

KAPPA-CASEIN AND PRL-RSA I GENOTYPIC FREQUENCIES IN TWO RUSSIAN CATTLE BREEDS

FRECUENCIAS GENOTÍPICAS DE KAPPA-CASEÍNA Y DE PRL-RSA I EN DOS RAZAS DE GANADO RUSAS

Alipanah, M.¹, L. Alexandrovna Kalashnikova² and G. Veladimirovich Rodionov³

¹Department of Animal Science. University of Zabol. Zabol. Iran. 98615-538. alipanahus@yahoo.com

²All-Russian Research Institute of Animal Breeding. Moscow. Russia. 141212.

³Department of Dairy Cattle Breeding. Timiriazev Agricultural Academy. Moscow. Russia. 127550.

ADDITIONAL KEYWORDS

Cattle. Kappa casein. PRL-Rsa I. Milk production. PCR-RFLP. Polymorphism.

PALABRAS CLAVE ADICIONALES

Vacuno. Kappa caseína. PRL-Rsa I. Producción de leche. PCR-RFLP. Polimorfismo.

SUMMARY

Casein is a family of milk proteins that exist in several molecular forms and are the main proteins present in the bovine milk. The B variant of bovine k-casein is reported to be favorable for milk quality and quantity of cheese derived from milk and considered to be included in breeding strategies of dairy cattle. Prolactin plays an important regulatory function in mammary gland development, milk secretion, and expression of milk protein genes. Hence the prolactin gene is a potential genetic marker of production traits in dairy cattle.

Genotypes of 72 Russian Black Pied and 98 Red Pied cows were determined for kappa casein and PRL-Rsa I loci by restriction fragment length polymorphism analysis (PCR-RFLP) of amplified DNA. This technique was used to determine the kappa casein and PRL-Rsa I allelic frequency in Black Pied and Red Pied dairy herds. Estimated gene frequencies were 0.83, 0.69 for the A and 0.17, 0.31 for the B k-casein alleles and 0.71, 0.79 for the A and 0.29, 0.21 for the B alleles PRL-Rsa I for Black Pied and Red Pied breeds, respectively. A significant difference was found between k-casein A and B alleles frequency in the black-pied and Red-pied cattle. There were no difference in the frequency of A and B alleles of prolactin gene.

The milk from cows with the BB genotype k-casein in two breeds had shown higher protein percentage than AA and AB individuals. A significant association between the PRL-Rsa I and milk yield, fat percentage is shown for two breeds.

RESUMEN

La caseína constituye una familia de proteínas lácteas que se presenta en diferentes formas moleculares y son las principales proteínas presentes en la leche bovina. Se ha señalado que la variante B de la k-caseína es favorable para la calidad de la leche y la cantidad de queso derivado de ella y se ha considerado integrarla en las estrategias de cría para el ganado lechero. La prolactina juega una importante función reguladora en el desarrollo de la glándula mamaria, secreción de leche y expresión de los genes de la proteína de la leche. Por eso el gen de la prolactina es un marcador genético potencial de caracteres de producción en el ganado lechero.

Los genotipos de 72 Berrenda en Negro y 98 Berrendas en Rojo rusas fueron analizados para los loci kappa caseína y PRL-Rsa I mediante análisis PCR-RFLP de ADN amplificado. Esta técnica fue empleada para determinar la frecuencia alélica de kappa caseína y PRL-Rsa I, en las razas lecheras Berrenda en Negro y Berrenda en Rojo. Las frecuencias génicas estimadas fueron 0,83 y 0,69 para el alelo A y 0,17 y 0,31 para el alelo B de k-caseína y 0,71 y 0,79 para el alelo A y 0,29 y 0,21 para el alelo B de PRL-Rsa I para Berrenda en Negro y Berrenda en Rojo respectivamente. Se encontró una diferencia significativa entre las frecuencias de los alelos A y B de la k-caseína para el ganado Berrendo en Negro y Berrendo en Rojo. No se encontraron diferencias para los alelos A y B del gen prolactina.

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La leche de las vacas con el genotipo BB de la k-caseína en las dos razas ha mostrado mayor porcentaje de proteína que la de los individuos AA y AB. Se ha detectado una asociación significativa entre PRL-Rsa I y rendimiento lechero y porcentaje de grasa en las dos razas.

INTRODUCTION

Milk protein polymorphisms have received considerable research interest because of their potential use as an aid to genetic selection and to genetic characterization of bovine breeds (Del Lama and Zago, 1996; Golijow *et al.*, 1996 and 1999; Kemenes *et al.*, 1999). The k-casein variants A and B differ in amino acid 136 and 148. In position 136, Thr (ACC) is changed for Ile (ATC) in position 148, and Asp (GTA) is changed for Ala (GCT) (Lin *et al.*, 1992, Strzalkowska *et al.*, 2002, Tinaev, 2003). Several studies have reported that some of these bovine protein variants, particularly certain k-casein, are associated with lactation performance and have a major influence on milk composition and its processing properties, including cheese yield (Kastolina *et al.*, 2004, Denisenko and Kalashnikova, 2004, Konovalova *et al.*, 2004, Romonasova, 1999, Marziali and Ng-Kwai-Hang, 1986; Aleandri *et al.*, 1990). Relationships between genotypes for different milk proteins and yield traits have been reported by several authors (Lin *et al.*, 1992). Although reports on the association between k-casein genetic variants and milk yield are somewhat conflicting. Whereas Strzalkowska *et al.*, 2002, Aleandri *et al.* (1990) found no significant associations; results from other groups (Pytlewski *et al.*, 2002, Ikonen *et al.*, 1999) indicate that there is indeed a relationship. However, because of economic interests, it has been suggested that favourable milk protein genotypes, k-casein BB, should be included into the criteria for selection dairy cattle. Genotyping of milk proteins, such as k-casein, now possible to include information on milk protein genotypes into selection programs,

which should result in more accurate predictions of breeding values of animals to be selected, and thus improve response to selection. Genetic variability in the k-casein locus has been reported for several breeds, with allelic frequencies incorporated into studies on genetic diversity among breeds (Golijow *et al.*, 1996; Del lama e Zago, 1996; Kemenes *et al.*, 1999).

PRL-Rsa I play an important regulatory function in mammary gland development, milk secretion, and expression of milk protein genes. Hence the PRL gene is a potential genetic marker of production traits in dairy cattle. The gene was mapped on chromosome 23 by Hallerman *et al.* (1987). It consists of 5 exons and four introns (Camper *et al.*, 1984) encoding the 199-amino-acid mature protein (Wallis, 1974). On the basis of sequence analysis of four different cDNA clones, seven possible nucleotide substitutions were described by Sasavage *et al.* (1974). One of them, recognized by *RsaI* endonuclease, has become a popular genetic marker used for genetic characterization of cattle populations by means of PCR-RFLP (Mitra *et al.*, 1995). Two allelic variants (A and B) have been distinguished at the DNA level, based on *RsaI* polymorphism in the third exon of the coding region. It has been suggested that PRL-Rsa I alleles correlate with milk yield (Lewin *et al.*, 1992).

The objectives of this work was to study gene frequencies at the k-casein and PRL-Rsa I loci in Black Pied and Red Pied cattle, and compare them with those reported for different commercial cattle breeds and to investigate the relationship between these polymorphisms and milk production traits of Black Pied and Red Pied cattle .

In Russia since 1977 began the work on the creation of new breed Red Pied. The Red Pied breed cattle was created via the crossing of Simmental cows with the bulls of the Red Pied Holstein with the high milk yield and milk fat 3.6-3.7%, live weight of 600-650 kg, with the evenly developed udder, suitable for the machine milking.

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The Black Pied breed developed from crossing the local cattle in various areas with the Dutch Black Pied and East Friesian breeds. Some animals were imported from Germany, the Netherlands, Estonia and Lithuania during 1930-40 and distributed in various parts of the Russia (Dmitriez and Ernst, 1989).

The Black Pied breed is noted for high milk production (the highest among the dairy breeds), good conformation and good beef qualities. Due to the high productivity, adjustment to machine milking, well-defined beef features and the ability to acclimatize, the population of this breed is increasing year by year.

MATERIAL AND METHODS

A total of 72 Russian Black Pied and 98 Russian Red Pied cows were genotyped. The cows were kept in the Gorki herd in Moscow state and in the Drydjba herd in Varonedj state of Russia, respectively.

Blood samples for DNA genotyping were collected from the jugular vein. The isolation of DNA from whole blood done with a method described by, Denicourt *et al.* (1990).

KAPPA CASEIN POLYMORPHISM

To analyze the k-casein (k-CN) *locus*, a 530-bp fragment covering the sequence containing the mutation site was amplified according to the procedure proposed by Medrano and Aguilar-Cordova (1990). The primer sequences used for the amplification of K-CN were as follows: Cas A 5'-ATA GCC AAA TAT ATCCA ATT CAG T-3', Cas B 5'- TTT ATT AAT AAG TCC ATG AAT CTT G 3'. Samples were amplified for 35 cycles under the following conditions: 95°C/1 min (denaturation); 58°C/1 min (primer annealing); 72°C/1 min (primer extension). The amplification was digested with *HindIII* restriction endonuclease at 37°C for three hours, to distinguish between A and B alleles the restriction fragments were separated in agarose gel 3 percent and etidium bromide

PRL-RSA I POLYMORPHISM

The *PRL-RsaI* genotypes were analysed using the PCR-RFLP method. PCR Primer Sequences was amplified using forward 5'-CGAGTCCTTATGAGCTTGATTCTT-3' and reverse 5'-GCCTTCCAGAAGTC GTT TGTTTTTC-3' primers (Mitra *et al.*, 1995). Cycles applied were: denaturation - 94°C/5 min, followed by 30 cycles - 94°C/30 s, primer annealing - 59°C/40 s, PCR products synthesis - 72°C/20 s, and final synthesis - 72°C/3 min. Amplified DNA was digested with *RsaI* enzyme. Digestion products were separated electrophoretically in 4% agarose gel. The polymerase chain reactions were performed using a PCR-mix with: 2, 5 µl 10 x PCR buffer (15 mM MgCl₂), 1, 5 µl dNTP-mix (2 Mm each), 1, 5 µl of primer (100 pmol/µl each), 0/5 U Taq.

Allele frequencies were determined by gene counting. A chi-square test was carried out to evaluate if the population was in Hardy-Weinberg equilibrium.

Data for 305-day milk production, including overall yields of milk, milk fat and milk protein, percent of milk fat and percent of milk protein obtained from the farm records. Milk samples were taken from each cow once a month during lactation, the milk samples from two control days were estimated for the contents of fat, protein on the basis of measurements by a milkoscan FT2 (Foss, Denmark) apparatus. Statistical calculations were performed using SAS procedures. Frequencies of distribution of alleles within the herds were compared with Chi-square test. The effect of k-cas and *PRL* genotypes on the milk production traits of cows were analysed using GLM procedure.

STATISTICAL ANALYSIS

The data obtained were analysis by the SAS procedure according to following model:

$$Y_{ijkl} = \mu + a_i + b_j + c_k + e_{ijkl}$$

Where:

Y_{ijkl} = observed mean value of the trait;
 μ = overall mean;
 a_i = effect of i -th year of lactation ($i = 1, \dots, 6$);
 b_j = effect of j -th lactation number ($j = 1, \dots, 6$);
 C_k = effect of k -th K-Cn or PRL-Rsa I genotype ($k =$
 AA, AB and BB);
 e_{ijkl} = random error.

RESULTS AND DISCUSSION

Genotypic frequencies k -cas for Black-pied were 68.89, 28.22 and 2.89 for AA, AB and BB, respectively and for Red Pied cattle were 44.12, 50.00 and 5.88 for AA, AB and BB, respectively. Frequencies of alleles A and B, for two breeds estimated from genotypic frequencies, were 0.83 and 0.17 for Black-pied and for Red Pied breeds 0.69 and 0.31, respectively (**table I**). Contrary to Black-pied, the frequency of desirable casein B allele in the Red Pied breeds was higher.

Nearly identical results of B variant of k -casein (0.13) for Black Pied cattle were obtained by Zinovieva and Gladir (2003). However, results of Solimova *et al.* (1992),

Tinaev *et al.* (2003) and Iolchiev (1993) showed frequency of B k -casein allele of 0.53, 0.40 and 0.42, respectively.

A allele was more frequent in both breeds than the k -casein B allele. The frequency k -casein B was higher in Red Pied (0.31) than in Black Pied cows (0.17). The genotypic frequencies of k -casein AA and AB are significantly different in the two breeds examined. The no significant departure from Hardy-Weinberg equilibrium ($p < 0.05$) was in the two breeds.

In studies of genetic characterization of cattle breeds, it has been found that the B allele of k -Cn occurs at higher frequencies in breeds originating from *Bos taurus* than in those of *Bos indicus* origin (Backer and Manwell, 1980; Golijow *et al.*, 1996; Del lama e Zago, 1996; Kemenes *et al.*, 1999). Black Pied and Red Pied breed shows a high degree of genetic variability for the k -casein locus, with a frequency of the B allele of 0.17 and 0.31, respectively.

In this study the frequencies of alleles PRL-Rsa I were as follows; A-0.71, B-0.29 for Black Pied and A-0.79, B-0.21 for Red Pied, respectively. The frequencies of AA, AB and BB genotypes were 0.500, 0.413 and 0.087 for Black Pied 0.598, 0.392 and 0.01 for Red Pied; respectively (**table I**).

Until now the frequency of PRL-Rsa I alleles in Russia has been analysed only for Russian Black Pied. Frequencies of PRL-Rsa I alleles obtained in this study are similar to results reported earlier for the Russian Black Pied cattle by Khatami *et al.* (2004) that genotyped 32 cows and found that the allele frequencies for PRL-Rsa I A and B were 0.95 and 0.05, respectively. While was observed by Udina *et al.* (2001) 0.80 and 0.20, for A and B alleles respectively. In other breeds higher frequency of the PRL-Rsa I A allele (0.95) in Holsteins was observed by Chrenek *et al.* (1998) while lower by Mitra *et al.* (1995) and Chung *et al.* (1996) 0.80 and 0.73, respectively. Dybus (2002) reported for Black and White cattle A-0.86 and B-0.14.

Table I. Polymorphism at the K-casein and PRL-Rsa I loci in Russian breeds Black Pied and Red Pied cattle. (Polimorfismo de los loci de la k -caseína y PRL-Rsa I en las razas bovinas rusas Berrenda en Negro y Berrenda en Rojo).

	Genotype	Frequency	Allele frequency	χ^2	
Black Pied	K-Casein	AA	68.89	A-0.83	0.70ns
		AB	28.22	B-0.17	
		BB	2.89		
	PRL-Rsa I	AA	50.00	A-0.71	0.02ns
		AB	41.30	B-0.29	
		BB	8.70		
Red Pied	K-Casein	AA	44.12	A-0.69	2.57ns
		AB	50.00	B-0.31	
		BB	5.88		
	PRL-Rsa I	AA	59.79	A-0.79	0.14ns
		AB	39.18	B-0.21	
		BB	1.03		

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Table II shows the effect of the k-casein and PRL-Rsa I genes on milk production traits in cows studied.

The results shown in **table II** indicate that in Black Pied breed the effect of polymorphism k-casein was significant ($p=0.05$) for fat and protein percentage. The milk from cows with the BB genotype showed the highest fat percentage (+0.37% and +0.49%, respectively) than AA and AB individuals and for protein percentage BB genotype showed higher (+0.19% and +0.19%) than AA and AB individuals. In Red-pied cows, statistically significant differences for milk yield, protein percentage and fat yield were found ($p=0.05$). Cows with genotype AA had higher milk yield (+93.28 kg and 204.02 kg, respectively) than AB and BB individuals and had higher fat content (+3.10 kg and +5.29 kg, respectively) than AB and BB animals. The milk from cows with the BB genotype showed highest protein percentage (+0.09% and +0.09%, respectively) than AA and AB individuals.

Effects of the PRL-Rsa I locus are shown in **table II**. In Black Pied breed the effect of polymorphism PRL-Rsa I was significant for milk yield and fat percentage ($p=0.05$). Milk of the cows with genotype BB of PRL-Rsa I contained more fat percentage (+0.19% and 0.12%, respectively) than AA and AB individuals. But AB genotype had higher milk yield (+356.37 kg and +761.17 kg, respectively) than AA and BB animals ($p=0.05$).

Results in Red Pied breed showed that cows with the BB genotype had higher milk yield, fat yield, protein yield but lesser fat percentage ($p=0.05$). Animals with BB genotype had higher milk yield (+681.62 kg and +906.73 kg, respectively) than AA and AB individuals. Milk fat yield differences ($p<0.05$) between the cows with different *PRL-RsaI* genotypes were observed. BB cows showed higher milk fat yield (+51.49 kg and +62.28 kg, respectively) than AA and AB individuals. AA cows yielded more milk fat (+10.79 kg) than AB animals. For milk fat content (%). AB genotype had higher fat

Table II. Effect of k-cas and PRL-Rsa I genotypes on the milk traits in Russian Black Pied and Russian Red Pied cows. (Efecto de los genotipos de k-cas y PRL-Rsa I sobre caracteres de la leche en vacas Berrenda en Negro y Berrenda en Rojo rusas).

Breed Genotype	Milk(kg)±SE	Fat(kg)±SE	Fat(%)±SE	Protein(kg)±SE	Protein(%)±SE
Black Pied k-cas					
AA	7807.04 ^a ±725.53	343.45 ^a ±32.92	4.42 ^a ±0.20	243.58 ^a ±20.59	3.12 ^a ±0.09
AB	6996.77 ^a ±719.35	296.20 ^a ±32.64	4.30 ^a ±0.19	218.19 ^a ±20.42	3.12 ^a ±0.09
BB	6821.83 ^a ±859.41	324.13 ^a ±38.99	4.79 ^b ±0.23	226.27 ^a ±24.39	3.31 ^b ±0.10
Red Pied k-cas					
AA	6047.34 ^a ±188.34	226.23 ^a ±7.47	3.75 ^a ±0.04	231.88 ^a ±7.49	3.26 ^b ±0.03
AB	5954.06 ^b ±161.92	223.22 ^b ±6.42	3.76 ^a ±0.04	233.30 ^a ±7.28	3.26 ^b ±0.03
BB	5843.32 ^b ±286.17	220.94 ^b ±11.35	3.79 ^a ±0.07	243.35 ^a ±15.71	3.35 ^a ±0.07
Black Pied PRL-Rsa I					
AA	7156.13 ^b ±397.75	299.65±15.45	4.19 ^b ±0.07	226.78 ^a ±12.30	3.17 ^a ±0.04
AB	7512.50 ^a ±397.75	311.00±15.45	4.16 ^b ±0.07	233.71 ^a ±12.30	3.12 ^a ±0.04
BB	6751.33 ^c ±694.53	295.27±25.24	4.38 ^a ±0.11	206.48 ^a ±20.08	3.07 ^a ±0.07
Red Pied PRL-Rsa I					
AA	6136.90 ^b ±178.03	236.46 ^b ±8.81	3.73 ^a ±0.04	236.46 ^b ±8.81	3.27 ^a ±0.03
AB	5911.79 ^b ±167.77	225.67 ^b ±9.43	3.78 ^a ±0.03	225.67 ^b ±9.43	3.26 ^a ±0.03
BB	6818.52 ^a ±576.92	287.95 ^a ±31.03	3.65 ^b ±0.12	287.95 ^a ±31.03	3.27 ^a ±0.11

^awithin columns frequencies bearing the same superscripts differ significantly at $p<0.05$.

Table III. Contribution of different mixed effects to the pleiotropic variation in daily milk yield and composition as referred to *K-Cas* or *PRL-Rsa I* genotype. (Contribución de diferentes efectos mezclados a la variación pleiotrópica en la producción diaria y composición de la leche, en relación con el genotipo *K-Cas* o *PRL-Rsa I*).

Source	Milk (kg)	Fat (%)	Protein (%)
K-Cas	2.93	13.96	9.14
PRL-Rsa I	13.57	37.03	4.77
Sire	4.44	0.03	1.17
Age at calving	42.48	0.30	2.92
Number lactation	24.72	8.80	2.82
Year lactation	0.81	28.50	46.21
Live weight	1.06	3.79	21.01
Weight at calving	9.99	7.59	11.96

content (+0.05 % and +0.13%, respectively) than AA and BB individuals. For milk protein yield the cows with the BB genotypes produced more milk protein (by 51.49 kg and 62.28 kg, respectively) than AA and AB individuals and cows with AA genotype produced more milk protein (+10.79 kg) than cows with AB genotype. For milk protein content (%) no differences were found between the cows of different *PRL-Rsa I* genotypes.

The results shows that the highest milk and milk fat yield were obtained by cows with genotype *PRL-Rsa I* BB. The results presented here show that the *PRL-Rsa I* gene may be considered as a marker for dairy traits in cattle

According to Denisenko (2004), cheese production can be increased by 5 percent if milk is from cows of the BB genotype for k-casein, when compared with milk from AA animals. In the Holstein and Jersey breeds it has been shown that the *B* allele is

associated with higher protein content in milk (Denisenko, 2004), and it has been suggested that appropriate weights could be given to genotypic information and polygenic breeding value in order to improve selection response (Van Arendonk and Bovenhuis, 1996).

This allele has been shown to be favorably related to milk composition in dairy cattle breeds. Therefore, studies aimed at establishing this possible relationship are of crucial importance, as selection could be enhanced by the inclusion of genetic markers in selection decisions.

The percent contribution of different effects to the variation in daily milk yield and composition is shown in **table III**. The *K-cas* genotype contributed mostly to fat content and protein content in milk (at the level of 13.96 and 9.14%, respectively), the contribution of *PRL-Rsa I* genotype varied from 37.03% for fat content to 4.77% for protein content.

The results presented here allow arranging the contribution of all factors studied to the milk production traits in following order: For milk yield: age at calving > number lactation > weight at calving > *PRL-Rsa I* > sire > k-cas > live weight > year lactation.

For fat% *PRL-Rsa I* > year lactation > k-cas > number lactation > weight at calving > live weight > age at calving > sire.

For protein%: year lactation > live weight > weight at calving > k-cas > *PRL-Rsa I* > age at calving > number lactation > sire.

Thus, it may be concluded that k-cas and *PRL-Rsa I* genotypes, when used as genetic markers in selection programmes, may moderately, but significantly contribute to the improvement of milk production traits in cattle.

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