making of April as well as a potentially linear not meaningful function for the cheese making of May. As concerns the ratio between: (i) saturated and unsaturated fatty acids changes a quadratic function ($P = 0.05 \div 0.01$) for all the cheese makings were observed; (ii) for the cheese making of March and April, -6 and -3 changed following a polynomial function of third order ($P = 0.01 \div 0.001$) whereas an increasing linear function ($P < 0.01$) for the cheese making of May was observed. The ratio between the single fatty acids, finally, changes according to different statistic models depending on the fatty acid considered. The trend of the fatty acids profile during the ripening period remarks the importance of microenvironmental factors of the breeding's bioterritory and, mainly, of the qualitative equilibrium between microorganism populations of the 'Caciocavallo' cheese, changing in relation to the duration and ripening conditions.

Shearing influences the milk fatty acid profile of dairy ewes

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ABSTRACT

In Mediterranean areas shearing is commonly performed during late spring and, therefore, ewes may be exposed to cold stress especially during the night. Short-term periods of cold exposure can increase hepatic glucose production, decrease insulin secretion and increase fat catabolism and plasma non-esterified free fatty acids (NEFA) concentration. These metabolic adaptations to cold exposure can increase the mammary uptake of long-chain fatty acid from plasma. The present study aimed to investigate the metabolic response of dairy ewes to shearing by monitoring their milk fatty acid (FA) profile. Twelve 2-4-year-old Sarda ewes, in mid-late lactation, were used. The trial lasted from 30th May to 9th June 2006. The pre-experimental period (pre-shearing, PrS) was from 30th May to 5th June (shearing day), being followed by the experimental period (post-shearing, PoS) until 9th June. On shearing day, the flock was divided in two groups (6 ewes each) which were then managed differently: non-confined group (NCG) and confined group (CG) which was kept in a sheepfold during the night. Four samplings during PrS and other four during PoS periods were performed. During the trial, ewes were fed concentrate at 1000g/d per head, during the two daily milking, and hay *ad libitum*, and grazed on green clover (3h/day). Daily milk production was recorded and daily milk samples were collected for analysis of fat content and FA profile. Shearing did not influence milk yield but increased significantly milk fat content (6.37 vs. 6.94% for PrS and PoS, respectively; $P < 0.01$). Ewes confinement during the night did not affect milk yield and its fat content. Shearing modified significantly the FA profile of milk. The concentration of C8, C10, C12 and C16 increased significantly from PrS to PoS. On the other hand, the content of long-chain FA (>C18:0) did not change between PrS and PoS (46.26 vs. 46.40mg/100g of FAME, respectively). These results suggest that the increase of milk fat after shearing was related to the increase of the main FA synthesized by the mammary gland. However, the unexpected increase in the synthesis of short- and medium-chain FA after shearing suggests that these animals were not subjected to cold stress. Therefore, the mechanism involved in the modification of the FA profile caused by shearing in dairy ewes should be elucidated.

Iodine supplementation in dairy ewes nutrition: effect on milk production traits and milk iodine content

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ABSTRACT

Iodine is a natural component of milk and its content is strictly related to the iodine content in feed. Usually, in ruminant nutrition iodine supplementation is based on the addition of KI salt in the concentrate feed. In literature conflicting results are reported for the effect of iodine supplementation on milk yield and composition and few data are available about the efficiency of transfer of iodine from feed to milk in dairy sheep. Aim of the study was to investigate the effect of two doses of iodine supplementation on milk fat yield and composition in a flock of Sarda dairy sheep. At this purpose, 24 pluriparous Sarda sheep at the second month of lactation were randomly assigned to: group A supplemented with a concentrate containing 1000 µg/kg DM of iodine (the dose usually recommended for concentrate) and group B containing 3000 µg/kg DM. Iodine was supplemented as KI salt in the concentrate feed. Ewes grazed the same pasture (a mixture of *Avena sativa* and *Trifolium repens*) and they were fed 700g/d of concentrate administrated during milking. The experiment lasted 4 weeks from February to March. Milk samples were weekly collected and for each sampling milk yield was recorded. Milk fat and protein contents were determined by Milkoscan, while iodine concentration of milk and feed was determined by acid digestion according to the colorimetric Sandell-Kolthoff reaction. Data were analysed by a repeated measure model with group (2 levels), week of the sampling (4 levels) and their interaction as fixed factors and sheep nested group as random effect. The average milk yield of group B tended to be higher than that of group A, but did not reach the statistic significance (1303 g/d and 1459 g/d of milk for group A and B respectively, P=0.1). Milk fat and protein contents, yield and somatic cell count did not differ between groups. These results confirmed what reported in a previous trial on Massese ewes, where increasing level of iodine supplementation led to a significant increase of milk yield. Average milk iodine concentration was higher in group B than in group A, increasing by 69.4% (163.5 µg/L and 277.0 µg/L for group A and B, respectively, P<0.001). The daily iodine secretion in milk was significantly higher in group B, increasing by 165% (222.6 µg/d and 391.0 µg/d for group A and B, respectively, P<0.001). The apparent transfer of iodine from feed to milk was higher in group A than in group B (31.8% and 18.6% for group A and B, respectively) and it was in agreement with data from previous study on cattle and sheep. In conclusion, data of the present study showed that higher levels of iodine in feed seemed to increase milk yield. Moreover, data confirmed that also in dairy ewes higher iodine supplementation led to increase milk iodine excretion, but the efficiency of transfer of iodine from feed to milk seemed to decrease.

Milk fatty acids of cows grazing a mountain diversified grassland is highly affected by the maturity stage of the grass

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ABSTRACT

In the last years many researches focused on the fatty acid (FA) composition of milk fat according to animal diet. They evidenced in particular that the content of monounsaturated (MUFA) and polyunsaturated (PUFA) fatty acids (FA), including Conjugated Linolenic Acid (CLA) and ω 3, is increased in milk and/or cheese from grazing cows in comparison with those from cows fed preserved forages. Nevertheless, even for cows only fed pasture, an important variability is often reported. This variability may be partly explained by the botanical composition of the grassland and also by the growing stage of the grass. The aim of this experiment was to quantify the effect of the development stage of the grass from one diversified mountain grassland pasture on the FA composition of grass and milk. On June (first growth) and October (regrowth), a diversified mountain pasture was continuously grazed by 6 cows (5 of Montbeliarde breed and 1 of Tarentaise breed) in a strip grazing system. FA profile was analysed twice a week both in June (9 dates) and October (2 dates) on samples of forage and individual milk by Trace-GC 2000 series gas chromatograph equipped with a flame ionization detector. Data were analyzed by the MIXED procedure of the SAS software, considering the sampling date (11 dates) as main effect, the animal within breed as random effect and the date as repeated measures. During the first growing phase, the grass content of C18:3 n-3 decreased from 58 to 43 g/100 g fat while the C16:0, the C18:1 cis9, and the C18:2 n-6 content increased from 15 to 19, from 2.6 to 6.4 and from 16 to 21 respectively. During the regrowth of October, the grass FA composition was similar to that observed in June for the 1st and 2nd samplings. During the first growth of the grass, the milk saturated FA content increased from 57 to 60 g/100 g fat and the PUFA content decreased from 4.2 to 3.1g/100 g fat, mainly due to the decrease observed for C18:3 n-3 (from 0.80 to 0.53 g/100 g fat) and c9t11-CLA percentages (from 1.45 to 0.79 g/100 g fat). The sum of the *trans* FA in milk fat also decreased from 6.8 to 4.0g/100g fat. At the start of October, the milk content of PUFA, total *trans* FA, C18:1t11(+t10), c9t11-CLA and C18:3 n-3 was higher to that observed at the start of June when the grass was still vegetative. For these FA, a strong decrease in their content was observed between the 2 samplings in October, and this trend could be explained by either the lowering availability of the grass or the grass FA composition differences observed during this short period. Variability observed in milk FA composition during one month in our study was high for c9t11-CLA, C18:3 n-3, C18:1t11, C16:0, certainly because of the botanical composition of this grassland pasture and the advanced mature stage of the grass due to the exceptional temperatures. These results underline the marked variability of the milk FA composition observed throughout a grazing period even when cows are fed a single grassland. They clearly evidence that the milk provided from pasture are not equivalent regarding their FA profile and that the best nutritional properties are observed when cows are grazing vegetative grass from the early growth or regrowth stages.

Quality evaluation of cheese from raw or pasteurized milk of ewes grazing sulla forage (*Hedysarum coronarium* L.) for different daily time

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ABSTRACT

Pasteurization is the more effective method for eliminating pathogens contaminating milk. However, the high temperature of pasteurization destroys either pathogens or lactic endemic flora, this latter involved in cheese ripening, thus impairing the development of sensory properties of cheese. It was previously observed that longer permanence at pasture allows the ewes to spend more time for eating; accordingly, ewes increase feed intake and milk yield. Aim of this experiment was to evaluate the effect of the prolongation of ewes daily grazing from 8 to 24 h and the effect of the milk pasteurization process on milk and cheese quality, with particular regard on fatty acid (FA) composition. In a semi-arid hilly area of Sicily, 14 Comisana ewes, averaging 157 ± 57 days in milk and 44.8 ± 7.3 kg of live weight, were divided into 2 groups. For 42d in spring, both groups continuously grazed sulla under a stocking rate of 34 ewes/ha, one group for 8h (8:00-16:00) (S8) and the other one for 24h (S24). At 2-week intervals, 3 cheesemaking trials were conducted in controlled condition and according to the Pecorino Siciliano technology. From each group, the 48-h bulk milk was collected and divided equitably into 2 inox vats. In a vat, milk was heated at 33°C (S8 and S24); in the other one, milk was pasteurized at 72°C for 20sec and added with starters (SP8 and SP24). Bulk milk was analysed for its components and coagulation properties. Determinations were executed on 15-day aged cheeses for chemical composition, colour, FA composition (by GC/MSD system with a flame ionization detector) and sensorial characteristics by triangular tests. Data were statistically analysed by GLM procedure of SAS 9.1.2 software, with grazing time, pasteurization and their interaction as effects. Ewes grazing for 24 h showed higher milk yield (929 vs. 817 g/d; $P < 0.05$) and urea (58 vs. 49 mg/dl; $P < 0.01$), and lower milk fat (6.3 vs. 6.8%; $P < 0.01$), somatic cells count (5.9 vs. $6.4 \log_{10}/\text{ml}$; $P < 0.05$), clotting time (τ) (22.3 vs. 19.9 min; $P < 0.05$) and curd firming time (k_{20}) (2.1 vs. 1.4 min; $P < 0.05$) than S8 ewes. Composition and properties of raw and pasteurized milk did not differ, except for bacterial count which was reduced by pasteurization action. Grazing time and pasteurization did not affect cheese yield and composition. Cheeses from pasteurized milk had a less intense yellow colour ($b^* = 15$ vs. 18; $P < 0.05$) than from raw milk. At triangular tests, significant differences emerged between cheeses in comparisons S8 vs. S24 ($P < 0.05$), S8 vs. SP8 ($P < 0.01$) and S24 vs. SP24 ($P < 0.05$). Grazing time did not influence significantly cheese FA profile, even though unsaturated FA and CLA were slightly higher in S8 (31.46 and 1.44% FA, respectively) than in S24 (29.51 and 1.16% FA, respectively) cheese. Also the pasteurization treatment did not modify cheese FA composition, in accordance with other investigations on cheese from cows and goats pasteurized milk. In conclusion, longer permanence of ewes at pasture improved milk yield without modifying cheese yield and FA profile. In front of the advantage of better cleanness, pasteurized milk did not lead to differences in cheese FA profile, in comparison to raw milk. However, milk pasteurization caused loss of typical taste and reduced yellow index of cheese, presumably due to variation in microbial flora.

Influence of extruded linseed on milk and cheese fatty acid composition in dairy cows

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ABSTRACT

Milk fat contains 60% saturated fatty acids (SFA) that contribute to human plasma LDL levels; unsaturated fatty acids promote HDL formation and have an important role in metabolism. Lipid supplementation can be provided through green forage or via the addition of oil and/or oil seeds in the ration. Fresh grass and pasture are rich in ω_3 linolenic acid, which is capable of affecting ω_3 acid levels in dairy cow milk. Oil seeds are also rich in long-chain fatty acids (C18:0, C18:1, C18:2, C18:3). Several studies have described changes in the acid composition of milk fat in cows fed seeds; in particular, linseed has been demonstrated to be an important source of ω_3 . In a trial conducted in a dairy farm, 80 lactating cows producing on average 30l milk/day were fed a control ration (DC) for 3 months followed by a ration supplemented with extruded linseed: first 400 g/d/head (DL₄) for 3 months and then 800g/d/head (DL₈) for another 3 months. All 80 cows were assigned to the same experimental treatment, because the farm's organisational structure did not allow for multiple groups. On the occasion of the monthly APA checks, milk was randomly collected and lyophilised for gas chromatographic analysis of fat. Six unifeed samples, taken from the mangers at the same times, were subjected to chemical analysis. Throughout the trial, the ration provided DM 72%, CP 16.2%DM, EE 3.53%DM, NDF 36%DM, and ash 9%DM. Cheese made from DC milk (DCC) and DL₈ milk (DL₈C) was sold after 20 day ripening. Data were subjected to analysis of variance with linseed supplementation as the effect. Analysis of the milk yielded significant differences (P<0.001) in relation to the higher linseed supplement (800g); in particular, ω_3 C18:3 rose from 0.56% and 0.61% in DC and DL₄, respectively, to 0.90%. Total SFA were significantly lower (P<0.001) in DL₈ milk (DC 62.7%, DL₄ 67.0%, DL₈ 57.8%). Significant differences (P<0.001) were also calculated for MUFA (DC 31%, DL₄ 25.9%, DL₈ 35.3%) and PUFA (DC 3.7%, DL₄ 3.9%, DL₈ 4.5%). Six cheeses per milk type were subjected to fat chemical and acidic composition analysis. There were no significant differences in the former (DCC: DM 63.8%, protein 40.7%DM, fat 49.3%DM vs. DLC: DM 61.7%, protein 42.2%DM, fat 48.6%DM), whereas fatty acid composition evidenced significant differences (P<0.01) in ω_3 C18:3 (DCC 0.51% vs. DLC 0.89%); SFA (DCC 68.4% vs. DLC 63.5%); MUFA (DCC 25.6% vs. DLC 30.6%) and PUFA (DCC 2.9% vs. DLC 4.1%). In conclusion, supplementation of the lactating cow ration with extruded linseed allows to modify the acidic composition of milk by increasing its content in unsaturated fatty acids, mainly ω_3 C18:3.