

# Goat Milk Quality

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## ABSTRACTS





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# Conformation of the udder, is that a problem in our dairy farms?

## Preliminary results.

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The AWIN project focuses on studying indicators that will help farms' certification in terms of animal welfare. Our team has been assessing dairy goats' welfare and one potential indicator is changes in the udder, namely the presence of pendulous and asymmetric udders. It was hypothesized that these conditions could affect productivity and milk quality and also be a source of pain.

We collected milk samples from each teat of 44 randomly selected goats, from three production groups in different stages of lactation (early, mid and late lactation). After milk collection the udders were photographed with a thermography camera and pressure was applied with an algometer to each side of the udder. Data concerning days in milking (DIM), average milk yield and day production was collected. The milk samples were submitted to somatic cell count (SCC) (Fossomatic™ FC) and to bacteriology analyzes.

The average SCC was 1,914 cells/ml and only 5 samples tested negative for microorganisms, being the most prevalent *Staphylococcus coagulase negative* and *Corynebacterium spp* (76% of the teats). Concerning udder conformation 45% of the udders were asymmetric and pendulous, 6% were just asymmetric or just pendulous. Asymmetric udders and asymmetric and pendulous udder had a significantly lower temperature (32.9°C,  $p=0.01$  and 33.49°C  $p=0.03$ , respectively) than the normal udders (udders that aren't asymmetric and/or pendulous) (34.5°C) and, although it wasn't statistically significant the average SCC for the animals with pendulous and asymmetric udder was almost the double than the SCC of the milk from goats with symmetric udders (2,911 cells/ml and, 1,664 cells/ml respectively). We also found that udders with SCC above 1,500 cells/ml had significantly lower temperature (33.69°C,  $p=0.011$ ) than udders with a SCC lower than 1,500 cells/ml (34.35°C). Although not statistically significant ( $p=0.08$ ), teats that showed both microorganisms had higher SCC (3,229 cells/ml) than the ones with just *Staphylococcus coagulase negative* or *Corynebacterium spp*. (1,691 cells/ml and 1,284 cells/ml, respectively). Reaction to pressure did not show correlation to any of the other variables analyzed. More studies are needed to evaluate pain in these animals. Milk yield data is still being analysed.

From this preliminary data we concluded that there are a lot of animals with subclinical mastitis that go undiagnosed. This shows that dairy goats' milk quality needs to be improved and that it may prove to be a problem if a SCC legal limit is introduced. There appears to be a correlation between udder conformation, SCC and the microorganism present in the udder. The lower temperature in pendulous udders can be related to the conformation or to a decrease in the vascularization of the mammary tissue due to chronic subclinical mastitis. This preliminary data shows that udders' conformation is an indicator of disease that may compromise dairy goat welfare.

# Environmental and genetic parameters of somatic cells and lactose contents in goat milk

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The research has been conducted for 11 years in a single herd. Milk yield, fat, protein and lactose contents, as well as SCC were recorded once a month in all lactations resulting in 4417 records for 118 Polish White Improved (PWI) and 96 Polish Fawn Improved (PFI) does. The animal multiple-trait model for variance component estimation accounted for breed, day of milking (112 classes), year of birth (13), year of milking (12), kidding season (October-March, April-September), feeding season (May-September, October-April), litter size (3), and parity (5). Kids were weaned at one month of age. The REML computations were run with the DMU package of Madsen and Jensen (2000). As expected, the highest content of lactose was found in milk of primiparous goats which gave birth to one kid; simultaneously, lowest milk yield was associated with this parity. No significant differences between breeds in lactose content were found. Yet, there was a lower SCC in milk of PWI than PFI goats. The highest SCC was recorded in milk of goats with twins and the lowest in milk with more than two kids, but the standard errors were very high. Youngest goats had lowest SCC and the lnSCC systematically increased with lactation number. The heritabilities for lactose content and SCC were 0.21 (se=0.06) and 0.27 (se=0.05), while repeatabilities were 0.31 (se=0.03) and 0.35 (se=0.03), respectively. Genetic correlation between milk yield and lactose content was -0.46 while between milk yield and lnSCC 0.59. Genetic correlation between lactose content and fat and protein contents were 0.62 and 0.54. No genetic correlation between lnSCC and protein content and low and negative correlations between lnSCC with fat (-0.19) and lnSCC with lactose content (-0.14) were found. All the standard errors of the latter parameters were high.

## **An impact of SRLVs infection on GSH level in goat milk**

Bagnicka E.<sup>1</sup>, Nowicka D.<sup>2</sup>, Jóźwik A.<sup>1</sup>, Kościuczuk E.M.<sup>1</sup>, Czopowicz M.<sup>2</sup>, Jarczak J.<sup>1</sup>, Horbańczuk K.<sup>1</sup>, Słoniewska D.<sup>1</sup>, Krzyżewski J.<sup>1</sup>, Kaba J.<sup>2</sup>

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The aim of the study was to estimate an influence of Small Ruminant Lentiviruses (SRLVs) infection on reduced glutathione (GSH) concentration in goat milk. Polish White Improved dairy goats were used in the study. Total number of 487 milk samples have been collected at the beginning, the peak and the end of three consecutive lactations. One hundred thirty eight records came from SRLVs-infected and 349 from non-infected goats. Relationship between GSH level in milk and SRLVs infection adjusted by year of study, parity and stage of lactation was evaluated using analysis of variance with GLM procedure (SAS, USA). Lower GSH level in milk of SRLVs-infected goats was observed (42,53 vs. 50,23;  $p < 0.01$ ). As GSH is a natural scavenger of reactive oxygen metabolites, the result may imply the occurrence of constant oxidative stress in SRLVs-infected goats.

## Feeding different lipid supplements during lactation cycle in dairy goats: 2 effect on mammary gene expression.

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To sustain the development and production of goat milk products, the guarantee of milk technological (high dry matter content, rennet coagulation) and sensorial (flavour) qualities is central. To achieve these goals along a lactation period, it is necessary to supply the goat with sufficient energy, which could be a challenge, especially for high yielding goats in early lactation. Dietary fat supplements are used as a mean to increase the total energy concentration of the diet. The aim of the present study was to examine the effect of different lipid supplements on mammary gene expression and milk production and composition in dairy goats over a lactation period.

Thirty Norwegian dairy goats with kidding in February 2011 were fed a control diet with a concentrate mixture (0.9 kg/d) consisting of barley, rape seed meal (expro 00SF), soy bean meal, beet pulp, molasses and mineral/vitamin premix until 60 days in milk (DIM). After 60 DIM and until the end of the experiment, the goats were assigned to three experimental groups (balanced for their parity, genotype at the  $\alpha$ S1 casein locus) each of 10 goats that received 3 dietary treatments: 'Control', 'Saturated' and 'Unsaturated' that differ in the composition of the concentrate mixtures. The two lipid supplemented treatments consisted of the same concentrate mixture as the 'Control', with addition of 8% of a source of 'Saturated' (Akofeed Gigant 60; rich in C16:0) and 'Unsaturated' (rapeseed oil, rich in cis-9-18:1 and cis-9, cis-12-18:2) fat. The experiment consisted of three different periods: 1) Spring indoor feeding period from 1 to 120 DIM; 2) Summer mountain grazing period from 120 to 200 DIM; 3) Autumn indoor feeding period from 200 to 230 DIM. In the indoor feeding periods during spring and autumn, the goats received silage according to appetite, and the silage intake was registered three subsequent days every week. Milk yield was measured three subsequent days every second week. The experiment included seven sampling points from 10 to 230 DIM including various milk analyses and body conditions measures as well as arterio-venous differences of metabolites across the mammary gland. Mammary biopsies were performed at 30, 60, 120, 200 and 230 DIM for analysis the mRNA abundance of 18 candidate genes by RT qPCR. These genes were involved in different pathways (lipid metabolism, lactose synthesis, apoptosis, glucose metabolism) or specifying the major milk proteins and proteins of the milk fat globule membrane. Data were expressed as mRNA copy number relative to the geometric mean of 3 reference genes.

Dietary treatments (addition of saturated or unsaturated fat to concentrate) had no effect on the mRNA abundance of the candidate genes in the mammary gland, that were not related to the observed increase in milk fat content in 'Saturated' compared to 'Control' and 'unsaturated' groups. Conversely, the lactation stage affected the mRNA abundances of most of the genes studied, in particular those involved in lipid metabolism that generally increased and then decreased over the lactation period, and their relationship with the milk components secretion need to be further explored.



# Breeding for goat milk quality in Norway

Thor Blichfeldt  
Norwegian Association of Sheep and Goat Breeders

Norwegian goat milk production is 19 million litres of goat milk in 340 herds. Ninety percent of the herds take part in the Goat Recording System operated by the dairy cooperative TINE. The Norwegian Association of Sheep and Goat Breeders (NSG) is responsible for the goat breeding activities based on the information from the recording system.

This paper reports on the genetic progress made for milk quality traits over the last 10 years. Breeding activities of vital importance for the genetic gain are described.

## **Breed**

We have one breed of milking goats in Norway: The Norwegian Dairy Goat. The basis of the breed is the feral goat which is of the North-European landrace type. The breed has an open herd book allowing in other breeds that could improve our own population (a composite breed). A few Saanen goats were imported in the 1970's, and semen from French Alpine has been imported in 2007 and in 2011. The French Alpine genetics have not yet made a significant impact, but will hopefully contribute to improvements of the Norwegian population and help keep the rate of inbreeding under control.

## **Breeding goal**

Eight traits that are included in the breeding goal. Milk production per day, dry matter content of the milk (protein%, fat% and lactose%) and udder/teat conformation have been traits in the breeding goal for more than 30 years. Speed of milking, free fatty acids and somatic cell count were included as new traits in 2008.

## **Breeding nucleus**

NSG is at present cooperating closely with 50 herds having a total of 6000 goats. These herds form the breeding nucleus. The main objective for the breeding nucleus is to create as much genetic progress as possible, which in turn should be disseminated to the rest of the population.

## **Estimating breeding values**

NSG is estimating breeding values monthly for all animals in the Goat Recording System using a multi trait BLUP animal model. The estimated breeding values for the 8 traits are presented to the farmers as an index score with a rolling average (goats born in the last 5 years) of 10 and a standard deviation of 1.

An aggregated breeding value (The Selection Index) is also calculated. The Selection Index has a rolling average of 100 and a standard deviation of 10. Selection decisions should be based on the Selection Index and not the estimated breeding values for the specific traits.

## **Progeny testing**

Traditionally, progeny testing has been organized in "buck circles", farmers cooperating in small breeding groups circulating bucks among them for natural mating. Due to the "healthier goat" project and improved protection measures against infectious diseases, the "buck circles" have stopped.

Progeny testing is now done within the individual herd in the breeding nucleus. The breeding nucleus is progeny testing around 100 bucks per year with on average 10 daughters each.

## **Artificial insemination**

When the progeny tested bucks are 2.5 years old, the 5-8 best ones are selected for use in artificial insemination (AI).

Herds in the breeding nucleus have to use AI every year inseminate at least 10-15 goats. The farmers inseminate their goats themselves with a simplified technique we call "a shot in the dark" (depositing the semen in the bottom of the vagina). Non-return rate with this technique is 60%.

AI has become an important tool in goat breeding:

- assures that all herds in the breeding nucleus breed potentially high merit buck kids for progeny testing
- improves genetic connectedness between herds removing bias in the genetic evaluation of animals across herds

### Null-alleles in the alfa-s1-casein gene

Two single point deletions in the CNS1S1 locus of chromosome 6 are present in Norwegian dairy goats, both associated with no synthesis of alpha-s1 casein (null-alleles). The deletion in Exon 12 seems to be unique for Norwegian goats. The other deletion in Exon 9 is well known in other breeds. A study of Hayes et al (2006) reported the gene frequency of the deletions in Norwegian breeding bucks to be 0.72 and 0.08, respectively.

Several studies have shown that the null-alleles in the alfa-s1-casein gene have a negative effect on milk quality. In Norway the increase of free fatty acids (FFA) has been emphasised, as high levels of FFA in the milk has been a major quality problem for the dairy industry. The reduced cheese making capability of milk from goats with null-alleles has also been of concern.

In a field study conducted in 2007-2010 (Blichfeldt et al, 2011) we investigated the effect of the three functional genotypes (“homozygous null”, “heterozygous null” and “homozygous not-null”) on production traits. In the “homozygous null” group FFA was 1.39 mmol per litre, significantly different from the two other groups with FFA levels of 0.84 and 0.86, respectively. Reducing the frequency of goats that are homozygous for a null-allele seems to have a substantial effect on milk quality.

Ten years ago 2/3 of the goats in Norway were of the genotype “homozygous null”. Reducing the frequency of null-alleles has become an important breeding objective to improve milk quality. From 2008 and onwards all goat milk producers have been offered to genotype their bucks. Close to a 1000 buck kids were genotyped in 2012.

The gene frequency of null-alleles of the genotyped young bucks approved for breeding in the breeding nucleus has decreased from 80% in 2005 to 16% in 2012.

### Genetic gain for the Selection Index

Figure 1 shows the genetic merit of the female kids tagged in the years 2002 to 2012. The genetic progress was rather low in the beginning of the 10 year period, but from 2007 and onwards yearly genetic gain increased substantially, more so in the breeding nucleus than in the outside herds. The genetic lag between the nucleus and the rest of the herds is now around 3 years.

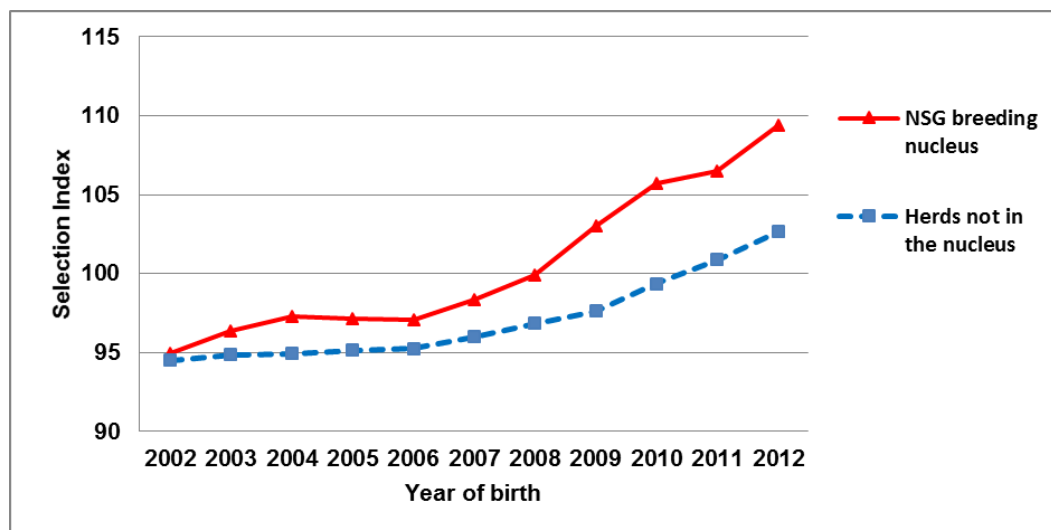


Figure 1. Genetic trend for the selection index for female kids tagged 2002-2012 in the 50 herds that are members of NSG's breeding nucleus and for the 225 herds in the recording system but not in the breeding nucleus.

### Genetic gain for milk yield, protein, fat and lactose

The annual genetic gain for percent of protein, fat and lactose in the milk in the breeding nucleus is presented in Figure 2. Over the 10 year period the percentage of solids (sum of protein, fat and lactose) in the milk has increased by 0.55 percent points, mainly due to the increase in fat percentage.

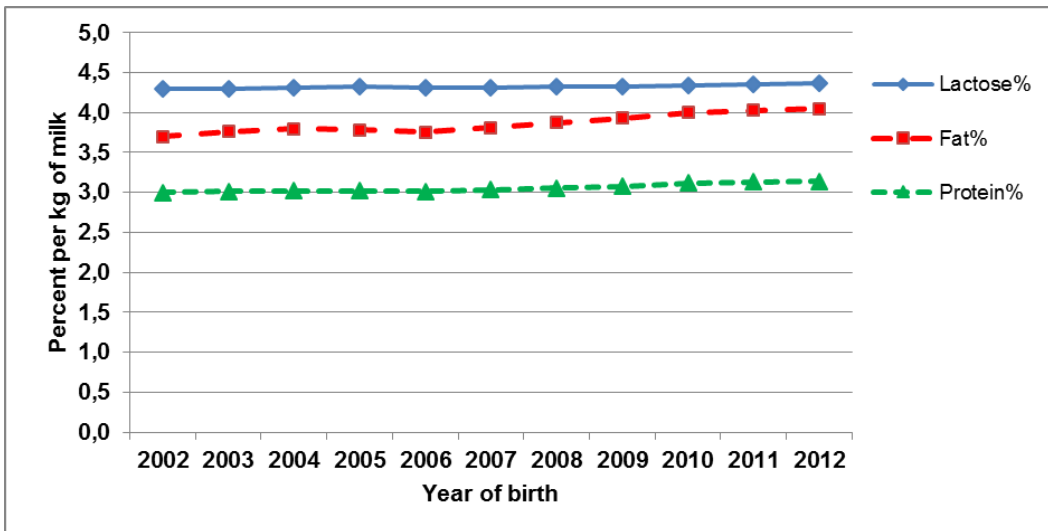


Figure 2. Genetic change in the percentage of protein, fat and lactose in the milk for female kids in the breeding nucleus tagged 2002-2012. Estimated breeding values in 2002 are set to 3.0%, 3.7% and 4.3%, respectively.

The annual genetic gain for milk yield per day and gain for solids (sum of protein, fat and lactose) per day is presented in Figure 3. Daily milk yield has decreased and yield of solids per day has not changed during the period from 2002 to 2012.

The breeding goal is to increase milk yield and percentage of protein, fat and lactose resulting in an increase in kg of solids per day. Daily milk yield has unfavourable genetic correlations to protein%, fat% and lactose% (-0.48, -0.46 and -0.36, respectively). It is therefore hard to make progress in milk yield and the percentage of the components per kg of milk at the same time.

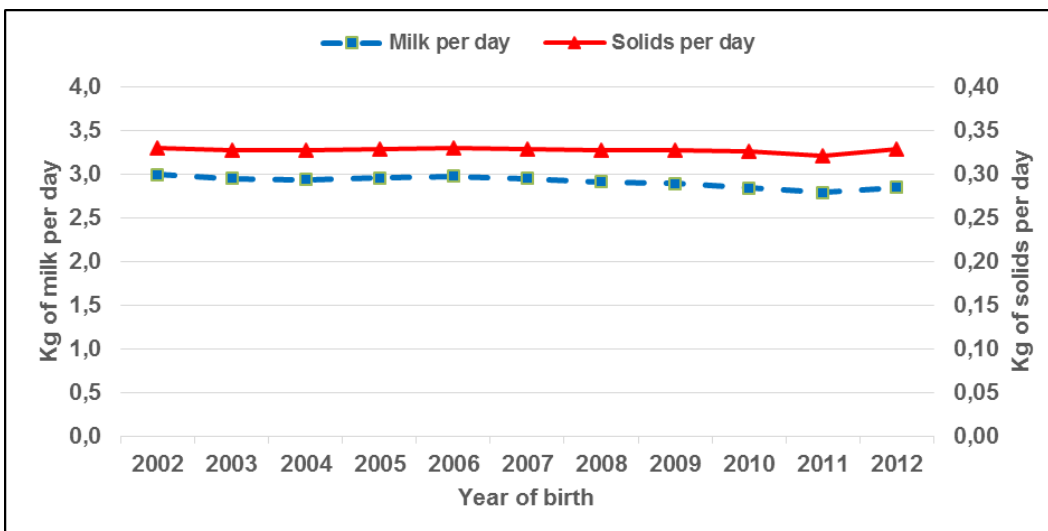


Figure 3. Genetic change in milk yield per day (left axis) and yield of solid per day (right axis) for female kids in the breeding nucleus tagged 2002-2012. Estimated breeding values in 2002 for milk and for percentage of solids per kg of milk (sum of protein%, fat% and lactose%) are set to 3 kg per day and 11% per kg of milk, respectively.

### Genetic reduction of free fatty acids

The observations of FFA in milk samples are recorded in mmol per litre. The observations are not normally distributed and are log transformed when estimating breeding values. The breeding values are then in turn converted into an index score where one standard deviation reduction of the breeding value equals one point increase in FFA index score.

From 2002 to 2008 there was little change in FFA index score, but from 2009 to 2012 the index score has increased by one index point. This translates to a reduction in FFA estimated breeding value of one standard deviation.

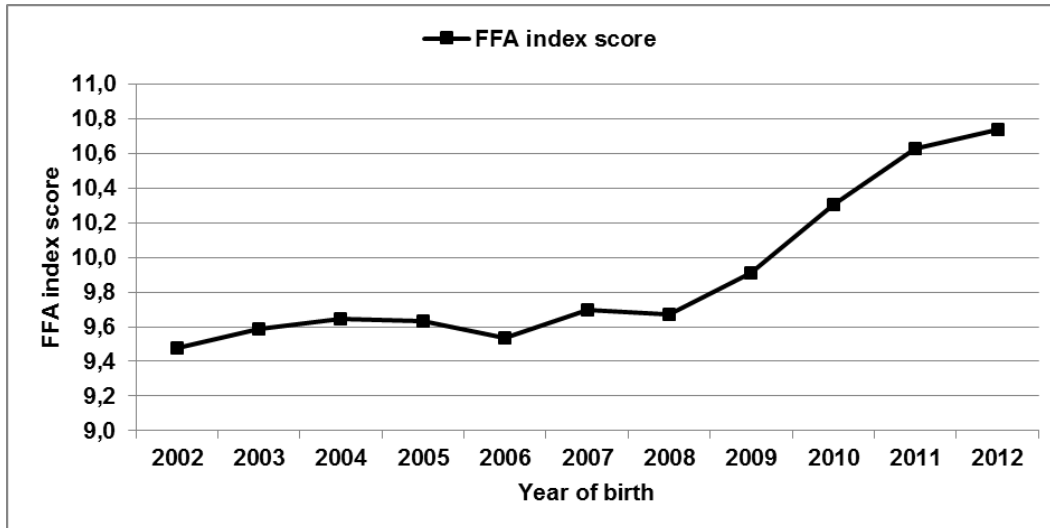


Figure 4. Genetic change in Free Fatty Acid (FFA) index score for female kids in the breeding nucleus tagged 2002-2012. An increase of one index point equals one standard deviation reduction in estimated breeding value for the log value of FFA.

### Genetic change to support revenue

In Norway we have quotas on goat milk production (kg of milk per herd per year). Due to the economic income structure specific for Norway (subsidies per goat, quality payment for increased percentage of solid per kg of milk, etc.) the priority of most farmers are to produce their quota on a low/medium level of kg per milk per goat in combination with a high percentage of solid per kg of milk. Emphasis is also given to the level of free fatty acid in the milk, as high levels will reduce the price of the milk.

The relative weights of the traits in the selection index reflect the priorities of the farmers. The genetic changes described for milk yield and percentage of solid are as expected, and assist the farmers in increasing the income of the milk sold.

The genetic decrease in free fatty acids is considered to be of vital economic importance.

In conclusion, the Norwegian goat breeding scheme supplies the farmers with improved genetics to support the economics of goat milk production. The rate of genetic gain per year has been speeded up the last years, mainly due to increased use of AI and intensive selection in the young breeding bucks against the null-alleles in the alfa-s1-casein gene.

## Effects of breed on milk quality traits from organic goat farms

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Quality traits of goat milk from five organic farms in the Veneto Region (North East of Italy) low mountain area (400-700 m) have been investigated for two years. In that area goat milk production is limited compared with other Italian Alpine regions, though it seems interesting and profitable for small-medium size farms producing artisan cheese for local markets.

Herd size was between 67 to 175 lactating goats of two breeds (Alpine and Saanen) with a majority of the second one (74 %); crossbred as well as goats from local breed were rare. Because of kidding season in that area is normally concentrated between February and the beginning of March, fresh milk samples, from bulk and selected group of goats, were collected monthly (from April to October) and analyzed for chemical composition and renneting properties (using a computerized renneting meter).

As expected, in the investigated farms, Saanen goats showed higher milk production (+ 13 %) compared to the Alpine ones. Milk fat and protein (%) were higher in Alpine goats compare to Saanen, respectively 3.40 vs 2.96 and 3.30 vs 2.84. No significant difference were found between the two breeds for pH (6.61 vs 6.65) and milk urea nitrogen (MUN, mg/dL 36.03 vs 35.87). Somatic cell counts (SCC) and standard plate counts (SPC) were slightly lower in Alpine goats but only SPC difference was significant (log-n 3.56 vs 4.32) probably due to a large variability between animals and farms for these traits. Fatty acid profile (SFA, MUFA and PUFA) and content of specific n-6, n-3 and CLA (conjugated of linoleic acid) did not differentiate between breeds. Renneting parameters: r (milk clotting time- min), K20 (curd firming time –min) and A30 (curd firmness– mm), measured on row fresh milk showed a large variability between animals, lactation stage (DIM) and farms; nevertheless the difference between the two breeds were significant for the three traits considered. Milk from the Alpine goats has shorter clotting time (r) and curd firming time (K20) compared to the Saanen, (15.27 vs 18.44 and 1.57 vs 3.04 respectively) and shows an higher curd firmness (38.61 vs 30.88). The three renneting traits seem to indicate a better milk quality in the Alpine goats; that might be important for small scale artisan cheesemaking because it facilitated clotting process, whey separation and cheese yield. The variability of renneting parameters of milk between animals within the same breed, might suggest to investigate their heritability, with the aim of considering these traits in the selection of goats population, similarly to dairy cows, to obtain goat milk with better cheese attitude.

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# Effects of feeding and physiological factors on goat milk fatty acid secretion and milk fat lipolysis

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This review is focused on the specificities of goats compared to cows, with specific emphasis on the responses of milk fatty acid (FA) secretion and milk fat lipolysis to physiological and nutritional factors, and possible underlying mechanisms.

The effect of lactation stage on milk fat yield and FA composition is similar between goats and cows, whereas the responses of milk fat yield and composition to dietary factors, in particular the types of lipid supplements, differ largely between the two species. With almost all studied lipid supplements, milk fat content increases in goats but not in cows. Marked interactions occur in both species between the composition of basal diet (forages, starchy concentrates) and lipid supplementation on milk FA responses, including trans-10 and trans-11 18:1 and isomers of conjugated linoleic acid (CLA). The goat is much less sensitive than the cow to alterations in ruminal biohydrogenation pathways causing the shift from trans-11 to trans-10 18:1 as a major intermediate which occurs on diets rich in starch and polyunsaturated FA (PUFA). Interestingly, changes in milk fat melting points to diet were small and of similar magnitude in goats and cows, despite of differences in milk fat secretion and FA profile responses between the two species. Goat milk cis-9,trans-11-CLA content increases greatly after either fresh grass feeding or vegetable oil supplementation, but does not change markedly when animals receive whole untreated oilseeds.

In goats, milk fat content and yield are not altered by dietary fish oil supplementation at doses which induce milk fat depression (MFD) in cows. However, significant reductions do occur in goats fed high-starch high-fish oil diets, but the relative decreases are lower compared with cows. Even during high starch and fish oil induced MFD in goats, milk trans-10-18:1 concentration did not increase (contrary to cows) whereas cis-9,trans-11CLA was substantially increased (more than in cows).

With regard to the regulation of mammary lipid metabolism, species differences have also been identified. Changes in the transcription of major lipogenic genes (mRNA abundances of genes involved in FA uptake (LPL), de novo synthesis (ACACA and FASN) and delta-9 desaturation (SCD)) in mammary tissue to nutritional factors do not always correspond with observed milk FA secretion responses. In goats as for cows, data suggest i) that the availability of substrates is more limiting than the lipoprotein lipase (LPL) activity in the uptake of long-chain FA, except with extreme diets fed to cows, in which mammary LPL expression decreased, and ii) that other proteins involved in the FA uptake and intracellular transport (e.g., fatty acid translocase, CD36; fatty acid-binding protein, FABP) may be implicated. In cows and goats ACACA and FASN mRNA abundances were linked to short- and medium-chain FA synthesis, even though the abundance of these transcripts are not always decreased by the addition of PUFA in the diet, in goats at least. In this species, ACACA and FASN mRNA are regulated by dietary factors at a transcriptional level, and SCD is regulated at a transcriptional and/or post-transcriptional level, depending on the lipid supplements. However, in cows, the abundance of SCD mRNA varies little with diet composition, except for a decrease when "rumen-protected" fish oil or docosahexaenoic acid (DHA)-rich algae were fed.

As previously stated for diet-induced MFD, feeding diets of similar composition to cows and goats does not substantially alter mammary lipogenic gene expression in the caprine. Altogether, these data suggest that variations between ruminants in mammary FA secretion and lipogenic responses to changes in diet composition reflect inherent inter-species differences not only in ruminal lipid metabolism, but also in mammary specific regulation of cellular processes involved in the synthesis of milk fat.

Post-ruminal infusions in cows have demonstrated that trans-10,cis-12-CLA or trans-10 18:1 have anti-lipogenic effects. Moreover, in cows, the responses of mRNA abundances of the lipogenic genes involved in de novo FA synthesis, FA uptake, transport and esterification to either trans-10,cis-12-CLA infusion or diets that induce MFD, showed a large decrease that occurred prior to any decrease in SCD1 mRNA. Conversely, in goats, administration of trans-10,cis-12-CLA at the duodenum or when fed as calcium salts lowered milk FA product/substrate ratios for SCD in the absence of, or only a small decrease in milk fat secretion. This suggests that the expression of mammary lipogenic genes is less sensitive to the anti-lipogenic effect of trans-10,cis-12-CLA in goats than cows, which was confirmed in vitro using bovine and caprine mammary slices. However, for SCD the converse is true with a higher sensitivity being reported in goats. This is in agreement with data on milk FA, since comparisons between studies in goats and cows with similar dietary changes showed that, in general, milk FA product/substrate ratios for SCD decreased in goats whereas these ratios increased in cows.

Furthermore, post-ruminal infusion studies in cows have shown that in addition to trans-10,cis-12-CLA, trans-10,trans-12-CLA and trans-9,trans-11-CLA reduced milk FA product/substrate ratios for SCD. This suggests that these two biohydrogenation intermediates could be specific inhibitors of SCD activity, since they were not associated with MFD. In particular, the large increase in milk trans-9,trans-11-CLA in goats receiving diets supplemented with sunflower oil could be involved in the typical decrease of milk FA product/substrate ratios for SCD in this species. In contrast, increases in milk trans-9,cis-11-CLA concentrations that may lower milk fat synthesis in cows, did not occur in goats receiving high starch-high PUFA diets.

The development of either goat flavour (linked to free, branched and medium-chain FA release) or rancidity (due to excessive release of free butyric acid) is related to the peculiarities of the goat milk FA composition and lipolytic system. The milk LPL activity is lower in goat than in cow. This enzyme has a higher affinity for fat globules with an activity more closely correlated with post-milking spontaneous lipolysis of milk fat in goats compared with cows. Goat milk lipolysis and LPL activity are low during early and late lactation, and decrease when animals are underfed or receive a diet supplemented with plant oils, varying considerably across goat breeds or genotypes. This could explain, at least in part, the observed decreases in the goat flavour of dairy products when animals receive lipid-rich diets.

In goats the alpha-s1-casein (CSN1S1) gene polymorphism affects milk composition, with a decrease in milk fat content, and 8:0-12:0 concentrations, and an increase in milk FA product/substrate ratios for SCD (without changing milk fat melting point), and in milk fat spontaneous lipolysis in the low CSN1S1 genotype. Moreover, with diets supplemented or not with extruded linseeds, several genotype x feeding interactions were observed, with lower responses in milk fat content and FA concentrations, and much higher response in milk fat spontaneous lipolysis in goats of the low than of the high CSN1S1 genotype. In the same way, genotype x feeding interaction could be responsible

for the lower amplitude of the response to food-deprivation observed on production and composition of milk as well as on mammary gene expression in goats carrying low compared to high genotype.

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## **Characterization of exon 14 and intron 5 of the SREBP-1 gene and its relationship with milk traits in Sarda goat**

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SREBP (sterol regulatory element binding protein) is a family of transcription factor that regulates the expression levels of some genes involved in fatty acid biosynthesis and uptake. SREBP-1 is an isoform member of SREBP family, and it controls the synthesis of fatty acids in various tissues such as the mammary gland. In cattle mutations in exon 14 and a deletion in intron 5 showed to influence the amount of milk fat yield and carcass traits. The aim of the present study was to screen single nucleotide polymorphisms (SNPs) or insertion/deletion in the exon 14 and intron 5 of the SREBP-1 gene and to evaluate possible relationship with milk traits in Sarda goats. Two-hundred multiparous goat, from 3 to 6 years-old and in their third to fourth lactation, were randomly chosen from four farm located in Sardinia. From each goat a blood sample was taken to DNA extraction and to perform PCR-SSCP analysis of exon14 and intron 5. Moreover, from each goats, every month, from 45th day to 140th day of lactation, milk yield was recorded and a milk sample was taken to assay fat, protein and lactose concentration. Ten randomly chosen PCR products were sequenced in both directions. No different migration patterns in SSCP analysis were found. Our data evidenced no variation in Sarda goat exon 14 and intron 5 of the SREBP-1 gene contrarily to that found in the cattle. Sarda goat produces a high milk fat concentration and this presumably is the result of a genetic selection made by farmers in several years. So this could have led to the removal of the genetic variants producing low-fat milk resulting also in little variability of these traits of the SREBP-1 gene analysed. However, to extend the knowledge about SREBP-1 gene in this goat breed it would be necessary to enlarge the number of samples and to study other parts of this gene.

## Factors influencing technological properties of goat milk

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The Polish goat population comprises more than 100 000 does. They are mainly dairy goats and their average milk yield reaches 600 – 700 kilos of milk per lactation with 3.3% of fat and 3.0% of protein. The goat milk production in Poland is about 40 million kilos a year. Even though drinking milk is still the main final product, cheese and yogurts are getting more popular every year. Therefore improving usefulness of goat milk to cheese production is an up-to-date issue in Poland. To improve and optimize the existing methods of processing, and to advance the manufacturing technologies of new milk products, more information is needed about the chemical composition of goat milk and curd making properties. The objective of the study was to evaluate the influence of pathogenic bacteria, leukocyte proportion and leukocyte subpopulations in somatic cell count (SCC) on physico-chemical properties of raw goat milk, cheese yield, and quality of curd and whey in fermentation tests.

The study covered three lactations in the years 2006 – 2008. Totally 487 milk samples were collected from separate udder halves of Polish White Improved and Polish Fawn Improved breeds, during the routine morning milking, on the 30th, 60th and 200th day of lactation. Leukocyte proportion and leukocyte subpopulations in SCC were determined with the flow cytometry method. Each foremilk sample was tested for pathogenic bacteria using standard microbiological techniques. Milk samples were divided into four groups according to the presence, type, and number of bacteria: pathogen-free samples, samples containing minor pathogens at concentration <103 CFU/ml, samples containing minor pathogens at concentration >103 CFU/ml, and samples containing major pathogens. Since the preliminary analysis revealed differences in chemical milk composition, cheese yield as well as curd and whey quality only between first three lactations, three parity classes were established: 1st, 2nd and ≥3rd lactation. The data were evaluated by the multivariate analysis of variance with the Bonferroni correction in SAS package. SCC was transformed into the natural logarithmic values. Significance level of 0.01 was assumed.

Year of study and stage of lactation were the only factors which influenced cheese yield, curd and whey quality and physico-chemical properties of goat milk. The effect could be observed both in pathogen-free and pathogen-contaminated samples. SCC had impact only on lactose content in pathogen-free milk samples whereas percentage of total leukocytes and their subpopulations in SCC were linked only with acidity of milk. Presence of bacteria does not seem to modify physico-chemical properties of raw milk, cheese yield, and quality of curd and whey in fermentation tests and milk containing bacteria can be processed by dairies. Although thermal processing kills bacteria thermostable toxins remain and may pose a threat to consumers' life.

## **Additive and dominance effects of casein haplotypes in Norwegian dairy goats**

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The four casein loci – CSN1S1, CSN2, CSN1S2 and CSN3 – encoding for the four caseins are found clustered within 250 kb in chromosome 6 of the caprine genome. The fact that the genes are closely organized implies that they have high tendency of being inherited together as haplotypes. This study investigates additive and dominance effects of casein haplotypes on milk composition and quality. In this study, 1825 Norwegian dairy goats (745 bucks and 1080 does) were genotype for 38 SNPs within the entire casein region. Casein haplotypes were inferred within each of the four loci using BEAGLE. Phenotype measurements on milk yield and composition were obtained from Norwegian dairy goat control recording system. Fixed effects of additive and dominance effects of casein haplotypes were estimated using single trait mixed model combined with principal component analysis (PCA) to solve multicollinearity in the design matrix. Additive effects of haplotypes of the CSN1S1 locus were observed for protein and fat percentages, free fatty acids (FFA) content and somatic cell count (SCC) in milk. The most frequent haplotype of the CSN1S1 locus had negative additive effect on protein and fat percentage and increased the FFA content and SCC in milk. This haplotype also had negative dominance effects for protein, fat and lactose percentages and positive dominance effect for milk yield in kg. Some haplotypes of the CSN2 locus had effect on protein and fat percentages, milk yield and FFA content. Additive effects of haplotypes of the CSN3 were found for protein. The observed effects of casein haplotypes on milk composition and quality traits indicate that there is an opportunity to select for specific haplotype as a tool to improve goat milk quality in the population.

## Consequence of overdominance in breeding

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Deletion in exon12 of CSN1S1, so far reported only in Norwegian goats, has been found in high frequency (0.73). This deletion reduces dry matter (DM) content of the milk and it is difficult to explain its high frequency in the population. In the study, 575 goats were genotyped for 38 casein SNPs and their milk production records were obtained from the Norwegian Dairy Goat Control. A test-day mixed animal model with additive and dominance fixed effects of single SNP were fitted including polygenic effects. The deletion (SNP 14) and a cluster of SNPs at CSN3 had additive effect on fat % and protein %. The deletion exhibited over-dominance effects on milk kg and lactose % and dominance effect on fat % and protein %. The observed non-additive effects reduced the additive genetic variance available for selection of the deletion allele at its current frequency, 0.73. This reduced the selection pressure of conventional breeding on the allele, and inclusion of molecular information in the national breeding could help to reduce its frequency in the population.

# Feeding different lipid supplements through lactation in dairy goats:

## 1) effects on energy balance and milk production

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Milk with high dry matter content, acceptable flavour and good rennet coagulation properties are important when developing new and improving existing goat milk products. To obtain goat milk with acceptable quality throughout the lactation period, it is necessary to secure an adequate supply of energy to the animals. This can be a challenge, especially for high yielding goats in early lactation. Dietary fat supplements can be used to increase the total energy concentration of the diet. The aim of the present study was to examine how supplements of saturated and of unsaturated fat would affect energy balance and milk production in dairy goats.

Thirty Norwegian dairy goats with kidding in February 2011 were fed a control diet with a concentrate mixture of barley, rape seed meal (expro 00SF), soy bean meal, beet pulp, molasses and mineral/vitamin premix until 60 days in milk (DIM). After 60 DIM and until the end of the lactation period (230 DIM), the goats were assigned to three experimental groups (balanced for parity and genotype at the  $\alpha$ S1 casein locus) of 10 goats receiving 3 dietary treatments differing in the composition of the concentrate. The 'Saturated' and 'Unsaturated' groups received the control diet, with an inclusion of 8% of saturated (Akofeed Gigant 60; rich in C16:0) and unsaturated (rapeseed oil, rich in cis-9-18:1 and cis-9, cis-12-18:2) fat, respectively. The experiment consisted of three different periods: 1) Spring indoor feeding period from 1 to 120 DIM; 2) Mountain grazing period from 120 to 200 DIM; 3) Autumn indoor feeding period from 200 to 230 DIM. The goats received 0.9 kg/d concentrate until the start of the mountain grazing period, thereafter 0.7 kg/d. During indoor feeding, the goats received silage according to appetite. Silage intake was measured on three subsequent days every week, and milk yield on three subsequent days every second week. Milk analyses, body weight, body condition and BMI (body mass index), body composition (computer tomography) and arterio-venous differences of metabolites across the mammary gland, were collected at seven sampling points from 10-230 DIM. Mammary biopsies were taken at 5 sampling points for gene expression studies.

We report the following findings:

- Generally, the goats lost body weight from kidding to 200 DIM, with a pronounced body fat mobilization during the mountain grazing period (120 to 200 DIM), followed by a body fat deposition towards the end of lactation (230 DIM).
- No effect of lipid supplements was observed on body weight changes, body condition score or amount of body fat during the lactation cycle.
- Milk yield was not affected by inclusion of dietary fat.
- Milk fat content was higher in 'Saturated' group compared to 'Control' and 'Unsaturated'.

- From 90 to 200 DIM daily milk fat yield was lower in the 'Control' group, compared to 'Unsaturated' and 'Saturated', while no difference was observed between the two dietary lipid sources.
- At 230 DIM the daily milk fat yield was generally low, and no effect of fat supplements was observed.
- Milk protein content was not affected by dietary fat supplements.

It is concluded that dietary fat supplements increase milk fat yield in dairy goats. Late lactating goats accumulate large fat deposits in preparation for their next lactation. Dietary lipid supplements had no effect on milk fat yield at this stage.

# Feeding different lipid supplements through lactation in dairy goats:

## 3) effects on arterio-venous differences of metabolites across the mammary gland

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Variations in goat milk flavour, sometimes including a prominent rancid-tart flavour, has made the development of new marketable products from Norwegian goats difficult. The occurrence of rancid and tart flavour is caused by increased concentration of free fatty acids (FFA) in the milk. Feeding dietary fat decreases milk lipolysis and FFA concentration in the milk. Supply of fatty acids to the mammary gland seems to be of fundamental importance to ensure stable and good milk quality.

The aim of the present study was to examine how dietary supplements of saturated and unsaturated fats affect blood concentrations and mammary gland extraction of milk precursors.

The experiment included 30 Norwegian dairy goats fed a control diet until 60 days in milk (DIM) and thereafter assigned to three different groups of 10 goats, receiving different supplements of concentrate differing in fat composition. The experimental design is described by Eknæs et al. (2013). Five times during the lactation period, at 30, 60, 90, 120 and 230 DIM, blood was sampled from the jugular vein (representing systemic blood supply to the mammary gland) and the milk vein three times with 2.5 hours intervals between morning and evening milkings. In addition, blood samples were taken from the jugular vein at 10 DIM and by the end of the mountain grazing period (at 200 DIM). Glucose, triglycerides (TAG),  $\beta$ -hydroxybutyric acid (BHBA), non-esterified fatty acids (NEFA) and cholesterol concentrations in plasma was measured by standard laboratory procedures.

We report the following findings:

- Dietary lipid supplements increased the jugular concentration of TAG, and this was associated with increased mammary extraction of TAG when dietary fat was fed, but no long-term effects was observed at 230 DIM.
- Jugular concentrations of NEFA were above 0.3 mmol/L from kidding until 60 DIM, indicating a negative energy balance with fat mobilization during the first two months of lactation.
- Jugular concentrations of BHBA decreased when dietary lipids were added. Dietary lipids could not prevent an increase in BHBA by the end of the mountain grazing period, where pasture availability or quality may have been limited causing mobilization of body lipids and increased hepatic ketogenesis.
- Total cholesterol concentration in jugular plasma increased when dietary lipids were added, but at 230 DIM the cholesterol AV-difference became negative in all groups, indicating a net synthesis or release from the mammary gland.

- Jugular glucose concentrations were not affected by lipid supplements. Mammary extraction of glucose followed milk production and increased towards peak lactation (90 DIM), but decreased thereafter.

In conclusion, fat supplementation in the diet can be used to regulate mammary lipid supply and uptake and hepatic ketogenesis. Dietary fat supplementation can not be used to prevent fat mobilization arising from an inadequate availability or quality of the basal ration by the end of the mountain grazing period.



# **Taurine Rich Goat Milk & its Products: Components of Functional Food, Nutraceuticals and Assurance to Sound Health**

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Climate, Environment and Health can not be separated; in fact they are spiral bonded. Any alteration in climate can be easily being notice in environment/ecology; subsequently reflected in health status. Now health issues are basically much more nature dependent; physically, chemically as well biologically (Genetics, physiology) and so on. Environmental issues are increasingly becoming part of discussion from coffee table to round table. Often while dinning or socializing this issue invisibly comes up with hot or chilled cold end, sometime with helplessness. Any serious change in natural condition affects our entire life activities this may be food, feed, or function. . To cope, such situation and to provide remedies; is the sincere demand from the all corner; hence the only best way is effective management of available space and resources with maximum gain to self, environment and beyond and to have healthy; happy man, animal and environment; to get the answers one has to look back the nature and the mother earth. Since ages milk is the first earthy substance which any mammal takes to extend his/her life at this planate and to survive Traditionally goat milk is regarded as poor man saver but now it is fast getting several labels, one of which is better for health, the such labels confer on it is, due to presence of superior and significant quantities of essentials molecules require for sound health like; Minerals, Vitamins, Protein & Amino Acids. These molecules are core of strength and wellbeing also. Goat milk is rich in various types of immuno protective proteins, several essential minerals, omega acids and a large number of vitamins. Though amino acids are building block of proteins but the presence of free amino acids not require for protein synthesis are equally important. Many of the free amino acids are integral part of several life processes; one of such free amino acid is Taurine. Taurine is sulfur containing amino acid and chemically it is 2-Amino Ethane Sulfonic acid which is surprisingly is in very high concentration in goat milk and has a 20-fold higher level than cow's milk, almost equal to that in human milk. Cow milk on which majority of infants survive almost lack taurine with time; as of its colostrums which suppose to have higher concentration of taurine is still below to goat milk concentration because of all this ,formula cow milk contains taurine concentration to make at per with human milk .Looking further, experimentation has proved a high content of taurine in all stages of lactation and new-born and infants fed goat milk do not need any addition of this amino acid. While going beyond the milk to milk products, it seems that taurine justifies all the physical parameter; the distribution of taurine among dairy products, their by-products and waste has been conformed while making cheese based on goat's milk compared with the amount of taurine present in the starting milk, the biggest proportion of taurine was found in whey while 12.5-16.5% was found in the goats' cheeses. Besides, a significantly higher content of taurine was found in Caciocotta goats 'cheese, obtained from milk heating at 95 °C , than in Caprino goat's cheese, at lower temperatures this signifies that taurine retention is not temperature dependent. Apart from above, taurine content did not significantly vary during both fermentation and the entire storage period. There is increasing evidences that sulfur amino acids (SAA) play an important metabolic and functional role in human health and decease prevention. It is further observed that SAA also provide elemental Sulfur require for growth and development, and in general, it is source of energy and nutrient needs of various life processes. Taurine has long been placed under such category. To add little more the best-known functional food until now is mother's

milk of which taurine is component. It is possible and feasible to modulate target functions via food supplement

# Can milk composition and individual cheese yield be influenced by suckling?

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## Introduction

Milk with high fat and casein content is required to achieve high cheese yields. Swedish dairy goats produce milk with low contents of fat, total protein and casein, which leads to low cheese yields. The objective of this study was to investigate if milk fat, casein content and individual cheese yield could be increased by suckling.

## Materials and methods

In study I, Swedish dairy goats (n=8) were kept together with one kid each in early lactation. On day 1, milk samples were collected continuously from one teat when the kid was suckling the other teat (S). On day 2, milk samples were collected from one teat during milking only (M). Blood samples were collected before, continuously during and after both S and M. The milk composition was analyzed by mid-infrared spectroscopy and plasma levels of oxytocin and cortisol were analyzed by ELISA.

In study II, milk composition and individual cheese yield was measured in milk from 12 goats, kept in 4 different MIX systems (milking combined with suckling) during 4 weeks in a cross-over design. In treatment 1 and 2, goats and kids were separated during 8h daytime and dams were milked twice daily. In treatment 1, kids suckled freely before each milking (S-8hS) and in treatment 2, kids suckled freely before each morning milking, but during afternoon milking, dams were milked only (S-8hM). In treatment 3 and 4 goats and kids were separated during 16h night-time and dams were milked once in the morning. In treatment 3 kids were allowed to suckle in 30 minutes before milking (S-16hS) and in treatment 4 dams were milked only (S-16hM). Total milk yield, i.e. both from milking and suckling were measured, the latter by a weigh-suckle-weigh method and number of sucklings recorded during 24h once a week. Casein content and individual cheese yield was measured by a rennet-coagulation method. The milk samples were clotted for 1h before the gel was vertically cut and centrifuged. SCC was analyzed by fluoro-opto-electronic cell counting and milk urea was analysed by an enzymatic colorimetric method.

## Results

In study 1, plasma levels of oxytocin increased during S, but not during M. The milk fat content was higher during S (P<0.05) than during M. In study 2, fat content and individual cheese yield were increased when dams were suckled before milking compared to milking only, despite no difference in total milk yield. Preliminary, there was no difference between treatments on SCC and milk urea.

## Conclusions

This study demonstrated that suckling before or in combination with milking gave a better udder emptying, most likely due to elevated plasma levels of oxytocin during suckling compared to milking only. Suckling thus increased both milk fat content and cheese yield in Swedish dairy goats.

## **Feeding different lipid supplements during lactation cycle in dairy goats: 4 Effects on fatty acid profile, free fatty acids and sensory properties of the milk**

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The aim of the present study was to examine the effect of feeding different lipid supplements on fatty acid composition, content of free fatty acids and sensory properties of goat's milk. Thirty Norwegian Dairy Goats kidding in February 2011 were fed a control diet with a concentrate mixture consisting of barley, rape seed meal (expro 00SF), soy bean meal, beet pulp, molasses and mineral/vitamin premix until 60 days in milk (DIM). Thereafter, the goats were assigned to three experimental groups each of 10 goats, called 'Control', 'Saturated' and 'Unsaturated'. The concentrate mixtures in the groups 'Saturated' and 'Unsaturated' were based on the same mixture as the control diet with addition of 8 % of a source of 'Saturated' (Akofeed Gigant 60; rich in C16:0) and 'Unsaturated' (rapeseed oil, rich in cis-9-18:1 and cis-9, cis-12-18:2) fat, respectively. The experiment consisted of three different periods: 1) Spring indoor feeding period from 1 to 120 DIM; 2) Mountain grazing period from 120 to 200 DIM; 3) Autumn indoor feeding period from 200 to 230 DIM. The goats received 0.9 kg concentrate per day until the start of the mountain grazing season, thereafter 0.7 kg per day. The experiment included six sampling points from 30 to 230 DIM, and the milk was analyzed for composition of fatty acids in triglycerides and free fatty acids, total content of free fatty acids and sensory properties. Different profiles of fatty acids (triglycerides) in milk were obtained from the different feeding regimes. Goats fed unsaturated fat had a higher content of the long- and unsaturated fatty acids, while milk from goats fed saturated fat had high content of palmitic acid. The 'Control' group produced milk with a higher content of odd-, medium and branched chain fatty acids compared to the two other groups. The content of free fatty acids in milk were low in the beginning and in towards the end of lactation, and highest at 90-120 DIM. High content of free fatty acids were highly correlated with poor sensory properties (tart/rancid flavor). The profile of free fatty acids was analyzed, but no specific fatty acids were found to be related to tart/rancid taste, because rancid/tart milk in general had high content of all the individual fatty acids. The results indicate that feeding unsaturated fat increases the content of long chain unsaturated fatty acids regarded as favorable in the human diet and decreases the content of palmitic acid as compared to feeding saturated fat.

## **Influence of environmental factors on acidity, citric acid and casein level in goat milk**

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Dairy goats have become popular animals kept on non-commercial farms in Poland in recent years. Those farms are often visited by families with children and that helps to promote goat milk products.

Milk goat products are usually recognized as functional and healthy. Variety of factors have an influence on milk yield and its physico-chemical composition. Milk acidity is associated with hygienic condition of animal environment. The high variability of milk acidity during the lactation indicates poor hygienic conditions during milking. Together with somatic cell count it can also serve as an indicator of health status of the udder because it decreases as a result of mastitis. Moreover, it is known that the average acidity of sheep milk is the lowest at the end of lactation. In this study an influence of stage of lactation and parity on milk acidity as well as concentration of citric acid, total protein and casein in goat milk were estimated.

The study was conducted on Polish White and Polish Fawn Improved dairy goats. The milk samples (1536 in total) had been collected each month for six years. Citric acid concentration, acidity, total protein and casein level in milk were evaluated and linked to the stage of lactation and parity of goats using the analysis of variance.

It turned out that the parity did not influence any studied milk parameter. However, the concentration of citric acid decreased while acidity increased during lactation. Lower citric acid concentration may worsen mineral absorption. The increase of acidity may mean that bacteria have better environment to grow in milk at the end of lactation. As expected the casein concentration followed that of total protein – it was the lowest in the middle of lactation and the highest at the end of lactation.

## High frequency of $\alpha$ S1-casein null variant in Swedish dairy goats

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Mutations within the casein genes are common in several species. These mutations affect the level of expression of corresponding proteins in different ways, some resulting in higher expression and some in lower expression. The latter gives a negative effect on the milk composition with a lower cheese yield as a consequence. The content of caprine  $\alpha$ S1-casein ( $\alpha$ S1-CN) in the milk is important for the cheese yield and unfortunately there is a mutation giving null expression of this casein in some goat breeds. To find out how spread this mutation might be in Sweden, a screening of goat milk samples was done.

Milk samples from 283 female goats, from 28 farms in ten different geographical regions of Sweden, were analysed for the caseins by capillary zone electrophoresis. The goats were of a Swedish landrace – a breed of ancient origin.

We found 65% of the screened goats to express very low or no content of  $\alpha$ S1-CN. Only 12% of the investigated individuals within the population showed high expression of this protein. These results are in agreement with the Norwegian goat population, where the frequency of low expressed  $\alpha$ S1-CN has been shown to be about 70%.

Since the Swedish goat population seems to be seriously affected by this unfavourable mutation of  $\alpha$ S1-CN gene, it is necessary to identify individual goats homozygous for strong  $\alpha$ S1-CN alleles, which could be used in the future breeding of dairy goats for higher cheese yield.

## Grazing preferences and diet composition of goats in diverse rangeland or cultivated pastures

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Norwegian goat milk production is based on summer grazing on diverse forest or alpine rangeland, and the quality of these pastures is important for milk quantity and quality. In the present study we compared grazing preferences of goats grazing on a heterogeneous rangeland with those grazing on cultivated pastures sown with timothy (*Phleum pratense*) and meadow fescue (*Festuca pratensis*). The experiment was performed during two periods in summer; early (beginning of July) and late (end of August), with ten goats per pasture type and period; 40 goats in total. The rangeland was mapped according to vegetation types. The goats in the rangeland pastures were fitted with GPS collars that recorded their position every 15 min during the two periods. We used n-alkanes and long-chain fatty alcohols found in plant waxes as markers to estimate diet composition. The goats were observed while grazing in both periods, and grazed plant parts and species were sampled together with faeces and analysed for alkanes and alcohols. Cluster analysis was used to group plant species according to alcohol and alkane profiles. The diet composition of each individual goat was obtained by comparing faecal alkane and alcohol profiles with those of the analysed plant groups using least square optimisation. The alkanes and alcohols analyses indicate a very diverse diet in the rangeland with bushes and trees, birch bark (*Betula pubescens*), ferns, grasses, sedges, blueberry (*Vaccinium myrtillus*) and some herbs. In late summer, the diet was particularly diverse, coinciding with a decline in protein content of the herbage. The GPS data indicated that the goats preferred spending time in the grass and herbs dominated vegetation types, although these occupied only a very small percentage of the area. They avoided or spent less time in the wet bogs dominated by sedges. In the cultivated pastures, goats preferred timothy in early summer (85% of the diet), while the diet in late summer was more diverse with more couch grass (*Elytrigia repens*) and tufted hairgrass (*Deschampsia cespitosa*) together with timothy and meadow fescue. The protein content of the diet in the cultivated pastures was stable during summer, while fat content declined and NDF content increased.

Keywords: Diet preferences, goats, nutrient content, plant wax markers, rangeland, cultivated pastures

# **MilkChEST, an integrative approach of the secretion pathways in the mammary epithelial cell: molecular dissection of milk fat adaptability**

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During lactation, mammary epithelial cells (MEC) secrete huge quantities of components, the biosynthesis of which are known in general outline. There are some evidences that a close mechanistic relationship exist between the biosynthesis and secretion pathways of the major milk components: casein micelles and milk fat globules (MFG). However, our knowledge of the molecular events occurring during assembly, intracellular transport and secretion of the micelles and MFG remains scarce. Lately there is also a realization that MEC release in milk microparticules, including exosomes, which contain mRNA and microRNA. To go further into the molecular dissection of the biosynthetic and secretion pathways of the major milk components, processes that determine their structure, as well as their biological and technological properties, a large collaborative project involving several French teams has been launched (funded by the French National Agency for Research and Apis-Gené, France).

Our strategy is based on the relevance of the goat model, with a “naturally occurring Knock Out (KO)” at the CSN1S1 locus and on the use of global approaches (including NGS, proteomics and lipidomics analyses) to decipher the multiple effects of this natural KO on milk secretion and quality.

Our main research goals will be: i) to achieve a better definition of the genome fraction which is expressed in goat MEC during lactation, ii) to obtain a better understanding of the role played by  $\kappa$ s1-casein in the export of caseins from the endoplasmic reticulum to the Golgi apparatus, iii) to identify factors that determine the fatty acid profile of milk fat, iiiii) to go further into the molecular dissection of the mechanisms driving lipid droplets formation and their interaction with the apical plasma membrane during the course of MFG secretion.

The project includes a comparative study of lipid droplet formation in and microparticules release by MEC versus adipocytes, the later cells producing large lipid droplets but lacking the machinery to secrete them. On the other hand, we will focus on the consequences of the absence of the  $\kappa$ s1-casein on the protein and fat secretory pathways, as well as on the fine composition of milk. The ultimate goal is to identify genes playing key roles in the production of milk fat by MEC on which selection and breeding program might be engaged to modulate the fat composition of milk.



## Metabolism Exploration Platform : Transcriptomic approach

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The Transcriptomic Platform is integrated into a larger PlatForm « Metabolism Exploration: from genes to metabolites » (PFEM), which is a scientific and technological infrastructure that brings together the skills and equipments of the Clermont-Ferrand/Theix INRA Centre and the Regional Center for Physical Measurements at the B. Pascal University. This larger structure consists of three components: metabolomics, proteomics and transcriptomics.

The transcriptomic component is dedicated to the gene expression profile analyses which have many applications in human nutrition, as well as in physiology and genetic of animals and vegetals or in microbiology. However, the techniques used require a significant investment in terms of equipment and expertise. This is why we provide the concepts, methods and tools devoted to the transcriptomic studies for the public and private scientific community. Our services include the implementation of DNA microarray and real-time quantitative PCR technologies, guaranteeing an optimal use of instruments and an appropriate analysis of the produced data.

What we can perform:

- Advice for planning biological experiments and transcriptomic experiments.
- Analyses of the samples quality (Nanodrop ND-1000, Agilent Bioanalyzer).
- Microarray analyses: samples labeling, slides hybridization and data acquisition (Ventana hybridization station, hybridization oven and scanner Agilent, Feature Extraction software Agilent).
- Real-time quantitative PCR analyses using TaqMan Low Density Arrays as well as more classical analyses in format 96 or 384-well (AB7900HT Applied Biosystems).
- Statistical analyses of transcriptomic data.

The platform also provides for softwares for bioinformatic analyses of transcriptomic data: GeneSpring, Pathway Studio and Genomatix.

We are at your disposal for any further information:

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## The norwegian Healthier Goats project

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The aim of the project is to eradicate the chronic contagious diseases CAE, CLA and Johne's disease from the Norwegian goat population

Goat production in Norway has changed during the last fifteen years. About 40 milk producing flocks (versus 1000 flocks fifteen years ago) are now producing 20 mill. liters pr year. The number of meat producing flocks is increasing. A health survey in 2000 showed high prevalence of Caprine arthritis encephalitis (CAE), Caseous lymphadenitis (CLA), and respiratory diseases. Also, Johne's disease is enzootic in parts of southern Norway, and vaccination is compulsory in these areas to avoid clinical outbreaks. Johne's disease is notifiable and by June 2008, 45 herds had restrictions. In 2004 88 % of the milk producing herds had CAE antibodies in bulk milk, and a questionnaire in 2003 showed > 70% flock prevalence for CLA. The last 20 years increasing disease problems and decreased milk yield, has been recorded. Therefore the project "Healthier goats" was started, in 2001, with the purpose of eradicating CAE, CLA and Johne's disease.

The eradication principles are built on culling of seropositive animals in flocks where the CAE prevalence < 10%. "Snatching" kids; Kids are taken from the mother and the "infected" barn immediately after birth. They are housed in a clean barn, given cow colostrum and raised on milk replacer, water, concentrate and hay. The goats are slaughtered at the end of the lactating period. Thereafter, the barn and the near surroundings are cleaned and disinfected. Healthy goats are then moved back to the barn to start lactation.

The sanitized flocks are monitored by clinical observation and antibody detection in serum and bulk tank milk. Kids are tested before 5 weeks to detect maternal CAE antibodies for control of the snatching. Thereafter one test before the doe is starting her first lactation. Bulk milk is now tested twice a year to detect antibodies within the flock.

### Applied tests:

Johne's disease: Interferon gamma, Paratuberculose-ELISA/ Pourquier, cultivating faeces, histopathology and pathology. Interferon gamma test is performed in disease eradicated flocks in areas where PTB is enzootic.

CAE antibodies : "Elitest MVV/CAEV" HYPHEN BioMed

CLA antibodies: "Elitest CLA #CK105A" HYPHEN BioMed

Building knowledge: A variety of educational efforts for farmers, advisors and veterinarians are carried out to supply information about the diseases, the project and it's methods.

### Results

By april this year 602 farmers have applied to join the voluntary project and 523 flocks are sanitized.

CAE testing in 137 flocks eradicated by snatching from 2001 to 2008 show 0,8% positive among kids < 5 weeks and 0,9% positive among goats > 6 months. Test results verify that farmers manage to do the sanitation process (snatching) and to follow the projects procedures very accurate. Test positive animals in sanitized flocks are slaughtered.

Out of the 523 sanitized flocks ( by snatching and culling), 3 CAE reinfections , 1 Johne's disease reinfection and 8 CLA reinfections have been observed. Re-infected flocks are carefully monitored and test positive animals are slaughtered.

During 2012 there where no new outbreaks of diseases caused by reinfection in sanitized herds.

By the end of 2013 all goatmilk used by TINE Dairies SA will come from sanitized herds.

## **AlphaS1-casein deficiency recorded for defective genotypes induces a chronic ER stress and deep changes in milk composition, signing a singular secretion process in goats**

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The extensive polymorphism recorded at the CSN1S1 locus has been shown to influence goat milk composition and its technological properties. A deficit in alphaS1-casein is responsible for the accumulation of immature caseins in distended rough endoplasmic reticulum (ER) cisternae of mammary epithelial cells (MEC). This triggers a chronic ER stress which induces, in turn, an adaptive unfolded protein response (UPR). Our data strongly suggest: i) the existence of a membrane-associated form of alphaS1-casein, which is required for efficient export of the other caseins from the ER to the Golgi apparatus; ii) that alphaS1-casein plays a key role in the early steps of casein micelle biogenesis. A differential proteomic analysis (2D-DIGE) of milks from goats of extreme genotypes (A/A vs. O/O) at the CSN1S1 locus revealed the over representation of ER-resident proteins in O/O milks, strongly suggesting a singular secretion mechanism for this genotype. In addition, goats of O/O genotype produce fat globules smaller in size and displaying significant differences in MFGM composition, including both MFGM proteins and polar lipids. A relationship between genotypes at the CSN1S1 locus and the profile (structure and composition) of milk free oligosaccharides (OS), which are also built within the ER, has been shown, thus providing additional evidence for the impact of alphaS1-casein deficiency on the functioning of MEC.

Finally, using different functional genomics approaches, we succeeded in highlighting the general dysfunction occurring in MEC from alphaS1-casein deficient animals, and in identifying genes contributing to the adaptive UPR and proteins involved in the transport between the ER and the Golgi apparatus, as well as enzymes participating to the biosynthesis of lipid droplets, the precursors of MFGs. Taken together our results demonstrate that a close mechanistic relationship exists between biosynthesis and secretion pathways of the main milk components: casein micelles, milk fat globules and oligosaccharides. We definitely demonstrated the relevance of the goat model as an experimental system to unravel the underlying mechanisms and to appraise the possibility to dissociate these biosynthesis pathways in order to modulate selectively one or the other.

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# **Cheesemaking properties of goat milk from different regions of Greece**

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Over the past years there has been an increased interest in goats. Farms have been appearing in regions and countries with a previous tradition in goats farming as well as in others with no such tradition. This has resulted in an increase in milk production and its quality. Therefore cheesemaking from goat's milk has been continuously rising.

In the present study, the research is focused on the cheesemaking properties of goat's milk. 1360 samples and 100 mixtures of them, from 22 regions of Greece were tested between March and July. Milk sample mixtures were resulted from separate temporal and regional origins. The Formagraph instrument was used for the measurement of three parameters of coagulation. These parameters are the clotting time ( $r$ ), curd firming rate (K20) and curd firmness (A30). The results are presented per region, per fortnight and per month. The results indicate that none of the parameters of coagulation have shown a variation per region. The samples from the 2nd fortnight of March had the higher mean coagulation time. The samples from the 2nd fortnight of May had the higher mean firming rate while the samples from the 2nd fortnight of April had the higher mean firmness. The results of the mixtures were similar except for the smaller values of clotting time and curd firmness as well as the higher means values for curd firming rate, in total. They had also smaller range of values in comparison with the samples. The mean values of the coagulation parameters in this study were: clotting time  $10.9 \text{ min} \pm 4.2$ , curd firming rate  $4.8 \text{ min} \pm 3.7$ , and curd firmness  $12.8 \text{ mm} \pm 7.8$ . The strategy applied in this study can be used to evaluate and compare cheesemaking properties of goat milk. In addition, it was demonstrated that goat's milk is suitable for cheesemaking, even under conditions applied in cheese manufacture using goat milk or its mixture with sheep milk, mainly during summer (June, July). This information is of great importance, as currently Greece is lacking far behind in sheep milk production. As a last, goat milk could be used on its own or in combination with sheep milk in cheesemaking.

## Effects of manufacturing processes on physicochemical and microbiological characteristics of soft goat cheese

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The aim of this work was to study the physicochemical, microbiological and sensory characteristics of a Greek traditional soft goat cheese, according to manufacturing processes. Two cheesemaking methods were evaluated, namely production of cheese using goats' milk without starter cultures (A), as traditionally manufactured by farmers (A), and with starter cultures and Rennet (B). Drainage ability and values of some physicochemical parameters, such as pH, titratable acidity, moisture, fat, proteins and NaCl content were determined. Cheeses were analyzed at 15d of storage for volatile compounds by GC/MS. In addition the levels of several microbial groups (mesophiles and thermophiles LAB, psychrotrophs, coliforms and yeast) were enumerated in the milk, curd and different stages of the 15-day storage period at 4°C. Comparing the two methods of manufacture, it can be concluded that the addition of lactic acid bacterial culture and rennet (cheese B), resulted an accelerated coagulation and draining of the milk, but led to a lower yield compared to the traditional way of manufacturing (cheese A). The last ones had significantly higher, moisture and ash as well as lower protein contents than cheese B. No significant differences in fat-in-dry matter, salt, pH, were observed between the two types of cheese. The flavor profile (number and concentration) of compounds was affected by the type of cheese and were greater in cheese A. A high number (> 9 cfu/g) of mesophilic and thermophilic cocci were identified in both cheeses during manufacture and storage. Cheeses B presented lower psychrotrophic bacteria and yeast count than cheeses A. Coliforms count decreased significantly during the storage time reaching 2 log cfu/g in cheeses B. The sensory evaluations of both cheeses studied showed that they have received high total scores.

## Mutations at the $\alpha$ s1-CN Gene in Ethiopian and Crossbred Goats: Effect on Casein Content, and Coagulation Properties of Their Milks.

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A previous study in some Ethiopian goat breeds indicated high casein content with good coagulation properties and strong  $\alpha$ s1-CN variant at protein level. The study also showed reduced content of caseins and coagulation properties in the cross between the local and exotic breed. This initiated a study to investigate the  $\alpha$ s1-CN gene in these breeds. Selected regions of the  $\alpha$ s1-CN gene were sequenced in 122 goats from 6 breeds (two indigenous: Arsi-Bale, Somali, one exotic: Boer and Cross: Boer x Arsi-Bale, Boer x Somali and Toggenburg x Arsi-Bale). The DNA analysis resulted in 36 new discovered mutations: 4 in exons, 3 in the 5' UTR, and 29 in the introns. A mutation at nucleotide 10657 (exon 10) involved a transversion CAG→CCG resulting in an amino acid exchange Gln77→Pro77. This mutation was found in the indigenous breeds only. Two mutations: at nucleotide 6072 (exon 4) and 12165 (exon 12) revealed synonymous transitions: GTC→GTT in Val15 and AGA→AGG in Arg100 of the mature protein respectively. The 4th mutation involved a transversion C→T at nucleotide position 15026, exon 15 in Toggenburg x Arsi-Bale crosses in a heterozygote form. This mutation results in a premature stop codon and is believed to have come from the exotic sire Toggenburg since it was not detected in the dam breed. The mutation however occurred in very low frequency and is associated with one buck and therefore is not included in further investigations. Transitions, G→A and C→T at nucleotides 1374 and 1866 respectively, occurred in 5' UTR while the third mutation involved a transversion T→G at nucleotide location 1592. The goats were then grouped into three different groups: homozygote new (CC), homozygote reference (AA) and heterozygote (CA) based on the nucleotide at the mutation position 10657 that resulted in shift of amino acid. The content of  $\alpha$ s1-CN (15.32 g kg<sup>-1</sup>) in milk samples of goats homozygous (CC) for this newly identified mutation, Gln77→Pro77 was significantly higher ( $P<0.001$ ) than in milks of heterozygous (CA) (9.05 g kg<sup>-1</sup>) and reference (AA) (7.61 g kg<sup>-1</sup>) genotype animals. The  $\alpha$ s2-,  $\beta$ - and  $\kappa$ -CN contents showed a similar pattern. Milk from goats with homozygote new mutation had significantly lower ( $P<0.001$ ) micellar size. Milk from both homozygote and heterozygote new mutation goats had significantly shorter coagulation rate ( $P<0.001$ ) and stronger gel ( $P<0.05$ ) than the reference genotype. Except the transversion, the sequence corresponded to allele A and presumably derived from it. Therefore this mutation is denoted with A3. All goats from the reference genotype (AA) were homozygote for the mutation at nucleotide position 1374 and 1866, while all mutations in the 5' UTR existed in a heterozygote form in both heterozygote (CA) and the new mutation (CC) genotype. The newly identified mutation (CC) detected in some of the goat breeds is therefore important in selection for genetic improvement and high quality milk for the emerging goat cheese producing industries in Ethiopia. The finding will also benefit farmers raising these goat breeds due to the increased selling price. Further studies should investigate the effect of this amino acid exchange on the secondary and tertiary structure of the  $\alpha$ s1-CN molecule and on the susceptibility of peptide hydrolysis by digestive enzymes.

## **A preliminary investigation on the variation of milk composition during lactation of ten pure bred Anglo Nubian goats from Trinidad**

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There are currently about 4000 dairy goats in Trinidad. Farmers not only sell goat milk but a few are involved in producing cottage type value added cheese and milk products such as paneer, and ice cream. Goat producers are working to improve their industry to one of processing of soft and hard cheeses. To achieve this purpose, producers have sought assistance from FAO, IICA, and more recently via collaboration between The University of Trinidad and Tobago (UTT) and The Trinidad and Tobago Goat and Sheep Society (TTGSS). The “up the hills” farm has invested in 200 imported pure bred Saanen, and Anglo Nubian animals in an entrepreneurial venture to move their enterprise to one of processing. However, the quality of processed milk products depends on its main components protein, fat and lactose on milk composition which is influenced by factors such as season, farming systems and farming methods. This study represents a first report on milk composition of lactating Anglo Nubian females of early weaned kids of the “up the hills” farm.

Milk samples were analysed over a seven week period from 10 pure bred Anglo Nubian goats without evidence of subclinical mastitis, intensively reared on an 18% Crude protein diet and at varying stages of lactation. Composition of the milk from individual goats were analysed using a lactoscan SP (Nova Zagora, 8900) and the pooled data subdivided into early (0-90d; n=42), mid (90-180d; n=23) and late lactation (> 180d; n=5). A one way ANOVA revealed lactose, Solids Non Fat, protein and salt composition was significantly higher ( $p < 0.05$ ) in early lactation compared with values in mid or late lactation. However, neither fat, temperature, salt concentrations nor the freezing point of the milk ( $p > 0.05$ ) varied with stage of lactation. Overall means for fat, lactose, Solids Non Fat, protein were 4.9 %, 4.8 %, 8.7 % and 3.2%, respectively. Average daily milk yields from a single milking of the does were between 1.3 to 1.5 litres.

Milk composition from these pure bred Anglo Nubian goats would be suitable for the production of hard and soft cheeses and other dairy products. The low average milk yields reported needs to be improved through a better system of feeding and management. Studies are under way to determine nutritional input pertaining to individual milk yields and milk composition of pure bred Anglo Nubian, Saanen and Alpine breeds of lactating goats from Trinidad.



# Modeling daily milk yield in sanitized Norwegian dairy goats using multilevel mixed-effects linear regression model.

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## BACKGROUND

In 2002, the Norwegian Goat Health Service initiated a program called the Healthier goats sanitation program (HGSP), with the aim to sanitize for the three diseases caprine arthritis encephalitis (CAE), caseous lymphadenitis (CLA) and paratuberculosis (Johne's disease) in Norwegian dairy goat herds. The sanitation by "snatching" method used in the HGSP is based on the principle of raising infection-free kids and stamp-out the old persisting herd. The kids are "snatched" in the birth canal and raised in a clean compartment using cow colostrum. By 2012, all dairy goat herds in Norway have signed up to join the HGSP. As a result, CAE, CLA and Johne's disease are no longer enzootic in the Norwegian dairy goat population. As an effect of eradication of these three chronic, wasting diseases through the HGSP, it will be expected that the milk production potential of the goats increases.

The aims of this study are to: (1) model milk yield using a mixed-effects regression model, (2) investigate how sanitation through the HGSP affects the milk yield and compare with milk yields from un-sanitized goats (shape and scale).

## MATERIALS AND METHODS

Individual records on daily milk recordings from the Norwegian Goat Herd Control Database (GHCD) were selected based on the following inclusion criteria:

(1) data collected between 1999 and 2008, and (2) minimum five records per lactation where the first record was within 60 days after kidding. Milk yields recorded before day 5 or after day 275 in lactation as well as milk records less than 0.2 kg were excluded. Lactations were separated into parities from 1 to 5 where the latter includes lactations 6 to 16.

The data material contained 135 446 registrations of daily milk yield from 28 636 lactations.

Data were grouped in sanitized and non-sanitized herds (controls). Further, the milk yield recordings were coded according to time of appearance in relation to year of sanitation to allow for comparison of milk yield records from before and after sanitation. For the controls, the data was split in two; 1999-2003 as "before" and 2004-2008 as "after". By doing so, the changes in milk yield independent of sanitation through HGSP can be expressed, and the actual effect of the HGSP on the milk yield change can be identified. The mixed-effects regression model was applied to the groups of data representing the situation before/after sanitation and the control group.

The data were analyzed using the statistical package STATA/IC 11.2©.

## RESULTS

Preliminary results show that the annual milk yield for the four groups sanitized before, sanitized after, control before and control after were 580.9 kg (SE=1.1 kg), 745.4 kg (SE=1.3 kg), 588.0 kg (SE=1.5 kg) and 657.6 kg (SE=1.2 kg), respectively. The lactation curves as well as the annual (275 day) milk yields from goats in sanitized herds, in comparison to goats from un-sanitized herds, will be presented.

# Effect of somatic cell count on some chemical, physical and bacterial properties of milk in a Hungarian Alpine goat farm

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Compared to the goat population being 880 million worldwide, the number of goats in Hungary (88000) is really low. However, the importance and prospects of goat milk production next to providing special needs is mainly in making the product range wider and in manufacturing premium products. For enhancing the competitiveness of goat milk production the quality of the commodity is essential. In order to this, we have to qualify not only the nutritional value, but the hygienic traits (somatic cell count and bacterial count) of the milk as well. Only a few studies dealing with the somatic cell count in small ruminants and its effect to the milk compound compared with dairy cattle. Our present study analyses the milk compound of Alpine goat, in particular to its somatic cell count, and certain physical and hygienic characteristics.

Milk samples were collected from mixed parity Alpine goats ( $n=32$ ) both in the morning and evening periods at the beginning, midpoint and end of lactation. Fat, protein, and lactose content of milk samples were measured, and their pH value, freezing point, somatic cell and bacteria counts were analysed, moreover Ca and Na were determined by inductively coupled plasma – optical emission spectrometry (ICP-OES).

The investigation showed a positive correlation ( $P<0.01$ ) between SCC and protein content ( $r=0.67$ ;  $P<0.001$ ), pH value ( $r=0.26$ ;  $P<0.001$ ) as well as Na ( $r=0.44$ ;  $P<0.001$ ), and negative correlation between SCC and lactose ( $r=-0.41$ ;  $P<0.001$ ) and freezing point ( $r=-0.33$ ). Furthermore, SCC correlated to total bacteria count ( $r=0.79$ ;  $P<0.001$ ). No significant relationship was found between the somatic cell counts (SCC) and milk Ca content in goat milk. Results indicate that higher SSC in raw goat milk is associated with disadvantageous milk properties, which may lead to reduced milk product quality.

## Acknowledgement

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## The effect of DDGS supplemented diet on fatty acid profile in acid- rennet goat cheese

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Supplementation of ruminant diets with unsaturated fatty acid sources results in improvement of unsaturated fatty acid (UFA) content in milk. The purpose of this study was to evaluate the applicability of dried distillers grains with solubles (DDGS) as a dietary supplement in dairy goat diets for production of milk as a source for production of acid-rennet curd cheese with higher level of UFA contents. In the experiment 66 milking goats were allocated to one of two groups (n=33) and fed with basal TMR diet (control) and basal diet plus 120 g/d DDGS cake. Goats were machine milked twice a day in their 4th and 5th months of lactation. Daily samples of milk from individual goats were prepared by mixing morning and evening milking (1:1). For analyses the composites were prepared in two batches: one, stored at 4°C and analysed for milk constituents (MilkoScan FT) and the other, stored at -20°C, and analyzed for the fatty acids profile using a gas chromatograph (Varian Star CP 3800).

DDGS cake used in the experiment contained the following fatty acids (g 100 g<sup>-1</sup> of identified fatty acids): C16:0 (13.4), C18:1 cis-9 (25.8), C18:2 cis-9 cis-12 (55.17), C18:3 cis-9 cis-12 cis-15 (1.8).

The fatty acid profile of raw milk from goats fed the experimental diet (DDGS) when compared to the control diet indicates a lower level of SFA and higher levels of MUFA and PUFA.

This milk was used to produce acid-rennet curd cheese with a mesophilic bacteria culture (FLORA DANICA) and rennet solution (NATUREN PREMIUM 225). The fatty acid profile of this type of cheese after production and 21 days of storage was similar to that of raw milk, but slightly altered as a result of used diet. There were not significant differences in the chemical composition or quality of goat acid-rennet curd cheese produced at the administration of the control and experimental (DDGS) diet.

## **Milk yield and composition variations of latvian breed goats depending on the length of the kids suckling period**

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The basic breed in Latvia is Latvian breed goats (LVK). The average milk yield from the goats in 2011 was 522 kg with the average fat content 3.81% and protein content 3.14%. In Latvia the goat kid suckling period traditionally lasts till the 60th day of lactation. Milk recording for the goats of this group started only after the 61st day of lactation. The aim of the research was to find out the changes of milk yield and composition of goat depending on the length of the kids suckling period. The research was carried out in 2011 and 2012 in a farm where goats of Latvian breed (LVK) were reared. Goats kidded in February and March in both years. For the research purposes three groups of goats (each 10 animals) were formed. Groups included goats with varied length of the suckling period. Kids in the first group were weaned on the day of birth. In the second group the suckling period lasted for 30 days, in the third – for 60 days. Goats of all research groups had the same conditions of housing care and nutrition. In winter the animals were kept in the stable and fed to hay, haylage and concentrate, but in summer they grazed in cultivated pastures. The average age of the animals was 4.7 lactations and there was no significant difference among the groups. The milk yield was measured in five successive days after kid weaning. Milk content for the total of 300 milk samples were analyzed in accredited milk quality laboratory. After the end of the suckling period the significantly highest average daily milk yield was obtained from the goats when kids were weaned after birth and milk samples were taken starting with the sixth day of lactation ( $2.10 \pm 0.092$  kg), while the lowest yield was from the goats with the suckling period of 60 days -  $1.68 \pm 0.099$  kg. The average fat content in milk from the first research group was significantly higher than in the milk from the second and third groups - respectively  $5.35 \pm 0.084\%$ ,  $4.38 \pm 0.087\%$  and  $2.89 \pm 0.090\%$ . The similar tendency was observed with the protein content, respectively  $4.20 \pm 0.064\%$ ,  $3.71 \pm 0.066\%$  and  $2.91 \pm 0.069\%$  ( $p < 0.05$ ). The highest average milk yield in a standard lactation was obtained from the first group goats –  $455.7 \pm 3.32$  kg, whereas the lowest from the third group  $404.84.5 \pm 3.56$  kg. The average fat content ( $4.58 \pm 0.047\%$ ) in milk from the first group goat was also significantly higher than from the goats of the third group ( $4.36 \pm 0.050\%$ ;  $p < 0.05$ ). The average milk protein content in a standard lactation did not significantly vary among the research groups. After weaning a kid set high milk yield composition variation are observed in all research groups, the coefficient of variation found from and 14.8% protein content to 23% in milk yield.

Keywords: goats, milk yield, milk composition

## Effects of the main variation factors on milk urea level in dairy goats in Northern Italy.

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Milk urea level (MUL) is used as a diagnostic tool of protein feeding in lactating ruminants. The recommended range for bulk cow MUL is 20-30 mg/dL. For dairy goats only a few studies give indications on the target MUL; in a previous study we recommended a level of 23-34 mg/dL. During the last decade (2002-2011), the average MUL in dairy goat farms of Lombardy (Northern Italy) was 40 mg/dL.

Aim of the present work was to study the effects of the main variation factors on MUL in dairy goats in Lombardy.

Nine commercial farms with a bulk MUL of  $40.9 \pm 7.4$  mg/dL and an individual milk yield of  $3.1 \pm 0.9$  kg/d (overall means of the entire lactation, in year 2009) were selected. During the years 2010 and 2011, the individual lactations (milk yield and quality) of 354 (2010) and 386 (2011) goats were studied. Individual milk yield (MY) was recorded monthly alternating the morning and evening milking; daily MY was calculated according to the milking interval time. Individual milk samples were analysed for fat, crude protein (CP), lactose and somatic cell count by infrared methods, and MUL by pH-differential technique. Chemical composition of feeds was determined by near infrared spectroscopy, with the exception of CP that was chemically determined. Net energy for lactation (NEL) of feeds was predicted by in vitro gas production (GP) method (Menke and Steingass, 1988) at 24 h of incubation. Body weight (BW) and diet composition were evaluated in early, mid and late lactation. Dry matter intake (DMI), energy and protein requirements and protein digestible in the intestine (PDI) allowances were calculated according to the French system (2007). NEL and PDI balances (%) were calculated as the difference between allowances and requirements.

Data were statistically analysed by SAS GLM and regression procedures.

One farm had to be excluded because it ceased the activity.

In the two years the average BW, DMI and MY were  $64.2 \pm 12.6$  kg, 2.41 kg/d, and  $3.01 \pm 1.06$  kg/d. Milk fat, CP and MUL were  $3.47 \pm 0.49\%$ ,  $3.50 \pm 0.35\%$ , and  $37.5 \pm 7.9$  mg/dL. The forage:concentrate ratio was on average 54:46. Chemical composition (g/kg DM) and NEL (MJ/kg DM) of the diets were, on average: 144 CP, 178 starch, 397 NDF, 6.30 NEL.

MUL was significantly ( $P < 0.001$ ) influenced by nutritional (diet CP and diet GP) and non-nutritional factors (milk CP and milk yield) as follows:  $MUL \text{ (mg/dL)} = +0.281 \text{ diet CP (g/kg DM)} - 0.503 \text{ GP (ml/200 mg DM)} - 3.0 \text{ MY (kg/d)} - 5.33 \text{ milk CP (\%)} + 49.3$  ( $n=52$ ;  $R^2=0.37$ ;  $RSD=6.34$ ;  $P < 0.001$ ).

MUL was lower (35.9 mg/dL) during early lactation (0-60 DIM), peaked (40.4 mg/dL) in mid lactation (61-150 DIM), and decreased (36.6 mg/dL) later in lactation (DIM>151) ( $P < 0.001$ ).

PDI allowances, using nitrogen as limiting factor for rumen microbial growth (PDIN), were always higher than requirements (on average, +30.6%) whilst NEL balance was negative in the early stage of lactation (on average, -5.4%) and slightly positive in mid (+2.1%) and late (+8.8%) lactation. The relationship between MUL and PDIN balance resulted as follows:

$MUL \text{ (mg/dL)} = 0.31 \text{ PDIN balance (\%)} + 27.2$  ( $n=52$ ;  $r^2=0.40$ ;  $RSD=5.97$ ;  $P < 0.001$ ).

# Microbiological quality and safety of raw and heat-treated goat milk and milk products

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In recent years, the popularity of goat milk and goat milk products has been growing in Poland, especially due to its low allergenic potential and good digestibility. This study focused on the assessment of the microbiological quality and safety of raw and heat-treated goat milk and milk products. The samples of raw goat milk were collected from October 2011 to January 2013. A total of 53 samples of raw goat bulk-tank milk collected from 21 different farms throughout Poland were examined. In order to assess the efficacy of pasteurization of goat milk alkaline phosphatase activity and the microbiological quality of raw milk samples, and after heat treatment at 63 °C for 30 minutes, were tested. The enzyme activity ranged from 34,550 to 374,200 mU.L<sup>-1</sup> in raw milk samples and from 30 to 330 mU.L<sup>-1</sup> in the milk samples after the heat treatment. Microbiological quality was determined in relation to the number of coagulase-positive staphylococci, *E. coli*, Enterobacteriaceae and the total bacteria count. Furthermore, the prevalence of selected foodborne pathogens such as *L. monocytogenes* and *Salmonella* spp. was identified. The average number of *E. coli* in raw milk samples was specified at the level of 3.7 x 10<sup>1</sup> cfu.mL<sup>-1</sup> (from <1.0 x 10<sup>0</sup> cfu.mL<sup>-1</sup> to 7.8 x 10<sup>2</sup> cfu.mL<sup>-1</sup>), Enterobacteriaceae of 3.4 x 10<sup>5</sup> cfu.mL<sup>-1</sup> (from 1.0 x 10<sup>1</sup> cfu.mL<sup>-1</sup> to 1.2 x 10<sup>7</sup> cfu.mL<sup>-1</sup>), coagulase-positive staphylococci of 9.3 x 10<sup>2</sup> cfu.mL<sup>-1</sup> (from <1.0 x 10<sup>0</sup> cfu.mL<sup>-1</sup> to 1.2 x 10<sup>4</sup> cfu.mL<sup>-1</sup>) and of total flora – 1.3 x 10<sup>6</sup> cfu.mL<sup>-1</sup> (from 9.1 x 10<sup>3</sup> cfu.mL<sup>-1</sup> to 8.6 x 10<sup>6</sup> cfu.mL<sup>-1</sup>). After pasteurization the number of total flora decreased to 5.2 x 10<sup>2</sup> cfu.mL<sup>-1</sup> (from 3.0 x 10<sup>0</sup> cfu.mL<sup>-1</sup> to 4.0 x 10<sup>3</sup> cfu.mL<sup>-1</sup>) and the other microorganisms to <1.0 x 10<sup>0</sup> cfu.mL<sup>-1</sup>. *Salmonella* spp. were not isolated from any of the raw milk samples. However, 5 (9.4%) of the raw goat milk samples were positive for *L. monocytogenes*, but after pasteurization this organism was not detected. The tests were also carried out for 81 samples of heat treated milk (pasteurized, UHT) and 87 samples of cheese (soft and hard cheese, cottage cheese and melted cheese) from retail outlets. The alkaline phosphatase activity was up to 278.6 mU.L<sup>-1</sup> in milk samples and 7.5 mU.g<sup>-1</sup> in cheese samples. *Salmonella* spp. and *L. monocytogenes* were not detected in any of the samples. In 10 cottage and soft cheese samples Enterobacteriaceae and *E. coli* were present in the number of 1.1 x 10<sup>6</sup> cfu.g<sup>-1</sup> (from 5.0 x 10<sup>1</sup> cfu.g<sup>-1</sup> to 8.5 x 10<sup>6</sup> cfu.g<sup>-1</sup>) and 2.0 x 10<sup>2</sup> cfu.g<sup>-1</sup> (from <1.0 x 10<sup>1</sup> cfu.g<sup>-1</sup> to 2.0 x 10<sup>3</sup> cfu.g<sup>-1</sup>), respectively.

## **Antimicrobial resistance of coagulase positive staphylococci isolated from goat and bovine raw milk in poland**

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The aim of this study was to determine the antibiotic susceptibility and resistance profiles of coagulase positive staphylococci (CPS) isolated from raw goat and bovine milk in Poland. In the years 2011 – 2012, a total of 111 samples of raw milk from dairy farms were collected. They were examined according to the ISO 6888-2 for CPS. Overall, 81 raw milk samples were found to be contaminated with CPS, 73 % of goat milk and 54% of cow milk samples, respectively. Susceptibilities of the isolates were determined for 11 antimicrobial substances such as penicillin, erythromycin, tetracycline, ciprofloxacin, gentamicin, ceftiofur, chloramphenicol, trimethoprim, sulfamethoxazole, streptomycin and florfenicol. The MIC (minimal inhibitory concentration) test was performed. Differentiation of isolates was done by the DKVP plate (SENSITITRE TREK Diagnostic Systems, England). The MIC criteria for *S. aureus* was defined by the European Reference Laboratory for Antimicrobial Resistance (EURL AR) and Clinical and Laboratory Standard Institute (CLSI). The analyzed 95 CPS isolates showed sensitivity for all antimicrobial agents (47.4%). Resistance to sulfonamides was the most common finding (29.5%) as well as to penicillin (23.2%). The analyzed strains isolated from cow milk were the most resistant to penicillin (53.8%) and the isolates from goat milk were the most resistant to sulfonamides (32.9%). Antimicrobial resistance profile for all of them was determined. Seventeen antibiotypes were identified by the MIC method. From 95 examined strains 38 (40%) were resistant to a single antimicrobial agent, 7 (7.4%) showed resistant to 2 antimicrobial substances. Multiresistance was found in 5 (5.3%) of CPS isolates.

## On effects of stage of lactation and subclinical mastitis on milk quality in goats

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In modern dairy goat farms, animals are milked at different stages of lactation, where a relatively large number (20 to 40% of the udders in a given herd) are infected with a variety of bacteria. Bulk milk is the mixture of all the milked udders in different stage of lactation. High quality milk is essential for making high dairy products, such as cheese and yogurt. This is particularly important for the goat industry because most of the milk is used to make dairy products. Bacterial infection, particularly with coagulase-negative staphylococci (CNS), and stage of lactation are the two most single important factors that affect milk quality, and hence the bulk milk used for consumption and processing. A positive relationship between % casein, lactose, and curd firmness (CF) and a negative relationship between somatic cell count and CF are associated with bacterial infection and with late lactation milk, hence with reduction in cheese yield and quality made from such milk. No correlation between the levels of fat, protein, and casein in milk and curd yield exist in goats. Thus, gross milk composition cannot be used as prediction for milk quality for cheese production. Research carried out in the past few years highlighted the effectiveness of lactose as a predictor of milk quality. The correlation between lactose and CF was higher than those for % casein and SCC. Lactose concentrations  $\leq 4\%$  are associated with non-clotting milk. Milk with  $\leq 4\%$  lactose is worthless for making cheese, but still meets the criterion for consumption as pasteurized liquid. A model that describes the simultaneous and close association between reductions in lactose concentration and milk yield, on the one hand, and reductions in lactose concentration and milk quality on the other hand, is presented.



# The influence of the $\alpha$ S1-casein genotype of goats on the quality of cheese milk and cheese quality

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The differences in milk quality between the  $\alpha$ S1-CN genotypes of goats have been studied in different goat breeds in several countries. It is in general accepted that the cheese making properties of the high  $\alpha$ S1-CN variants are preferable. But few studies have investigated their effect in ripened cheese. The objective of this study was therefore to investigate the differences on the cheese making properties and cheese ripening between milk from  $\alpha$ S1-CN genotype goats and from the “null” genotype goats with absence of  $\alpha$ S1-CN of the ordinary Norwegian goat breed. The cheese making was standardized so that the cheese was comparable from production to production without any other experimental factors than genotype. The study included analysis of free fatty acids (FFA), free amino acids (FAA), organic acids, dry matter, microbiology, pH and sensorial analysis. In addition coagulation properties (formagraph) and composition of milk from each goat was analysed one week after each cheese making. The composition (fat and protein) and the coagulation properties (K20 and A30) of milk from goats of the high  $\alpha$ S1-CN variant were preferable for cheese making. Further it appears like the milk from the high  $\alpha$ S1-CN variant leads to a better and more stabile cheese quality. The cheese from the low  $\alpha$ S1-CN variant milk had a frequent rancid flavour and a lower % dry matter content, which implies that the cheese matrix is trapping more water.

## Effect of pasture type compared with hay diet on dairy goat milk casein composition

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The objective of the present study was to examine the effect of grazing on different pasture types and hay feeding on dairy goat milk casein composition in early and late grazing season. Eighty goats were grouped according to genotype at the  $\alpha$ S1-casein locus and number of lactations and randomly divided into two groups (Early and Late) with approximately 8 weeks difference in kidding dates. Goats within each of the two groups were further allocated to four forage treatment groups accounting for genotype and lactation number: R, forest rangeland pasture; C, cultivated pasture; HH, high quality hay; HL, low quality hay. The goats in Early were subjected to forage treatments in early grazing season, while the goats in Late received the forage treatments 8 weeks later. There was a strong effect of genotype but no genotype by diet interaction on casein content and composition. Goats grazing R yielded less milk (1.6 vs. 2.2 kg/d,  $P < 0.001$ ) with higher milk fat content (48 vs. 38 g/kg,  $P < 0.001$ ) than goats on C. Pasture type had no effect on total protein or casein content. However, milk from goats on R compared to C had lower content of  $\alpha$ S1-casein (2.57 vs. 3.82 g/L,  $P < 0.01$ ) and  $\kappa$ -casein (4.51 vs. 5.22 g/L,  $P < 0.05$ ) but higher content of  $\beta$ -casein (13.1 vs. 11.7 g/L,  $P < 0.001$ ). Grazing compared to hay gave similar milk yield with higher content of total casein (24.2 vs. 21.0 g/kg,  $P < 0.001$ ),  $\alpha$ S2-casein (3.48 vs. 3.04 g/L,  $P < 0.001$ ) and  $\beta$ -casein (12.4 vs. 11.7 g/L,  $P < 0.01$ ). Grazing compared to hay feeding improved the milk casein composition important for cheese making, while cultivated pasture were superior to rangeland.

## How does grazing species-rich rangeland or cultivated species-poor pasture affect goat milk quality and milk quantity compared to hay feeding?

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Traditionally, Norwegian dairy goats graze on diverse forest or alpine rangeland during summer, and these pastures are important both as a feed source, and for keeping the traditional image of goat milk being produced on local “natural” resources. Simultaneously, the grazing goats keep the landscape open. The quality of goat milk often declines during summer, with increased problems with free fatty acids (FFA) in the milk. This seems to coincide with the latter part of the grazing season, when goats generally also are in a later lactation stage, which also can cause problems with FFA. To elucidate the effects of pasture quality on milk production and quality we conducted an experiment where we grouped eighty goats according to genotype and lactation. They were randomly divided into two groups with approximately 8 weeks difference in kidding date and start of feeding experiment in Early (beginning of July) and Late (end of August) grazing season on improved cultivated pasture (PC) or rangeland (PR). Grazing was compared with hay of high (HH) or low (HL) quality. We used n-alkanes and long chained alcohols found in plant waxes as markers to estimate diet composition, and dosed the animals with the even-chained alkane C32 to estimate intake. Grazed plants were analysed also for feed quality.

The forage intake was generally high, on average 1.2, 1.9, 2.1 and 1.6 kg DM day<sup>-1</sup> per goat for PC, PR, HH and HL, respectively. The intake in the cultivated pasture the diet was predominantly timothy (*Phleum pratense*) in early season, while meadow fescue (*Festuca pratensis*) and couch grass (*Elytrigia repens*) dominated in 2nd period. In the rangeland, the diet was diverse and consisted of ferns, sedges, blueberry (*Vaccinium myrtillus*) and birch (*Betula pubescens*) in early summer. In late summer the diet was particularly diverse, coinciding with a general decline in plant quality.

R yielded less milk (1.6 vs. 2.2 kg d<sup>-1</sup>) and lower milk protein content (32 vs. 33 g kg<sup>-1</sup>), but higher milk fat (48 vs. 38 g kg<sup>-1</sup>) and DM content (122 vs. 114 g kg<sup>-1</sup>) than C. Milk content of free fatty acids (FFA) was not affected by pasture type. The effect of pasture type on milk yield and milk constituents were similar in early and late grazing season. Grazing resulted in similar milk yield but higher milk fat (43 vs. 35 g kg<sup>-1</sup>), protein (32 vs. 30 g kg<sup>-1</sup>) and DM (118 vs. 107 g kg<sup>-1</sup>) content and lower content of FFA (0.25 vs. 0.31 mEq L<sup>-1</sup>) than hay feeding.

## **Milk protein genes (CSN1S1, CSN1S2, CSN2 and CSN3) and their effect on qualitative milk parameters, and technological properties (renetability) of goat milk in Czech dairy goat breeds.**

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The objective of this study was to assess the relationships between polymorphism at the calcium-sensitive casein genes and yield, milk parameters and technological properties of caprine milk. Czech dairy goat breeds were used to type at the CSN1S1, CSN2, CSN1S2 and CSN3 genes. To determine genotype frequencies were used methodology PCR-RFLP, AS-PCR and PEA. We used individual raw goat milks to screen milk parameters: protein content, casein content, fat content, total dry matter, non-protein nitrogen, renetability properties, souring ability and casein number. The yield, total pure protein (%), protein content (%) ( $P \leq 0.05$ ) and casein content ( $P \leq 0.01$ ) was influenced by the effects of CSN1S1 (AA>FA>FE>FF>F0) within genotype group. Genetic polymorphism at the CSN2 locus not showed any association effect on the followed milk parameters even rennet coagulation time (min) or milk yield (sj). Non-protein nitrogen ( $P \leq 0.05$ ) was significantly affected by genetic variants at the CSN1S2 locus (FN>FF>NN) and genetic polymorphism at the CSN3 locus showed significant differences ( $P \leq 0.05$ ) in rennet coagulation time (min) (BD>AA>AB>BB>AD).

## Udder health in Norwegian goat dairy herds

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Elevated bulk milk somatic cell count (BMSCC) has been a challenge in dairy goat milk production. In Norway BMSCC level last decades has been over 1.000.000 cells /ml. The SCC in healthy goats is expected to be below 500.000 cells / ml.

In 2004 a national study showed 88% prevalence of CAEV antibodies in bulk tank milk and clinical Caseous Lymphadenitis in 71% of the milk producing flocks. 40 herds was restricted by the authorities due to Paratuberculosis. CAEV can cause indurative mastitis in addition to arthritis and neurological dysfunctions. Infected goats show reduction in milk yield and increase in SCC.

Norwegian Goat Health Services will during 2014 finish a sanitizing program for CAE, CLA and Paratuberculosis in all milk producing herds, 423 in total.

Several studies conclude that *S. aureus* is the dominating infection isolated from clinical mastitis in Norwegian goats. Infected udders are the main reservoirs but recent studies show considerable occurrence at extramammary body sites such as nose and vagina. *S.aureus* infection is a well known cause of high SCC in goat milk.

Reports from TINE Goat Health Recording System show a mastitis treatment incidence of 2-3%. These reports probably underestimate the mastitis incidence because the farmers tend to slaughter or leave them untreated. Control of goat milking equipment too often reveal severe dysfunctions which may have serious negative effects on udder health.

Eight sanitized erds in Telemark county participated in a study on udder health control measures from 2009-2011. All herds got their milking equipment examined and after a VADIA test equipment was optimized. Farmers were committed to collect DHI samples from all lactating goats at least 5 times during lactation. DHI samples were analyzed for protein, fat, lactosis and SCC. Before drying off autumn 2009, after kidding winter 2010 and before drying off autumn 2010 quarter milk samples were analyzed from all goats. A total of 1385 lactations were included. Goats infected with *S.aureus* or *Str.dysgalactiae* were treated with antibiotics at drying off (n=48)

Prevalence of *S.aureus* infected goats at drying off in 2009 was 7.4% (2.1–19.2) and in 2010 4.8 % (0.0 – 11.1). *S.aureus* prevalence 5.9% after kidding in 2010.

Geometric mean SCC for *S.aureus* infected goats at drying off were 2.842.000 cells/ml, and 547.000 cells/ml for the uninfected. Geometric mean at first DHI sampling after kidding were 114.000 cells/ml for the treated goats, and 161.000 cells/ml for the not infected goats.

Eigthyfive% of the *S.aureus* infected goats treated at drying off did not show infection after kidding. Seven % of 374 goats uninfected at drying off had *S.aureus* infection after kidding.

Geometric mean SCC for the lactations where *S.aureus* infection was treated at drying off were 549.000 cells/ml, following lactations 415.000 cells/ml.

In 52% of the lactations the DHI samples analyzed had SCC lower than 1 mill cells/ml in all samples. Prevalence of DHI samples lower than 200.000 cells/ml increased from 24 to 26 from 2009 to 2010.

Geometric mean BMSCC for the participating herds was 943.000 cells/ml in 2009, 839.000 cells/ml in 2010, 842.000 cells/ml in 2011, 824.000 cells/ml in 2012.

Most herds did not take action during lactation to handle with the high SCC goats. Additional udder health control measures during lactation is needed to lower the bulk milk somatic cell count.

## Effect of breed, parity, and milking interval on concentration of lactose in blood plasma

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Lactose is a disaccharide derived from the condensation of galactose and glucose. This milk component is synthesized only in the mammary gland and is not secreted basolaterally in significant quantities, so the plasma level of lactose provides a measure of the leakage rate through tight junctions (TJ), allowing its movement from the lumen of the mammary gland into the blood stream. The objective of this study was to evaluate differences in plasma lactose concentration at different milking intervals in goats traditionally milked once a day. 32 dairy goats (16 primiparous and 16 multiparous) of two breeds (Majorera and Palmera) in mid lactation were milked at different intervals (10, 24, 28, and 32 h). Goats were milked in a double 12-stall parallel milking parlor (Alfa-Laval, Madrid, Spain). Blood samples were taken at each milking. The enzymatic assay for determination of lactose (Boehringer Mannheim / R-Biopharm) is based on two reactions, one measuring galactose and the other measuring lactose and galactose; the difference between the two provided a measurement of lactose concentration. The analysis was performed in the Laboratory of Research Unit at University Hospital (Tenerife, Spain). Repeated measures analysis, with adjustments for non-sphericity (Greenhouse-Geisser correction) followed by LSD post-hoc tests, were used for statistical analysis. Lactose concentration was not affected by breed factor (Majorera: 197.01  $\mu\text{M}$ ; Palmera: 181.81  $\mu\text{M}$ ). However, parity affected lactose content in blood. Thus, primiparous goats showed lower values (135.83 vs. 242.99  $\mu\text{M}$ ) than multiparous goats. Finally, lactose concentration was affected by milking interval, a significant increase was observed between 24 and 28 h for both breeds (Majorera: 152.55 vs. 349.19  $\mu\text{M}$ ; Palmera: 144.00 vs. 241.47  $\mu\text{M}$ , at 24 and 28 h, respectively). However, no differences were found between 28 and 32 h for both breeds. In conclusion, the results demonstrated that TJ disruption occurs after 24 h of milk accumulation. Nevertheless, degree of TJ leakiness differed according to parity.

## **Pasture fatty acids profile and Stearoyl-CoA desaturase expression in milk somatic cells of goats**

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CLA in ruminants milk results from the isomerization and biohydrogenation of unsaturated fatty acids [octadecatrienoic (C18:3) and ocatdecadienoic (C18:2) acids] by rumen bacteria as well as the activity of Stearoyl-CoA desaturase (SCD) in the mammary gland on trans-11 C18:1 (TVA, transvaccenic acid), intermediate product of several polyunsaturated fatty acids (PUFA) biohydrogenation. SCD is also the rate-limiting enzyme in the biosynthesis of mono-unsaturated fatty acids (MUFAs) by the introduction of a cis double bond between carbons 9 and 10 in a spectrum of saturated fatty acids, with preference for C14:0, C16:0 and C18:0. The expression of SCD is known to change according to animal species, tissue, dietary conditions and environmental factors such as age, insulin and CLA. Some PUFA are thought to inhibit SCD by down-regulating its gene expression. In goats the relationship between pasture and milk fatty acid profile including CLA has been investigated, but information on the influence of pasture fatty acid profile on mammary SCD gene expression are limited. Therefore, aim of this study was to assess the effects of grazing season, particularly referred to C18:2 and C18:3 levels in the pasture, on SCD gene expression in goats mammary gland by extraction of total RNA from milk somatic cells. The trial was effected using 30 pluriparous goats, delivered in February. The animals had free access to pasture constituted by 60% Leguminosae and 40% Graminee, and received 700 g/head/day of concentrate. From the second half of April, goats were milked twice a day for 5 months. Daily milk yield was recorded and, monthly, representative individual milk and pasture samples were analysed for chemical composition and fatty acid profile. The SCD expression was studied by extraction of mRNA from milk somatic cells and analyzed by RT-PCR. Average milk yield, fat and protein were 1420 (g/d), 4.45 (%) and 3.62 (%) respectively. Milk yield decreased along the lactation ( $P<0.01$ ) while milk fat was higher in August. Milk total CLA showed the highest levels ( $P<0.01$ ) in June and August (mg/100 g fat: 0.98 and 1.21, respectively) as consequence of the highest levels of pasture C18:2 and C18:3 in June (% of total FA: 34.0 and 46.0, respectively) and August (% of total FA: 46.5 and 54.6, respectively). The grazing season affected the SCD expression; indeed, its values (arbitrary units) progressively decreased from April (1.95) until June (1.40), increased in July (1.70) and decreased again in August (0.83).

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## The effect of false cake (*Camelina sativa*) diet supplementation in dairy goats on fatty acid profile of kefir

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Supplementation of ruminant diets with unsaturated fatty acid sources results in improvement of unsaturated fatty acid (UFA) contents in milk. The purpose of this study was to evaluate applicability of *Camelina sativa* (CS) cake, a by-product of vegetable oil production process, as a dietary supplement in dairy goat diets to produce milk for the production of kefir with higher UFA levels. In the experiment 66 milking goats were allocated to one of two groups (n=33) and fed with basal TMR diet (control) and basal diet plus 120 g/d CS cake. Goats were machine milked twice a day in their 4th and 5th months of lactation. Daily samples of milk from individual goats were prepared by mixing morning and evening milking (1:1). For analyses the composites were prepared in two batches: one, stored at 4°C and analysed for milk constituents (MilkoScan FT) and the other, stored at -20°C, and analyzed for the fatty acids profile using a gas chromatograph (Varian Star CP 3800).

*Camelina sativa* cake used in the experiment contained the following fatty acids (g 100 g<sup>-1</sup> of identified fatty acids): C16:0 (7.3), C18:1 cis-9 (16.1), C18:2 cis-9 cis-12 (26.2), C18:3 cis-9 cis-12 cis-15 (38.8), C20:1 n9 (11.6).

The fatty acid profile of raw milk from goats fed the experimental diet (CS) when compared to the control diet indicate higher levels of MUFA (either cis or trans forms), PUFA (n-3 and n-6) and lower SFA levels. This milk was used to produce kefir with a kefir DC starter culture (*Lactococcus lactis* spp. *lactis*, *Streptococcus delbrueckii* spp. *bulgaricus*, *Leuconostoc* and kefir yeasts) by Danisco Biolacta. The fatty acid profile of kefir after production and 21 days of storage was similar to that of raw milk, but slight differences were the result of used diet. No significant differences were found in the chemical composition or quality of goat kefir produced when administering the control and experimental (CS) diets.

## Breeding and environment info in FTIR milk spectra

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Fat, protein, and lactose content in milk is often found routinely by Fourier transformed infrared spectra (FTIR) analysis. Other milk composition information such as fatty acids and to some extent casein composition may also be found.

We have seen that variation in the spectra themselves for different milk samples, without predicting fat% or other components, may be attributed to genetic and environmental, in addition to unmodeled causes. Ratios of explained variation are given as: heritability for the additive genetic cause, as variance ratio explained by animal permanent environment, and by variance ratio for herd test day, in addition to the remaining residual variance.

Knowing these variance components we may predict breeding values for individual animals, but also predict their values including effects of permanent environment and herd test day. This gives us a means of detecting whether an animal is out of its normal milk composition: if its value deviates too much from the prediction, it may be sick or not receive adequate feeding. Also today information on fat% and other measures coming from the FTIR specter are used for this purpose.

However we advocate that this prediction should rather be based on the variance components of the FTIR spectra than on the variance components of milk components derived from them. It is known that multivariate is better than univariate when there is relevant information in the former. We have shown this for breeding values.

Breeding values are now found indirectly by predicting the phenotypic values for each milk sample, then estimating variance components, and then blup breeding values for individuals. We propose to use the heritable part of the FTIR spectra to predict breeding values of these traits, and possibly for other quality traits not available today. 28000 FTIR spectra from 14869 goats in 271 herds were used of which 20000 for calibration. The >500 specter frequencies were reduced to 8 factors by PCA, and their REML estimates of the four variance components were found. PLSR analysis established regression coefficients of spectra on the existing fat, protein, and lactose% already recorded in the Dairy Goat Control. 8000 remaining spectra validated the usefulness of the method. Blup breeding value scores were found for each factor for each animal. These carry info on the heritable part of spectra. Predicted breeding values for the spectra were transformed to breeding values for known chemical components of the milk (fat, ...) using PLSR regression of milk spectra. Using the same 8000 spectra, predicted phenotypical chemical components were found using the same PLSR regressions for each trait, and univariate blup values calculated for fat, protein and lactose. Compared to the indirect method, prediction error variances for the direct method are 3.2% better for fat, 6.1% for protein and 4.1% for lactose percent. Multivariate blup values based on the 3 phenotypic traits had prediction errors between the two mentioned methods. We also hypothesize that the heritable part of the spectra may be transformed into predictions of other quality measures such as coagulation and taste, which are difficult to measure in sufficient numbers without use of the spectra. We recommend predicting breeding values for traits derived from the FTIR spectra from the heritable part of the spectra.

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