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Effects of polymorphism at 5'-noncoding regions (promoters) of αS1- and αS2-casein genes on selected milk production traits in Polish Black-and-White cows*

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The effects of cow's genotype at αS1- and αS2-casein gene 5'-noncoding regions (promoters) were determined on selected milk production traits of the 135 Polish Black-and-White (Polish Friesian) cows as related to the animal's age, lactation parity and stage, and somatic cell count. Cows of the *AA* genotype of αS1-casein gene yielded more milk daily than *AG* heterozygotes. Also, the daily yield of solids-non-fat, protein and lactose was higher in *AA* genotype cows. Milk of the cows with genotype *CC* of αS2-casein contained more lactose but less protein than that of the *CT* heterozygotes. The daily protein yield was slightly (but significantly) higher in the cows of the *CT* αS2-casein genotype. In summary, the results showed that genetic variants of αS1- and αS2-casein 5'-noncoding regions had only a slight effect on milk production traits of the Polish Black-and-White cows. Nevertheless, the *AA* genotype of αS1-casein seemed favourable for higher milk yield, as well as for lactose and protein content.

KEY WORDS: casein genes / cows / milk / polymorphism / promoter

In bovine milk six major protein fractions – caseins αS1, αS2, β, κ, α-lactalbumin, and β-lactoglobulin – are coded by autosomal single-copy genes. Four genes coding for caseins are clustered within less than 300 Kb on bovine chromosome 6 in the following order: αS1, β, αS2, and κ [Feretti *et al.* 1990, Rijnkels *et al.* 1997]. It was assumed

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that the three genes coding for the calcium-sensitive αS1-, αS2- and β-caseins evolved from one ancestral gene by exon shuffling and intra- and intergenic duplications [Jones *et al.* 1985, Yu-Lee *et al.* 1986, Bonsing and Mackinlay 1987]. In contrast, the κ-casein encoding gene evolved differently [Alexander *et al.* 1993]. Lien *et al.* [1993] supported a strong genetic linkage of the casein genes by using the "single sperm typing" method. So, it may be supposed that close localization and linkage of the casein genes might influence a common inheritance of these genes with only a little recombination. Moreover, the close proximity of the casein genes supported the hypothesis of common hormonal regulation of the entire casein gene complex [Rosen 1987].

Genetic polymorphism of milk proteins in cattle is well documented [Grosclaude 1988, Martin *et al.* 2002]. The proteins differ in amino acid substitutions or deletions resulting from the differences in the coding sequences of corresponding genes. Associations have been described between polymorphism in the coding regions of the milk protein genes and the level of expression of milk proteins in cattle [Van Eenennaam and Medrano 1991]. Variable sites were also identified in 5'-noncoding sequences of bovine milk protein genes [Schild and Geldermann 1996, Kamiński 1996, Bleck *et al.* 1996, Geldermann *et al.* 1996, Van Ehrmann *et al.* 1997]. At least some genetically variable sites are located in putative regulatory sequences, e.g. in transcription factor-binding sites [Schild and Geldermann 1996, Szymanowska *et al.* 2003], and thus they may affect the gene expression. It has been suggested that differential expression of various alleles of milk proteins possibly resulted from linkage between variants of coding and regulatory regions of their genes [Van Eenennmaan and Medrano 1991].

The objective of this study was to examine the effect of polymorphism in the 5'-noncoding region of the bovine αS1- and αS2-casein genes on daily milk yield and composition in Black-and-White dairy cows during the whole lactation period. Moreover, the contribution of casein genotype and animal's age, lactation parity and stage, and somatic cell count were assessed, and their effects on the pleiotropic variation in milk production traits were estimated.

Material and methods

Animals

The Black-and-White (BW) cows were maintained at the Polish Academy of Sciences Experimental Farm, Kosów in a herd yielding on average 8,300 kg of milk containing 4.01% fat and 3.45% total protein. For this study 135 cows, with more than 80% of Holstein-Friesian (HF) blood, were randomly chosen. Only 4-5 cows were daughters of one sire and for this reason the sire effect was not included in the statistical model. During the whole period the cows were kept in loose barn with outside run. During the test period animals were fed complete TMR diet (total mixed ratio) of corn silage, wilted grass silage and concentrates, supplemented with mineral and vitamin mixture, according to the INRA system. Water was available *ad libitum*.

The cows were milked twice a day. Milk samples were taken from each cow once a month during three consecutive lactations, starting from lactation I.

All procedures carried out with the use of animals were approved by the Local Ethical Commission; permission No 67/2001).

DNA isolation from whole blood

Blood samples for DNA genotyping were collected from the jugular vein by an authorized veterinarian on K_2EDTA and stored at -25°C for a few weeks, or at -75°C up to several months. The isolation of DNA from whole blood was done with a rapid method described by Kanai *et al.* [1994].

Determination of αS1- and αS2-casein genotype with PCR-RFLP method

Detection of restriction fragment length polymorphism (RFLP) based on the polymerase chain reaction (PCR) was carried out according to Koczan *et al.* [1993] and Schild and Geldermann [1996]. The sequence of primers and conditions of PCR are summarized in Table 1. The PCR was performed in a reaction volume of 25 µl containing approximately 100 ng of bovine genomic DNA, 0.25 µM of each primer, 160 µM dNTPs and 2 units of Taq polymerase (PolGen, Poland). All PCR reactions were performed in MJ Research PTC-225 Thermal Cycler. The PCR-amplified DNA fragment (from -1150 to -872 nt) of the αS2 casein gene was digested at 37°C for 3 hours with 5 units of the *Mae*II nuclease (FERMENTAS, Lithuania). For the αS1-casein, gene fragments: -1145/+101 or -372/+36, were amplified and digested with *Ssp*I or *Mae*III restriction endonucleases, respectively. The digested products were

Table 1. PCR primers and conditions of DNA amplification used for RFLP genotyping in 5'-noncoding regions (promoters) of αS1- and αS2-casein genes in the Polish Black-and-White cows

Gene/position of mutation	Restriction nuclease	Sequence of primers	Location	Amplified fragment (bp)	Number of PCR cycles	Temperature/time (min)		
αS2-casein/[illegible]	MaeII	[illegible] [illegible]	-1150/-872	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
αS1-casein/[illegible]	MaeIII	[illegible] [illegible]	-372/+36	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
αS1-casein/[illegible]	SspI	[illegible] [illegible]	-1145/+101	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]

separated on 2% agarose (GIBCO-BRL, England) gels in 1 × TRIS-borate-EDTA (TBE) buffer. The gels were stained with ethidium bromide and visualised and scanned in FX Phosphoimager (Bio-Rad).

Milk composition

The fat, protein and lactose content was estimated in fresh milk samples using Milko Scan 104A/B, and somatic cell counts (SCC) were determined by means of Fossomatic apparatus. Per cent of total solids in each milk sample was expressed as a sum of per cent of fat, total protein, lactose and minerals. The concentration of minerals was calculated according to the Sherman equation: P = 0.1 × per cent of total protein + 0.38.

The milk samples were divided according to the age of cows into three groups: cows in lactation I, II and III (or further). The whole lactation period was divided into three post-calving stages: 6-60 days, 61-210 days, and 211 days up to the end of lactation. According to the SCC the milk samples were divided into three classes: up to 400 thousand, 401-800 thousand and >801 thousand cells/ml. The SCC values were transformed to the natural logarithm scale.

Statistical

The data were evaluated by the analysis of variance according to Harvey [1990] using the following fixed model:

$$Y_{ijklm} = \mu + a_{i} + b_{j} + c_{k} + d_{l} + e_{ijklm}$$

where:
Y_{ijklm} – observed mean value of the trait;
μ – overall mean;
a_i – effect of i-th age of cow (i = 1, 2, 3);
b_j – effect of j-th stage of lactation (j = 1, 2, 3);
c_k – effect of k-th αS1- or αS2-casein genotype (k = 1, 2, 3, 4);
d_l – effect of l-th class of SCC (l = 1, 2, 3);
e_{ijklm} – random error.

The reference genotypes were: *AA*, *AG* for αS1-casein gene, and *CC*, *CT* for αS2-casein gene.

Results and discussion

Frequencies of genotypes and alleles at 5'-noncoding regions (promoters) of the αS1- and αS2-casein genes in the studied group of cows are shown in Table 2. RFLP at the bovine αS2 casein gene promoter was investigated at the site previously reported as polymorphic by Schild and Geldermann [1996]. The polymorphisms occurred at posi-

Table 2. Frequency of genotypes and alleles in 5'-noncoding regions (promoters) of αS1- and αS2-casein genes in the Polish Black-and-White cows

Locus/position of polymorphic site	Restriction nuclease	Genotype	Number of animals	Allele frequency
αS2-casein/-1084	*Mae*II	*CC*	100	
		CT	42	*C*: 0.85
		TT	1	*T*: 0.15
			total: 143	
αS1-casein/-175	*Mae*III	*AA*	126	*A*: 0.97
		AG	9	*G*: 0.03
			total: 135	
αS1-casein/-728	*Ssp*I	(-/-)	126	(-): 0.97
		(*T*-)	9	(*T*): 0.03
			total: 135	

tion -1084 relative to the transcription start point. It was a single nucleotide substitution (SNP) – *C/T* (transition) – recognizable by PCR-RFLP with the nuclease *Mae*II. All three genotypes were found, although the *TT* genotype was rare and appeared only in one animal. The *CC* genotype and allele *C* were the most frequent – 70 and 85%, respectively. The results showed that the *C*→*T* transition in the αS2-casein gene promoter at position -1084 was rare, similarly as in other cattle breeds. Previously, Schild and Geldermann [1996] among seven cattle breeds showed *C*→*T* mutation in one Zebu (*Bos indicus*) and in one German Simmental individual only. In our earlier study on Polish native cattle breeds [Klauzińska *et al.* 2003] among 195 Polish Red cows no *TT* genotype was identified.

In this study the RFLP of the bovine αS1 casein gene promoter was investigated at two polymorphic sites reported by Koczan *et al.* [1993] and Schild and Geldermann [1996]. The mutation in αS1-casein gene found at position -728 was a deletion/insertion of T nucleotide (Tab. 2). An amplified DNA fragment was digested with restriction endonuclease *Ssp*I, and two genotypes: (-/-) and (T/-) were observed. The frequency of allele (-) was 97% (Tab. 2). No *TT* animals were found in the studied group of cows. The high frequency of the allele (-) was also reported by Schild and Geldermann [1996] who found only two *TT* animals out of 13 belonging to seven cattle breeds. We also found no *TT* genotype in Polish Red cattle [Klauzińska *et al.* 2003], but the allele *T* appeared slightly more frequent in Polish Red than in BW cattle (0.12 and 0.03, respectively). Another polymorphism studied in the αS1-casein gene 5'-noncoding region was A/G transition at position -175 [Koczan *et al.* 1993]. Since *A*→*G* substitution creates new restriction site for *Mae*III nuclease it can be analysed by the PCR-RFLP method. While studying polymorphism of casein genes in individual animals we noticed the complete associations between specific variants of αS1-casein at positions -175 and -728. All animals of genotype (-/-) at position -728 appeared *AA* for nucleotide at position -175,

Table 3. Least squares means (LSM) and their standard errors (SE) for daily milk yield, milk energy and per cent of major milk constituents as affected by αS1 and αS2 genotype in the Polish Black-and-White cows

Variation source	n[1]	Milk (kg)		Fat-corrected milk (kg)		Gross energy (MJ)		Total solids (%)		Solids-non-fat (%)		Fat (%)		Protein (%)		Lactose (%)	
		LSM	SE	LSM	SE	LSM	SE	LSM	SE	LSM	SE	LSM	SE	LSM	SE	LSM	SE
αS1 genotype																	
AA	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
AG	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
αS2 genotype																	
CC	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
CT	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
Lactation stage																	
6–60 days	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
61–140 days	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
> 140 days	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
Lactation																	
I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
II	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
III and further	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
SCC/ml																	
≤400 thousand	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
401–800 thousand	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
>801 thousand	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]

[1] Number of milk samples analysed.

[a,b] Means within columns and variation source bearing different letters are significantly different: small letters – P≤0.05, capitals – P≤0.01.

Table 4. Least square means (LSM) and their standard errors (SE) for daily yield of major milk components as affected by αS1 or αS2 genotype in the Polish Black-and-White cows

Variation source	n[1]	ECM (kg)[2] LSM	ECM (kg)[2] SE	Total solids (g) LSM	Total solids (g) SE	Solids-non-fat (g) LSM	Solids-non-fat (g) SE	Fat (g) LSM	Fat (g) SE	Protein (g) LSM	Protein (g) SE	Lactose (g) LSM	Lactose (g) SE
αS1 genotype													
AA	1016	11.0[a]	0.1	1136	17	1347[a]	19	717	9	605[a]	8	817[a]	11
AC	166	19.9[b]	0.6	2147	61	1419[b]	47	713	10	558[b]	16	753[b]	14
αS2 genotype													
CC	1385	10.1	0.1	1190	17	1471	17	718	11	571[a]	10	780	13
CT	607	10.7	0.4	1110	44	1501	11	710	13	591[b]	11	787	17
Lactation stage													
6–60 days	796	13.3[a]	0.4	1817[a]	31	1901[a]	76	913[a]	16	718[a]	11	1011[a]	10
61–140 days	1034	10.8[b]	0.4	1111[b]	40	1511[b]	19	710[b]	17	598[b]	11	801[b]	16
>140 days	741	13.1[c]	0.4	1361[c]	41	1077[c]	19	318[c]	14	419[c]	11	310[c]	16
Lactation													
I	447	19.1[a]	0.4	1073[a]	34	1794[a]	79	681[a]	18	341.1[a]	13	779[a]	11
II	607	19.9[a]	0.3	1173[a]	43	1440[a]	71	694[a]	13	366[a]	17	759[a]	18
III and further	1146	11.1[b]	0.1	1791[b]	17	1614[b]	36	766[b]	11	619[b]	10	857[b]	14
SSC/ml													
<400 thousand	1301	11.0	0.1	1186[a]	40	1361[a]	36	711	11	601[a]	10	817[a]	14
401–800 thousand	130	10.1	0.3	1167[b]	37	1471[b]	41	696	19	573[ab]	16	773[b]	11
>801 thousand	441	10.1	0.4	1147[b]	47	1414[b]	71	711	13	367[b]	17	740[b]	18

[1] Number of milk samples analysed

[2] ECM = 0.327 daily milk (kg) + 12.86 x fat (kg) + 7.65 x protein (kg), Orth et al. (2001)

[a–c] Means within columns and variation sources bearing different letters are significantly different: small letters – P≤0.01, capitals – P≤0.01

and all (*T*/-) animals were *AG* heterozygotes (Tab. 2). These results suggest a tight linkage between both polymorphic sites located within a distance of 553 bp and the existence of intragenic haplotypes within the αS2-casein gene. Therefore, only one polymorphism of the αS1-casein gene – the *A*/*G* transition at position -175 – was included in our further calculations.

The individual effects of αS1- and αS2-casein genotypes on the milk yield and composition are shown in Tables 3 and 4. Cows of the *AA* genotype of αS1-casein yielded more milk daily than *AG* heterozygotes (Tab. 3), the difference being 1.2 kg milk/day in favour of the *AA* genotype. However, the milks of *AA* cows contained significantly less gross energy (by 0.07 MJ/l) and fat (by 0.22 per cent units). This resulted in a not significant difference in FCM yield between cows of genotypes *AA* and *AG*. The difference in dairy performance between *AA* and *AG* cows appeared evident when the milk corrected for both fat and protein (VCM) was considered (Tab. 4). The difference at VCM value was significant and amounted to 1.1 kg in favour of the αS1 *AA* genotype. This was due to the higher (though statistically not significant) concentration of protein in the milk of the *AA* genotype cows. In addition, the *AA* homozygotes yielded significantly more milk protein and lactose daily than those of *AG* genotype; the daily yield of fat was nearly the same in both groups (Tab. 4).

The αS2-casein genotype influenced only the protein and lactose per cent of milk (Tab. 3). Milk of the cows with genotype *CC* of αS2-casein contained more lactose but less protein than that of the *CT* heterozygotes. The *TT* genotype was not considered in the calculations since only one animal of this genotype was identified. The genotype of αS2-casein affected only the daily protein yield, which was slightly, but significantly, higher in the *CT* cows (Tab. 4).

The results presented so far show that genetic variants at the 5'-noncoding region of αS1-casein gene have a marked effect on daily milk yield and yield of milk main components, as well as their content of milk. The *AA* genotype of αS1-casein seemed favourable for higher milk yield, and higher lactose and protein content. On the other hand, the αS2-casein gene genotype affected only lactose and protein content of milk.

Effects of lactation stage, cow's age (lactation parity), and somatic cell count (SCC) on milk yield and composition are shown in Tables 3 and 4. Older cows (lactation III) produced more milk – both total and fat-corrected – than did the younger ones. The milk yield depended significantly on lactation stage, being highest in early lactation (6-60-days period). Milks from the late stage of lactation (>240 days) contained more gross energy, total solids, fat, and protein than those from earlier lactation stages. High SCC was adversely related to milk yield (but not to FCM yield). Milks of cows with high SCC (>801 thousand) contained less solids-non-fat and lactose but significantly more fat and protein. The yield of milk components – total solids, protein, and lactose – was much smaller ($P<0.01$) in cows with high than in those with low SCC (Tab. 4).

The contribution of different fixed (genotype) and random (lactation parity, lactation stage, SCC) factors to the variation in daily milk yield and composition is shown

in Table 5. The calculated contribution of casein genotype to milk yield was low and for αS1 amounted to 0.79%, while for αS2-casein to 0.24% of total phenotypic variation. The αS1-casein genotype contributed mostly to fat content (10.10%), while the αS2 was shown to affect mostly the phenotypic variation of lactose (16.36%). The contribution of lactation parity was high and varied from 44% for fat per cent, to more than 60% for milk yield, and up to 93% for per cent of protein. SCC mostly affected the lactose content of milk (50% of contribution of all factors analysed).

Very few studies have been done so far of the nucleotide sequence polymorphism in the 5'-regulatory regions of the milk protein genes and its effects on milk yield and composition. Voelker *et al.* [1997] examined 5'-flanking region of the bovine α-lactalbumin gene for potential sequence variations. They identified a single base pair difference, the *A*/*G* transition, located at position -1689 from the transcription start point. A higher expression of allele *A* has been described in heterozygous (*AG*) animals by Graml *et al.* [1989]. Lum *et al.* [1997] investigated the role of the G to C transversion within a consensus binding site for activator protein-2 (AP2) at position -430 in bovine β-lactoglobulin gene. A possible regulatory role of AP2 in the transcriptional regulation of the β-lactoglobulin gene has been proposed [Lum 1997]. Folch *et al.* [1999] showed differential expression of a reporter gene fused to bovine β-lactoglobulin *A* or *B* promoter variants in transiently transfected HC11 cells, the *A* variant driving more efficient expression of the reporter than the *B*

Table 5. Contribution* of different fixed and random effects to the phenotypic variation in daily milk yield and composition as related to αS1- or αS2-casein in the Polish Black-and-White cows

Variation source	Milk (kg)	Fat-corrected milk (kg)	ECM (kg)	Fat (%)	Protein (%)	Lactose (%)	Total solids (%)	Solids non-fat (%)	Gross energy (kJ/kg)
αS1-Casein genotype	0.79	0.14	0.71	10.10	0.60	0.56	1.36	1.04	3.37
αS2-Casein genotype	0.24	0.01	0.23	3.0	1.31	16.36	1.83	0.43	1.72
Lactation stage	61.06	64.13	50.80	43.86	93.06	3.51	79.39	85.57	72.41
Age (lactation parity)	4.11	3.76	4.55	7.06	1.13	22.78	6.95	4.94	6.14
SCC/ml	1.05	0.41	0.50	6.32	1.57	50.21	0.11	4.98	1.46
Remainder (e.g. year or season)	32.75	31.55	43.21	29.66	2.33	6.56	10.36	3.04	14.90
Total	100.00	100.00	100.00	100.00	100.00	100.00	100.00	100.00	100.00

*Least squares constant for each factor: 100 + sum of least squares constants for all factors

variant. Polymorphism within 5'-flanking region of the bovine β-lactoglobulin gene was also studied by Kamiński and Zabolewicz [1998] in the dairy Polish BW cattle. Several point mutations were found by SSCP analysis. Statistical evaluation revealed significant associations between the β-lactoglobulin genotypes and protein content of milk during the first complete lactation [Kamiński and Zabolewicz 2000].

Kamiński [1996] identified a *Dd*eI RFLP polymorphism within the 5'-upstream region of the bovine κ-casein gene, containing five potential consensus sequences for different transcription factors. Associations between individual κ-casein genotypes and milk production traits were investigated and significant differences were found for protein content of milk [Kamiński 2000].

In our earlier study [Martin *et al.* 2002] based on SDS-PAGE and HPLC techniques, differences were shown in casein content between milks obtained from cows carrying specific mutations at position -1084 and -728 of the αS2- and αS1-casein genes, respectively. Milk of BW cows with (*T*/-) genotype of αS1-casein gene promoter was found to contain on average 11% more αS1-casein than that of cows with (-/-) gene. Also the polymorphism within αS2-casein gene promoter was shown to affect the content of the relevant protein of milk; milk from BW cows with *CT* genotype of αS2-casein gene at position -1084 contained twice as much αS2-casein than that from *CC* animals. Moreover, differences were found in the expression rates of the different αS2-casein alleles using semi-quantitative RT-PCR analysis performed on RNAs isolated from biopsies of mammary glands or from somatic cells derived from cow's milk [Szymanowska *et al.* 2003]. These results show that nucleotide sequence variations in the 5'-noncoding regulatory regions of milk protein genes may influence expression of individual proteins in the cow's milk.

The results presented here show that such genetic variants in the bovine casein genes may also be related to the milk yield, as well as to milk components yield and content.

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Wpływ polimorfizmu w rejonie niekodującym 5' (promotorze) genów kazein αS1 i αS2 na wybrane cechy mleczności polskich krów rasy czarno-białej

S t r e s z c z e n i e

Zbadano wpływ polimorfizmu w rejonie niekodującym 5' genów kazein αS1 i αS2 na cechy charakteryzujące mleczność i skład mleka 135 polskich krów rasy cb (wydajność dzienna, zawartość suchej masy, suchej masy beztłuszczowej, tłuszczu, białka i laktozy) zależnie od wieku zwierząt, stadium laktacji i liczby komórek somatycznych (SCC) w mleku. Stwierdzono, że krowy o genotypie *AA* kazeiny αS1 produkowały więcej mleka niż heterozygoty *AG*. Także dzienna produkcja niektórych składników, w tym białka i laktozy, była większa w mleku krów o genotypie *AA*. Mleko krów o genotypie *CC* kazeiny αS2 zawierało więcej laktozy, lecz mniej białka niż mleko heterozygot *CT*. Dzienna produkcja białka była nieznacznie, ale istotnie większa w mleku krów o genotypie *CT* kazeiny αS2. Uzyskane wyniki świadczą, że w porównaniu z wyraźnym wpływem okresu laktacji, wieku krów i SCC, warianty genetyczne niekodujących rejonów 5' genów kazein αS1 i αS2 wpływają w niewielkim stopniu na cechy produkcji mleka krów rasy cb. Tym niemniej, genotyp *AA* kazeiny αS1 wyraźnie korzystnie wpływa na wydajność mleka oraz zawartość w nim laktozy i białka.