Effect of a_{S1} -casein genotypes on yield and chemical composition of milk from Skopelos goats

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Background

a_{s1} casein (CN) polymorphism

- Extensive polymorphisms of the caprine gene (CSN1S1), which encodes the a_{S1} -CN fraction, have been reported in different goat breeds to be associated with milk yield and composition.
- Different alleles have been identified and are classified in 4 groups:
 - strong alleles (A, B1, B2, B3, B4, B', C, H, L, M) are associated with increased a_{S1}-CN in milk (3.6 of g/L),
 - intermediate alleles (E, I) at 1.6 g/L,
 - weak alleles (F, G) with 0.6 g/L,
 - **null** alleles (01, 02, N) which are characterized by absence of a_{S1} -CN in milk.





Objective

To assess the effect of a_{s1} -casein genotypes on milk yield (MY) and milk composition (MC) of Skopelos Greek dairy goats





Materials and Methods

Animals: 235 randomly selected from two herds in Skopelos and Alonnisos islands in Greece



- Individual milk samples over two successive milking periods (5 months)
- Blood samples
- Milk was analyzed for protein (PRO), fat (FAT), lactose (LAC), solid non-fat (SNF) concentration and total viable count (TVC).











Materials and Methods:

Genotyping of the CSN1S1 locus

- DNA was extracted from 200µL of blood using the GeneJET Whole Blood Genomic DNA Purification Mini Kit (Thermo Scientific Inc.).
- Identification of CSN1S1 alleles was done:
 - 1. by PCR-RFLP (Ramunno et al., 2000, 2005)
 - A* (including A, G, I, H),
 - B* (including B1, B2, B3, B4 and C),
 - F and N alleles
 - 2. by AS_PCR (Torres-Vázquez et al., 2008 and Cosenza et al., 2003)
 - E and 01 alleles.





Statistical analysis

Univariate Analysis of Covariance (ANCOVA)

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X_{gijk} = m_{gijk} + A_g + H_i + M_j + Y_k + a_1 \cdot milk + a_2 \cdot log TVC
where,
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 X_{gijk} = variable in question (protein, fat, lactose, SNF) m_{gijk} = intercept,

A_g= fixed effect of genotype (g= 9 levels),

H_i= fixed effect of herd (i= 2 levels),

M_i= fixed effect of stage of milking period (j= 5 levels),

 Y_k = fixed effect of year of sampling (k= 2 levels),

 $a_1 - a_2$ = linear regression coefficients of standardized values of:

- milk yield
- log transformed value of TVC





Results

A total of 9 genotypes were identified in the studied population. Genotype A*B* was the most common (23.8%) followed by genotypes B*B* and A*A* (21.7% and 21.3%, respectively). The less frequent genotype was FB* (1.3%).





Table 1. Effects genotypes and other factors used in the general linear model on milk yield (gr) and milk quality traits (protein, fat, lactose and solid not-fat concentration (%).

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	Protein (%)	Fat (%)	Lactose (%)	SNF [†] (%)	12-hours mill yield (gr)	
AA	0.25***	0.36**	0.09	0.34*	-37.2	
AB	0.15	0.24	-0.06	0.05	-0.8	
BB	0.20**	0.27*	0.08	0.28	1.9	
FA	-0.04	-0.19	-0.03	-0.08	171.1***	
FB	0.18	0.59*	-0.04	0.12	131.6*	
FF	0.16	0.80**	0.07	0.23	-70.6	
NA	-0.02	0.11	0.02	0.01	85.2**	
NB	0.03	0.02	0.00	0.02	52.0	
NN		Reference category				
Farm 1	-0.27***	-0.16	-0.08	-0.38***	-410.6***	
Farm 2	Reference category					
1 st	0.54***	0.68***	0.57***	1.15***	352.7***	
2 nd	0.36***	0.27**	0.39***	0.79***	317.4***	
3 rd	0.03	0.17	-0.06	-0.03	209.4***	
weaning 4th	-0.20***	0.04	0.13*	-0.06	64.6**	
5 th	Reference category					
Year 1st	0.08*	0.12	0.23***	0.31***	-52.2***	
2 nd	Reference category					
Continuous	-0.19***	-0.39***	-0.02	-0.21***	NA	
Continuous	0.16***	0.11***	-0.07***	0.10*	-57.8***	
	AB BB FA FB FF NA NB NN Farm 1 Farm 2 1st 2nd 3rd 4th 5th 1st 2nd Continuous	AA 0.25*** AB 0.15 BB 0.20** FA -0.04 FB 0.18 FF 0.16 NA -0.02 NB 0.03 NN Farm 1 -0.27*** Farm 2 1st 0.54*** 2nd 0.36*** 3rd 0.03 4th -0.20*** 5th 1st 0.08* 2nd Continuous -0.19***	AA 0.25*** 0.36** AB 0.15 0.24 BB 0.20** 0.27* FA -0.04 -0.19 FB 0.18 0.59* FF 0.16 0.80** NA -0.02 0.11 NB 0.03 0.02 NN Farm 1 -0.27*** -0.16 Farm 2 1st 0.54*** 0.68*** 2nd 0.36*** 0.27** 3rd 0.03 0.17 4th -0.20*** 0.04 5th 1st 0.08* 0.12 2nd Continuous -0.19*** -0.39***	AA 0.25*** 0.36** 0.09 AB 0.15 0.24 -0.06 BB 0.20** 0.27* 0.08 FA -0.04 -0.19 -0.03 FB 0.18 0.59* -0.04 FF 0.16 0.80** 0.07 NA -0.02 0.11 0.02 NB 0.03 0.02 0.00 NN Reference cate Farm 1 -0.27*** -0.16 -0.08 Farm 2 Reference cate 1st 0.54*** 0.68*** 0.57*** 2nd 0.36*** 0.27** 0.39*** 3rd 0.03 0.17 -0.06 4th -0.20*** 0.04 0.13* 5th Reference cate 1st 0.08* 0.12 0.23*** Reference cate 1st 0.08* 0.12 0.23***	AA 0.25*** 0.36** 0.09 0.34* AB 0.15 0.24 -0.06 0.05 BB 0.20** 0.27* 0.08 0.28 FA -0.04 -0.19 -0.03 -0.08 FB 0.18 0.59* -0.04 0.12 FF 0.16 0.80** 0.07 0.23 NA -0.02 0.11 0.02 0.01 NB 0.03 0.02 0.00 0.02 NN Reference category Farm 1 -0.27*** -0.16 -0.08 -0.38*** Farm 2 Reference category 1st 0.54*** 0.68*** 0.57*** 1.15*** 2nd 0.36*** 0.27** 0.39*** 0.79*** 3rd 0.03 0.17 -0.06 -0.03 4th -0.20*** 0.04 0.13* -0.06 5th Reference category 1st 0.08* 0.12 0.23*** 0.31*** Reference category 1st 0.08* 0.12 0.23*** 0.31*** Reference category Continuous -0.19*** -0.39*** -0.02 -0.21***	

[†]SNF: Solid Not-Fat, [‡]Z: Standardized value, [§]TVC: Total Viable Count; *P<0.05, **P<0.01, ***P<0.001

Conclusions

 The high frequency of the strong genotypes A* and B* in Skopelos goats is associated with the production of milk with high fat and protein content and with optimal technological properties; caseins are important for cheese making.

- The results could be used in genetic improvement programs:
 - select animals carrying the strong alleles
 - select animals that carry the null (N) allele and produce milk for specialized applications (i.e. milk with low allergenic potential).





Thank you for your attention

Acknowledgements

Dairy Goat Farmers







