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Polymorphism of the *PGLYRP1* gene, the value of selected performance and functional traits, and causes of culling in Holstein-Friesian red-white cows

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Abstract: This research paper addresses the hypothesis that the peptidoglycan recognition protein 1 (*PGLYRP1*) gene polymorphism (Tyr76His; dbSNP ID: *ss104796364*) has an influence on some performance traits and causes of culling in Polish Holstein-Friesian red-white cows. The study involved 134 cows kept on a farm in the south-west of Poland. *PGLYRP1* genotypes *TT*, *CT,* and *CC* were detected. It was shown that compared with cows with genotypes *CT* and *TT*, the individuals with genotype *CC* were characterised by higher lifetime yields and higher amounts of lactation milk, fat, and protein. A beneficial effect of genotype *CC*, compared with genotype *TT*, was also noted in the case of the lifespan and, consequently, the length of the productive life and the average number of lactations. Diseases of the musculoskeletal system (genotypes *CC* and *TT*) and disorders of the reproductive system (genotype *CT*) were the most common causes of culling. An essential practical observation was the potentially higher susceptibility of cows with genotype *CC* to mastitis, which resulted in the necessity to cull over one-fifth of the animals in this group. Simultaneously, no cows in this group were culled due to low performance or metabolic, gastrointestinal, and respiratory diseases. Therefore, the *PGLYRP1* gene seems to be a promising potential herd health marker; however, to consider it the main gene, it is necessary to extend the investigations to include more individuals and other breeds of dairy cattle.

Keywords: dairy cattle; lactation; lifetime performance; length of production life

Breeding work focused on maximisation of milk production and an increase in the content of protein and fat in milk has negative consequences, e.g. reduced fertility and increased susceptibility of cows to bacterial diseases and infections, which are directly reflected in the economic value of the herd (Zemanova et al. 2022). This problem affects not only the most productive breeds and varieties

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(Holstein-Friesian) but also those characterised by lower performance parameters, e.g. Holstein-Friesian red-white cows. Currently, it is important to search for genes responsible for not only performance traits but also reproductive disorders (Guarini et al. 2019), length of productive life, and especially the health status in the herd (Hu et al. 2021). To improve the health of cows and thus extend their productive life, research is carried out to detect nucleotide substitutions (QTN) associated with functional traits (Yudin and Voevoda 2015) and to identify genes involved in immune response (Yashin et al. 2021).

Peptidoglycan recognition proteins (PGLYRPs) play a key role in innate immunity due to their ability to bind various pathogen-associated molecular patterns, including lipoteichoic acid, lipopolysaccharide, and peptidoglycans (Tydell et al. 2006). Peptidoglycan recognition protein 1 (PGLYRP1) was first identified in *Bombyx mori* hemolymph as a molecule with a strong affinity for peptidoglycan in Gram-positive bacteria (Yoshida et al. 1996). Genetic analyses have shown that genes coding for this protein constitute an evolutionarily highly conserved family present in both insect (Kurata 2014) and mammalian genomes (Dziarski 2004). Recent studies have shown that the Tag7 protein (PGLYRP1) can activate cells involved in anti-cancer activity (Sharapova et al. 2018) and can serve as a potential marker in the diagnosis of rheumatoid arthritis (Luo et al. 2019).

The *PGLYRP1* gene in cattle is located on chromosome 18 (BTA18) (https://www.ncbi.nlm.nih.gov/gene/282305). It contains three exons and encodes a protein composed of 190 amino acids. An analysis of the coding sequences and flanking regions of the *PGLYRP1* gene in different cattle breeds has revealed many single nucleotide polymorphisms (SNPs), two of which are non-synonymous (Seabury et al. 2010). A genome-wide association analysis of selected performance, reproductive, health, and body-type traits in Holstein-Friesian cows has demonstrated a strong relationship between the value of the analysed traits and the BTA18's *PGLYRP1-IGFL1* region (Cole et al. 2011). Similarly, Sablik et al. (2020) have reported a relationship between the *PGLYRP1* gene polymorphism and susceptibility to certain diseases in Holstein-Friesian black-white cows.

The aim of the study was to analyse the relationship between non-synonymous polymorphism in the *PGLYRP1* gene (g.254T>C) and selected performance and functional traits of Polish Holstein-Friesian red-white cows.

MATERIAL AND METHODS

A veterinarian took blood samples for genetic testing from animals during routine and mandatory testing for brucellosis and leukaemia in dairy cows. The procedure was carried out in strict compliance with the recommendations specified in Directive 63/2010/EU and the Journal of Laws of the Republic of Poland of 2015 on the protection of animals used for scientific or educational purposes. The other test procedures were conducted without the use of animals.

The study involved 134 Polish Holstein-Friesian red-white cows kept on a farm in south-western Poland. Descriptive statistics of the lifetime and lactation milk, protein, and fat yields, as well as the lifetime and lactation percentage of protein and fat in the milk of cows from the analysed herd, are shown in Table 1.

Experimental design

Blood was collected from the jugular vein into K_3EDTA-containing test tubes. DNA was isolated with the salting out method (Master-Pure™ DNA Purification Kit for Blood, Madison, WI, USA).

Table 1. Descriptive statistics of the lifetime and lactation milk, protein, and fat yields as well as lifetime and lactation percentage of protein and fat in the milk of cows from the analysed herd

Parameter	Mean	Median	SD	Min.	Max.	CV (%)
Lifetime yield						
Milk (kg)	40 419	37 097	20 016	1 941	127 318	49.52
Protein (kg)	1 388	1 289	679	61	4 261	48.90
Protein (%)	3.44	3.44	0.22	2.78	4.03	6.30
Fat (kg)	1 613	1 496	809	80	5 230	50.15
Fat (%)	4.00	4.01	0.50	2.77	5.49	12.44
Lactation yield						
Milk (kg)	9 435	9 611	2 126	1 941	13 823	22.54
Protein (kg)	320	325	70	61	470	21.84
Protein (%)	3.40	3.42	0.21	2.78	3.91	6.32
Fat (kg)	372	377	87	80	567	23.39
Fat (%)	3.96	3.96	0.50	2.71	5.49	12.50

CV = coefficient of variation; SD = standard deviation

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The identification of the 254T>C substitution in the *PGLYRP1* gene (Tyr76His; dbSNP ID: *ss104796364*) was carried out with the PCR-RFLP method. To this end, the *PGLYRP1* gene sequence (GenBank: EU746452.1) and the Primer3 program (http://bioinfo.ut.ee/primer3-0.4.0/) were used to design primers 5'-TGCAGCCAGAGGCTAAGA-3' and 5'-GGCTTCACCAGGCACTAGA-3' (Sablik et al. 2020). The PCR reactions were performed in a total volume of 15 µl containing ~50 ng of genomic DNA, 1.5 mM of $MgCl_2$, 0.2 mM of each dNTP, 15 pmol of each primer, and 0.3 units of *Taq* Polymerase (Thermo Fisher Scientific, Waltham, MA, USA). The 441-bp DNA fragments were amplified in TGradient and TPersonal thermal cyclers (Biometra, Göttingen, Germany) using the following thermal profile: 94 °C – 3 min, 94 °C – 30 s, 55 °C – 50 s, 72 °C – 30 s, 30 cycles, 72 °C – 7 minutes. For quantitative and qualitative evaluation, 5 µl of the PCR products were taken and separated on 1.5% agarose gel with ethidium bromide (buffer 1 × TAE, 30 min, 120 V). To genotype the T/C substitutions (*ss104796364*, Tyr76His), a PCR-RFLP test was developed, in which 10 µl of the amplification products were digested with three units of the restriction enzyme *Rsa*I (Thermo Fisher Scientific, Waltham, MA, USA). Next, the restriction fragments were separated on 2% agarose gel with the addition of ethidium bromide for 50 min at a voltage of 120 V.

Data on the production traits and handling of the cows were obtained from the AfiFarm (https://www.afimilk.com/) and Obora systems (http://www.obora-system.pl/) used for recording the breeding documentation and herd management. The following data on each cow were collected: the length of animal life and productive life (number of days from birth and the first lactation to the day of culling, respectively), the number of lactations, the average length of a single lactation (days), the total number of milking days (number of milking days in all lactations), the lactation and lifetime yields of milk, fat, and protein (kg), and the percentage contents of fat and protein. The causes of culling and the health history of the animals were determined based on veterinary documentation recorded and stored in the AfiFarm system.

Statistical analysis

The statistical analysis was performed using the STATISTICA v7.1 statistical package (StatSoft Inc., Tulsa, OK, USA). The normality of the distribution was verified with the Shapiro-Wilk test, and one-way analysis of variance (ANOVA) was employed to analyse normally distributed data (milk yield and composition, lifespan, length of productive life, number of lactations, and number of milking days). The ANOVA model had the following form:

$$y_{ij} = \mu + \alpha_i + e_{ij} \quad (1)$$

where:

y_{ij} – yield of the j-th cow from the i-th genotype group, i-th genotype group, $i = 1, 2, 3$; $j = 1, 2, \ldots, n_i$ and n_i is the size of the group determined by the i-th genotype;

μ – overall mean of the considered yield;

α_i – effect of the i-th genotype group and $i = 1, 2, 3$;

e_{ij} – vector of specific effects for the j-th cow from the i-th genotype group, $i = 1, 2, 3$; $j = 1, 2, \ldots, n_i$ and n_i is the size of the group determined by the i-th genotype.

The significance of the genotype effect on each analysed trait was tested with Duncan's test for normally distributed data. In turn, the chi-square test with the Yates correction was used for the qualitative traits (causes of culling, incidence of disease). The results are presented as the mean ± standard deviation (SD).

RESULTS

Three genotypes were detected in the analysed polymorphism: *TT* (332 and 109 bp; Tyr/Tyr), *CT* (441, 332, and 109 bp; Tyr/His), and *CC* (441 bp; His/His), with a frequency of 0.51, 0.36, and 0.13, respectively. The chi-square test revealed that the analysed population was in the Hardy-Weinberg equilibrium ($P = 0.088$).

The mean number of lactations ranged from 3.68 (genotype *TT*) to 4.11 (genotype *CC*), which was correlated with the average duration of the productive life of the animals, i.e. from 1 380 to 1 574 days, respectively ($P < 0.05$). There were also statistically significant differences in the total number of milking days between cows with the different *PGLYRP1* genotypes (Table 2).

Cows with genotype *CC* lived, on average, 197 days longer than those with genotype *TT* (Table 3), and these differences turned out to be statistically significant ($P \leq 0.05$). These animals

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Table 2. Length of productive life of Polish Holstein-Friesian red-white cows in relation to the *PGLYRP1* genotype

PGLYRP1 genotype	*n*	Length of productive life (days)	Number of lactations	Total number of milking days
CC	18	1 574^{a} ± 574	4.11^{a} ± 1.56	1 318^{c} ± 444
CT	48	1 451^{ab} ± 611	3.77^{ab} ± 1.46	1 191^{b} ± 494
TT	68	1 380^{b} ± 667	3.68^{b} ± 1.52	1 125^{a} ± 532

$^{a–c}$Means in the columns marked with different letters differ statistically significantly ($P \leq 0.05$)

were also characterised by a higher mean lifetime yield of milk, fat, and protein than the cows with genotypes *CT* and *TT* and a higher percentage of fat than those with genotype *TT* ($P < 0.05$).

We also found that, despite the similar average length of lactation (262–272 days), the *CC* homozygotes produced, on average 9 981 kg of milk per lactation, i.e. by 710 and 574 kg higher amounts than the individuals with genotypes *CT* and *TT*, respectively ($P < 0.05$). A positive and statistically significant effect of the *CC* system was noted in the case of the lactation yields of protein and fat (Table 4).

The results of the present study indicate a significant correlation between the genotype and the percentage of cows culled in subsequent lactations (Table 5). In comparison with the other genotypes, *CC* was found to be responsible for the increased percentage of cows left in the herd during subsequent lactations. Between the third and fifth lactations, the percentage of cows remaining in the herd was clearly higher in this group than those with *CT* and *TT* genotypes. In the latter two groups, which were substantially larger than the *CC* group, there was no simple correlation between the genotype and the survivability of the cows in the herd. It was found that the culling percentage was lower in the second and third lactations in the group of cows with genotype *CT* and in the first and fourth lactations in the case of the *TT* cows. The proportion of culled cows in the subsequent lactations was similar in both groups.

The study showed that the cows were mainly culled due to musculoskeletal system diseases, infertility, reproductive disorders, and udder diseases, which accounted for nearly 70% of the causes of culling in each of the genetic groups (Table 6). Due to infertility and reproductive system diseases, cows with genotype *CT* were culled more frequently than the *CC* and *TT* animals (33.3, 22.2, and 22.1%, respectively). In turn, the *CC* individuals were more susceptible to musculoskeletal system diseases and udder inflammations. It was observed that only cows with genotypes *CT* and *TT* were culled due to low yields, metabolic and gastrointestinal disorders, and respiratory diseases (in total 16.6% and 17.6%, respectively). Noteworthy,

Table 3. Length of lifespan and lifetime productivity of Polish Holstein-Friesian red-white cows in relation to the *PGLYRP1* genotype

PGLYRP1 genotype	*n*	Lifespan		Lifetime yields (kg)			Lifetime content (%)	
		days	years	milk	fat	protein	fat	protein
CC	18	2 372^{a} ± 580	6.50^{a} ± 1.59	45 227^{a} ± 15 431	1 879^{a} ± 706	1 574^{a} ± 580	4.11^{a} ± 0.59	3.45 ± 0.28
CT	48	2 265^{ab} ± 598	6.21^{ab} ± 1.64	40 607^{b} ± 19 801	1 612^{b} ± 776	1 383^{b} ± 658	4.01^{ab} ± 0.42	3.43 ± 0.23
TT	68	2 175^{b} ± 669	5.96^{b} ± 1.83	39 014^{b} ± 20 873	1 544^{b} ± 835	1 342^{b} ± 703	3.97^{b} ± 0.51	3.45 ± 0.18

^{a,b}Means in the columns marked with different letters differ significantly ($P \leq 0.05$)

Table 4. Length of lactation and lactation yields of Polish Holstein-Friesian red-white in relation to the *PGLYRP1* genotype

PGLYRP1 genotype	*n*	Length of lactation (days)	Mean per lactation				
			kg of milk	kg of fat	kg of protein	% of fat	% of protein
CC	18	272 ± 27	9 981^{a} ± 1201	400.8^{a} ± 58.9	337.2^{a} ± 45.6	4.04 ± 0.55	3.38 ± 0.25
CT	48	262 ± 43	9 271^{b} ± 2507	363.8^{b} ± 96.9	312.7^{b} ± 81.7	3.96 ± 0.43	3.38 ± 0.23
TT	68	265 ± 39	9 407^{b} ± 1980	369.5^{b} ± 83.5	320.6^{ab} ± 64.5	3.95 ± 0.52	3.42 ± 0.19

^{a,b}Means in the columns marked with different letters differ statistically significantly ($P \leq 0.05$)

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Table 5. Culling of Polish Holstein-Friesian red-white cows in subsequent lactations in relation to the *PGLYRP1* genotype

Number of lactation	*CC*			*CT*			*TT*		
	n	P1	P2	*n*	P1	P2	*n*	P1	P2
1	1	5.5	94.5	3	6.2	93.8	2	2.9	97.1
2	3	16.7	77.8	6	12.5	81.3	14	20.6	76.5
3	2	11.1	66.7	12	25.0	56.3	21	30.9	45.6
4	3	16.7	50.0	13	27.1	29.2	11	16.2	29.4
5	5	27.8	22.2	8	16.8	12.4	11	16.2	13.2
6	4	22.2	0	4	8.3	4.1	6	8.8	4.4
7	–	–	–	2	4.1	–	2	2.9	1.5
8	–	–	–	–	–	–	1	1.5	–
Total	18	100.0	–	48	100.0	–	68	100.0	–

% distribution: chi-square = 36.78; *P*-value = 0.000 7; Yates chi-square = 27.84; Yates *P*-value = 0.014 9; *n* distribution: chi-square = 11.40; *P*-value = 0.654 2; Yates chi-square = 6.83; Yates *P*-value = 0.941 1

P1 = % of culled cows per lactation; P2 = % of cows left in the herd

Table 6. Percentage of culled cows in relation to *PGLYRP1* genotype and causes of culling

Causes of culling	*CC*			*CT*			*TT*			Total	
	n	P1	P2	*n*	P1	P2	*n*	P1	P2	*n*	P3
Musculoskeletal diseases	7	38.9	18.8	10	20.8	27.0	20	29.5	54.2	37	27.6
Infertility, reproductive system disorders	4	22.2	11.4	16	33.3	45.7	15	22.1	42.9	35	26.1
Udder diseases	4	22.2	19.1	6	12.6	28.6	11	16.2	52.3	21	15.7
Old age	2	11.1	28.6	2	4.2	28.6	3	4.4	42.8	7	5.2
Low yields	–	–	–	3	6.2	60.0	2	3.0	40.0	5	3.7
Random causes	–	–	–	3	6.2	37.5	5	7.3	62.5	8	6.0
Metabolic and gastrointestinal diseases	–	–	–	4	8.3	44.4	5	7.3	55.6	9	6.7
Respiratory diseases	–	–	–	1	2.1	16.7	5	7.3	83.3	6	4.5
Sale for further rearing	–	–	–	1	2.1	100.0	–	–	–	1	0.8
Other	1	5.6	20.0	2	4.2	40.0	2	2.9	40.0	5	3.7
Total	18	100.0	–	48	100.0	–	68	100.0	–	134	100.0

% distribution: chi-square = 51.64; *P*-value = 0.000 1; Yates chi-square = 37.32; Yates *P*-value = 0.004 7; *n* distribution: chi-square = 14.97; *P*-value = 0.696 2; Yates chi-square = 6.025; Yates *P*-value = 0.996

P1 = % of sick cows within the genotype; P2 = % of sick cows within the cause of culling in relation to the cause of culling; P3 = % of sick cows in the entire herd in relation to the cause of culling

a greater percentage of *CC* cows (11.1%) than individuals with the other two genotypes (4.2 and 4.4%, respectively) were culled due to old age.

DISCUSSION

The present study is the first to analyse the lifespan and lifetime productivity of Polish Holstein-Friesian red-white cows considering the *PGLYRP1*/*Rsa*I genotypes; therefore, comparing these findings with results reported by other authors is difficult. Nevertheless, Gopi et al. (2022) studied the relationship between the polymorphism of two SNPs (*rs68268263* and *rs110217377*) in the *PGLYRP1* gene in an Indian cattle population and the susceptibility of the host to *Mycobacterium avium* ssp. *Paratuberculosis* (MAP) infection. This bacterium causes incurable, chronic, granulomatous inflammatory disease in ruminants not only resulting in significant economic losses but also shortening the lifespan of cows. Although the statistical analysis did not show significant relationships between the polymorphism of the analysed SNPs and the

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risk of paratuberculosis (PTB) in cattle, the presence of the *C* allele in *rs68268263* SNP and the *G* allele in *rs110217377* SNP was associated with a lower risk of PTB. On the other hand, Pant et al. (2011) identified three SNPs within the *PGLYRP1* gene (c.102G>C, c.480G>A and c625C>A) and found that SNP c.480G>A in exon 3 was marginally (P = 0.054) associated with susceptibility to MAP infection. Cows with the *G* allele in the analysed locus were 1.5 times more likely to be infected than cows with the *A* allele. More recently, Okuni et al. (2021) analysed exactly the same SNPs within the *PGLYRP1* gene in Ankole Longhorn cattle; however, they did not show any significant differences between seropositive and seronegative individuals, which indicates an ambiguous impact of the analysed gene on resistance to MAP disease, and thus a relationship with the lifespan of cows.

An increase in the lifetime yield of cows is accompanied by a shortening of their lifespan and an increase in the percentage of early cow culling. This is confirmed by findings presented by other authors (Brickell and Wathes 2011; Litwinczuk et al. 2016; De Vries and Marcondes 2020), who demonstrate that the actual length of cow productive life has been shorter than the natural lifespan in recent years. Brickell and Wathes (2011) demonstrated that 43% of cows were culled before the third calving, and Horvath et al. (2017) showed that as many as 26% of cows were culled during the first lactation. The productive life of cows in the herd should span from five to eight lactations, which indicates that the cows from the analysed herd were culled too early, as the average number of lactations ranged from 3.78 to 4.31 (in the animals with genotypes *TT* and *CC*, respectively). This, however, may have been associated with their high lifetime milk yield, which was approximately 20 000 kg higher than the national average value.

The intensity and causes of culling are determined by many random factors and intentional measures undertaken by humans. The results of studies carried out in Poland indicate that infertility and reproductive disorders, which are directly related to high milk yields, are one of the main causes of culling cows in the herd (Pokorska et al. 2012). This was confirmed in the present study, where reproductive system disorders, besides musculoskeletal diseases (26.1% and 27.6%, respectively), were the most common causes of cow culling. Noteworthy, infertility and reproductive system diseases accounted for one-third of all cases of culling in the group of heterozygous *CT* cows. The alcove-keeping system, which is becoming increasingly divergent from natural conditions, results in problems with limbs in approximately 30–70% of animals in herds, which consequently leads to the elimination of animals from production (Randall et al. 2016). In the analysed herd, cows with genotype *CC* were the most susceptible to this type of problem, which was the cause of culling in 38.9% of cases. The percentage of culling in the group of cows with genotype *CT* was nearly 20% lower. The only investigations of the relationship between the causes of cow culling and the *PGLYRP1* genotypes were conducted by Sablik et al. (2020) in a herd of Polish Holstein-Friesian black-white cows. They showed that the highest percentage of culled cows had genotype *CT*, while the lowest culling rate was noted in a group of cows with genotype *CC*. It should be emphasised, however, that both in the present study and in the investigations mentioned above, genotype *CC* was detected at the lowest frequency, i.e. 0.13 and 0.09, respectively.

As Horvath et al. (2017) demonstrated, the duration of lactation may determine the frequency of culling, as an increase in its length is accompanied by an increase in the percentage of cows culled due to reproductive disorders. The present study has shown no statistically significant differences in the duration of lactation, which ranged from 262 (genotype *CT*) to 272 (genotype *CC*) days. However, it was found that the homozygous *CC* individuals were characterised by the highest average milk yield per lactation, with significant differences ($P \leq 0.05$) from the yields of cows with the other genotypes. This is in agreement with the results obtained by Sablik et al. (2020) in a study of milk yields from first-lactation cows with different *PGLYRP1* genotypes.

A consequence of selection aimed at improving performance traits, especially milk yield, is the reduction of the resistance of the mammary gland to inflammation (Bludau et al. 2014), which may lead to cow culling (Gussmann et al. 2019). This is confirmed by the results of the present study suggesting that cows with genotype *CC* may be the most susceptible to udder inflammation, as this was the cause of the culling of nearly one-fifth of the animals in this group. The relationships between other polymorphisms in the *PGLYRP1* gene and the suscep-

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tibility of cows to mastitis were analysed by Wang et al. (2013) and Shivashanker et al. (2018). The results of their studies were inconclusive, i.e. Wang et al. (2013) showed that genotype *GG* was associated with a higher number of somatic cells. In contrast, Shivashanker et al. (2018) found a significant correlation between genotype *GG* and lower susceptibility to mastitis. More recently, Zabolewicz et al. (2022) examined the relationship between polymorphism in the *PGLYRP1* gene and the number of somatic cells in milk in Holstein cows and found a significantly lower number of somatic cells in cows with genotype *TT* within the *rs68268284* SNP than in cows with genotypes *CC* and *CT*.

For many years, researchers have attempted to find tools to improve the broad-sense health status of cows with maintenance of high milk yields, which is a prerequisite for the profitability of dairy herds. Scientists expect to improve animal health through marker-assisted selection (MAS). The implementation of MAS for selection of animals with lower susceptibility to mastitis (Dusza et al. 2018) or reproductive disorders (Miglior et al. 2017) may help eliminate the undesirable effect of traditional selection leading to reduced genetic variability. Therefore, the choice of the *PGLYRP1* gene as a potential health marker in the herd seems relevant.

CONCLUSION

In conclusion, it should be emphasised that the relationships shown in the present study seem to be promising. It was found that *PGLYRP1* genotype *CC*, compared to *CT* and *TT*, was associated with higher values of the lifespan, productive lifetime, lactation milk yields, and lifetime milk yields and with a lower frequency of culling due to reduced fertility. An important practical observation is that cows with genotype *CC* were more susceptible to udder inflammation. Therefore, cows with genotype *CC* should be subjected to careful control and sanitary regimen during milking and multidirectional prevention of udder inflammation in the lactation and drying-off periods. In addition, they can serve as specific "bio-indicators" of irregularities in the herd mastitis prevention program.

Based on the results obtained in the analysis of one breed only, it is difficult to identify unequivocally a genetic variant that is the most favourable for the length of the productive life of cows and their milk production efficiency. Nevertheless, the present results should serve as an important preliminary step in more extensive research comprising a larger number of individuals and other dairy cattle breeds to assess the possibility of using the *PGLYRP1* gene as a marker of herd health and the length of productive life in dairy cattle.

Conflict of interest

The authors declare no conflict of interest.

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