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The role of polymorphism at α_{s1}-casein *locus* on milk fatty acid composition in Girgentana goat

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ABSTRACT – Sixteen lactating Girgentana goats were used to evaluate the effect of polymorphism at α_{s1}-casein locus on milk fatty acids composition. Animals, homogeneous for milk production, days of lactation and body weight, were divided into two groups: eight homozygous for strong allele (AA group) and eight homozygous for weak allele (FF group). The experimental diet, identical for the two groups, consisted of alfalfa hay (1.5 kg), whole barley, whole maize, pelleted sunflower and whole faba bean (0.5 kg each). In spite of identical selected diets, also in terms of fatty acids, milk fatty acid composition resulted different between the two groups. In particular, except for C8:0, short and medium chain fatty acids and odd chain fatty acids resulted in higher percentage in the AA group. Taking in account that the difference reported in our experiment concerns above all de novo synthesized fatty acids, our results seem to confirm the hypothesis that polymorphism at α_{s1}-casein locus can influence milk fatty acid composition in goats.

Key words: α_{s1}-casein, Fatty acid composition, Genetic polymorphism, Goat milk.

Introduction - α_{s1}-casein polymorphism has been recognized as one of the major responsible for the casein content variation in goat milk (Leroux et al., 1992) and its technological properties. Most of the 17 alleles detected at this locus are associated with four levels of α_{s1}-casein (CSN1S1) in milk ranging from 0 (CSN1S1 0_1, 0_2, N) to 3.6 g/L (CSN1S1 A, B_1, B_2, B_3, B_4, C, H, L) per allele (Martin et al., 1999). As compared to weak alleles, milk from goats with strong alleles at this locus, shows a greater total milk protein content, better cheese making properties, a higher fat milk concentration and seems to have a different fatty acid composition (Chilliard et al., 2006). Data on the effect of α_{s1}-casein locus polymorphism on goat milk fatty acid composition are lacking and sometimes in disagreement. The aim of this research is to provide new data to better understand the influence of polymorphism at α_{s1}-casein locus on fatty acid profile in goat milk.

Material and methods – The experiment lasted 3 weeks. Sixteen lactating Girgentana goats, homogeneous for milk production (1.94±0.24 kg/d), days of lactation (110±15 d) and body weight (37.6±5.1 kg) were divided into two groups: eight homozygous at α_{s1}-casein locus for strong allele (AA group) and eight homozygous for weak allele (FF group). All the animals, housed in individual pens, were given, separately, alfalfa hay (1.5 kg), whole barley, whole maize, pelleted sunflower and whole faba bean (0.5 kg each). Goats were hand-milked twice per day. Daily, individual intakes of each feed were recorded and samples were taken for the chemical analyses. Twice a week, milk productions were recorded and samples were collected from each animal. Feeds were analyzed for dry matter, crude protein (AOAC, 1990), NDF (Van Soest et al., 1991), water soluble carbohydrates (WSC) (Deriaz, 1961), starch (Megazyme International Ireland Ltd.), and fatty acids profile (Palmquist & Jenkins, 2003).

Milk samples were analyzed for fat and protein by infrared method (Combi-foss 6000, Foss Electric, Hillerød, Denmark) and for fatty acid profile (Chouinard et al., 1999). Total nitrogen (TN), non-protein nitrogen (NPN), and non-casein nitrogen (NCN) were determined by FIL-IDF standard procedures (1964). From these nitrogen fractions, total protein (TN*6.38) and casein ((TN–(NCN*0.994))*6.38) were calculated. Data were analyzed using the GLM procedure for repeated measures of SPSS (SPSS for windows, SPSS Inc., Chicago, IL).

Table 1. Milk production and chemical composition.

		Genotype		*P*-values	Error
		AA	FF	(1)	M S
Milk yield	(g/d)	925.3	801.2	ns	3693.72
Fat	%	2.54	2.7	ns	0.10
Protein	%	3.64	3.2	***	0.01
Casein	%	2.84	2.4	***	0.01

*(1) ns=not significant; ***=P<0.001.*

Results and conclusions – No significant differences were reported between the two groups for DM intake, choice within the 5 feeds, crude protein and carbohydrates content of the selected diets.

As expected, casein level resulted significantly higher in AA goats. Consistently with Chilliard et al. (2006), but in disagreement with Avondo et al. (2009), genotype did not affect milk yield. In contrast with Chilliard et al. (2006) and Schmidely et al. (2002), fat percentage did not show differences between groups (Table 1); moreover, both genotypes had lower milk fat than usually reported for Girgentana goats (Avondo et al., 2008) in all probability because of the diet rich in concentrates offered to the animals (Slater et al., 2000). In our case the phenomenon of fat-protein inversion occurred, and probably this masked the higher proportion of fat that would be expected for the AA group.

Milk fatty acid composition resulted affected by genotype. Among all the fatty acids investigated, ten showed statistically significant differences between the two groups (Table 2). These findings are partially in contrast with Schmidely et al. (2002) who reported differences only for C14:0, which was higher in FF group, and for odd fatty acids C15:0 and C17:0, that similarly to our findings, were higher in the AA group. However, in that case, as suggested by Chilliard et al. (2006), the results might have been due to the negative energy balance of the AA goats. Except for C8:0, fatty acid profile obtained from Alpine lactating goats differing for the genotype at the at α_{s1}-casein locus (Chilliard et al., 2006), showed a trend similar to ours, but a wider range of fatty acids resulted affected by genotype; in fact, they found that also long chain fatty acids were higher in the AA group. However, it is not possible to exclude that the higher presence of long chain fatty acids in AA milk arose from a different fatty acid profile consumed with diet because it was not determined for each group. Taking in account that, in our conditions, the selected diets were identical also in terms of fatty acids, the differences found in the milk fatty acid profiles of the two groups seem to have a genetic origin. In this direction, it is

Table 2. Effect of genotype on milk fatty acid composition (% of total fatty acids).

	Genotype		*P*-values	Error
	AA	FF	(1)	M S
C8	2.89	3.12	*	0.14
C9	0.32	0.25	*	0.01
C11	0.47	0.29	*	0.02
C12	7.66	5.92	***	0.32
C12:1	0.35	0.21	***	0.01
C13	0.31	0.21	*	0.01
C14	14.56	13.55	*	0.86
C15 anteiso	0.37	0.24	**	0.01
C15	1.62	1.15	**	0.18
C16	24.14	26.40	*	3.78
C16:1	0.92	0.74	*	0.01

*(1) *=P<0.05; **=P<0.01; ***=P<0.001.*

noteworthy that Ollier et al. (2008) showed that weak alleles at α_{s1}-casein locus negatively affect the gene expression of FANS of lactating mammary gland. This gene encodes the fatty acid synthase, which is a multifunctional protein that catalyzes the mammary de novo synthesis of fatty acids. Moreover, also the activity of this protein turned out to be lower in animals with weak genotype, and this could explain why the biosynthesis of milk short and medium-chain fatty acids and odd and branched chain fatty acids resulted lower in the FF group. In conclusion, this study seems to confirm that polymorphism at α_{s1}-casein locus can play a role on goat milk fatty acid composition, in particular for the de novo synthesized fatty acids. However, on account of the particular experimental conditions, further studies with different feeding system are needed to better assess the role of the genetic α_{s1}-casein polymorphism on milk fatty acid composition.

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