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DEPENDENCIES BETWEEN *PIT-1* GENE POLYMORPHISM AND PRODUCTION PROGRESS IN POLISH HOLSTEIN-FRIESIAN BLACK-AND-WHITE COWS

ZALEŻNOŚCI MIĘDZY POLIMORFIZMEM GENU *PIT-1* A POSTĘPEM PRODUKCYJNYM U KRÓW RASY POLSKIEJ HOLSZTYŃSKO-FRYZYJSKIEJ ODMIANY CZARNO-BIAŁEJ

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Streszczenie. Celem badań była analiza zależności pomiędzy polimorfizmem genu *PIT-1* w obrębie 6 eksonu pierwszego bydłowego chromosomu (*c.1178G>A*) a wielkością postępu produkcyjnego u krów rasy polskiej holsztyńsko-fryzyjskiej odmiany czarno-białej. Stwierdzono, że największym rocznym postępem produkcyjnym i postępem kumulowanym w wydajności mleka i tłuszczu charakteryzowały się homozygoty AA. W przypadku wydajności białka w mleku korzystniejszymi wartościami obliczonych parametrów odznaczały się homozygoty GG.

Key words: cattle, polymorphism, *PIT-1*, production progress.

Słowa kluczowe: bydło, polimorfizm, *PIT-1*, postęp produkcyjny.

INTRODUCTION

Pituitary transcription factor *PIT-1* (POU1F1) plays a significant role in developmental processes as an activator of the growth hormone gene [GH] (Bodner et al. 1988), the growth hormone releasing hormone receptor [GHRH-R] (Rhodes et al. 1993), prolactin [*PRL*] (Nelson et al. 1988) and the thyroid-stimulating hormone [*TSH*β] (Lin et al. 1994; Augustijn et al. 2002). In view of the multifaceted action of its product this gene has been selected as a candidate gene for studies on the relationships with numerous production traits, e.g. growth, slaughter performance traits and milk yield (Stancekova et al. 1999). Georges et al. (1995) and Woolard et al. (2000) reported that the POU1F1 locus on chromosome 1 (1q21-22) affects production traits in dairy cattle.

Results of studies conducted by various authors concerning dependencies between genetic variants of *locus c.1178G>A* and production traits were inconclusive. Most probably it does not result from a lack of effect of this polymorphism on the function of the gene. For this

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reason analyses presented in this paper may provide novel information on the relationship between genotypes at *locus c.1178G>A* and production progress in Polish Holstein-Friesian Black-and-White cows. It is most advantageous to obtain considerable production progress within a short period of time with no deterioration of functional traits in cows and no increase in financial outlays on milk production. Atashi et al. (2006) suggested that it is possible to simultaneously improve lactation persistency and milk yield. Finding a respective genetic marker to reach this breeding objective within a short time would be highly advantageous for dairy cattle breeders and milk producers.

Literature sources lack results concerning a relationship between genetic variants at *locus c.1178G>A* and the level of production progress in Polish Holstein-Friesian Black-and-White cows. In view of the practical aspect of this problem and a lack of studies on the subject it was decided to undertake research to realise the proposed objective.

The aim of this study was to analyse the dependence between polymorphism of the *PIT-1* gene within exon 6 of bovine chromosome 1 and the level of production progress in Polish Holstein-Friesian Black-and-White cows.

MATERIAL AND METHODS

Analyses were conducted on 1099 Polish Holstein-Friesian Black-and-White cows (PHF). Cows were kept on six farms in the Wielkopolska region (Poland).

The study comprised the analysis of the polymorphic site (*c.1178G>A*) in gene *PIT-1* located at chromosome 1 in exon 6 (G→A mutation).

Analyses were conducted using PCR-RFLP.

The experiment consisted of the following stages:

- a) isolation of genetic material – DNA (from peripheral blood) using phenol extraction;
- b) amplification of a DNA fragment (451 bp) – conducted using a TGradient thermocycler (Biometra). Primer sequences provided by Woollard et al. (1994) were applied: Pit-1E6F-(5'-AAACCATCATCTCCCTTCTT-3'), Pit-1E6R-(5'-AATGTACAATGTCCTTCTGAG-3'). The reaction mixture of 15 µl contained 100 ng genomic DNA, 0.6 U *Taq* polymerase, 10 pmol of each primer, 1.5 mM MgCl₂, 200 µM dNTP, 1.5 µl PCR buffer – (NH₄)₂SO₄ (10x) and 0.75 µl DMSO. Preliminary denaturation (97°C/300 sec) was followed by 30 cycles of denaturation (95°C/30 sec), primer annealing (51°C/30 sec) and synthesis (72°C/40 sec), completed with final synthesis (72°C/300 sec);
- c) digestion of PCR products using the restriction enzyme. Amplification products were digested at 37°C for 3 h using the restriction enzyme (*Hinf*I) and R buffer. The composition of the reaction mixture (11 µl) for one sample was as follows: 5 µl PCR product, 1 µl restriction enzyme at 10 U/µl (Fermentas), 1 µl enzymatic buffer (Fermentas) and 4 µl H₂O;
- d) verification of digestion products by agarose gel electrophoresis. Following digestion with restriction enzymes each sample was supplemented with 2 µl loading buffer (Gel Loading Solution type I) 6x. Afterwards digestion products were verified by electrophoresis in 3% agarose gel (BASICA GQT, Prona) in 1 x TBE buffer. The DNA Gene Ruler™ marker was used in the DNA Ladder Mix composed of 2 µl loading buffer, 1.5 µl DNA marker and 10.5 µl H₂O. The following settings were applied: electrophoresis time of 30 min and electric current of 140V. Digestion products were observed in UV light;

- e) genotype identification. The amplified fragment of the *PIT-1* gene was 451 bp in length. The following genotypes were identified: homozygote AA (-,-) – 451 bp (no site identified by the *HinfI* restriction enzyme), heterozygote AG (-,+) – fragments of 451, 244 and 207 bp, and heterozygote GG (+,+) – fragments of 244 and 207 bp;
- f) statistical analysis. Results of laboratory analyses were subjected to the Hardy-Weinberg theorem. The χ^2 test was applied in statistical calculations. The frequency of alleles A and G at *locus c.1178G>A* was 0.1965 and 0.8035, respectively. In turn, the observed genotype frequency was: AA – 0.0446, AG – 0.3039 and GG – 0.6515. The applied χ^2 test showed genetic equilibrium in the analysed population of cows.

Cows came from herds with average milk yields in 305-day lactation ranging from 5000 to 8000 kg milk. The animals were in their 1st to 10th lactation. Data on 3365 305-day lactations were collected from milk recording documentation from the period of 2002–2009. The shares of successive lactations in their total number were as follows: 1 – 28.4%, 2 – 25.5%, 3 – 20.1%, 4 – 13.4%, 5 – 7.0%, 6 – 3.3%, 7 – 1.5%, 8 – 0.5%, 9 – 0.2% and 10 – 0.1%, respectively. Milk yield and yields of milk fat and protein were recorded for each cow.

In this study annual production progress was calculated for the period of 2002–2009 along with cumulative progress for milk yield and yields of fat and protein for the entire analysed cattle population and in terms of division into genotypes at *locus c.1178G>A*.

Statistical analyses were performed using the following linear model:

$$Y_{ijklmnop} = \mu + H_i + R_j + S_k + L_l + G_m + \beta_1 hfn + \beta_2 wco + e_{ijklmnop}$$

where:

$Y_{ijklmnop}$ – phenotypic value of analysed trait,

μ – population mean,

H_i – fixed effect of herd ($i = 1, \dots, 6$),

R_j – fixed effect of year of calving ($j = 1, \dots, 8$),

S_k – fixed effect of season of calving ($k = 1, \dots, 4$),

L_l – fixed effect of lactation rank ($L = 1, \dots, 10$),

G_m – fixed effect of cow's genotype at *locus c.1178G>A* ($l = 1, \dots, 3$),

β_1, β_2 – partial first-order linear regression coefficients:

hfn – share of HF genes in the genotype,

wco – age at first calving in days,

$e_{ijklmnop}$ – random residual effect.

Statistical calculations were performed using the SAS® statistical package (2011) with the MEANS and GLM procedures.

The Duncan multiple range test was applied to compare object means.

RESULTS

Table 1 presents calculated values of annual production progress and cumulative progress for milk yields in the years 2002–2009 for the entire population of cows and in terms of division into genotypes at *locus c.1178G>A*.

Table 1. Production progress for milk yield [kg] in the years 2002–2009 in the whole studied population of Holstein-Friesian Black-and-White cows^a and with regard to genotyping in *locus c.1178G>A*

Tabela 1. Postęp produkcyjny dla wydajności mleka [kg] w latach 2002–2009 w całej badanej populacji krów rasy polskiej holsztyńsko-fryzyjskiej odmiany czarno-białej^a, z uwzględnieniem podziału na genotypy w *locus c.1178G>A*

Year Rok **	Analysed population Badana populacja					Genotype – in <i>locus c.1178G>A</i> – Genotyp w <i>locus c.1178G>A</i>														
						AA **					AG **					GG **				
						\bar{x}	x_i-x_{i-1}	%	x_i-x_0	%	\bar{x}	x_i-x_{i-1}	%	x_i-x_0	%	\bar{x}	x_i-x_{i-1}	%	x_i-x_0	%
2002	5795.0	A		ABCD EFG		5531.9	A		ABCD EFG		5843.8			ABC DEF		5794.7	A		ABCD EFG	
2003	6105.4	310.4 AB	105.4	310.4 A	105.4	6086.0	554.1 A	110.0	554.1 A	110.0	5954.4	110.7 a	101.9	110.7 101.9	101.9	6168.8	374.1 AB	106.5	374.1 A	106.5
2004	6534.1	428.7 BC	107.0	739.1 B	101.3	6619.8	533.8 B	108.8	1087.9 B	119.7	6421.5	467.1 a	107.8	577.7 A	109.9	6577.4	408.7 BC	106.6	782.8 B	113.5
2005	7058.0	523.9 C	108.0	1263.0 C	121.8	6945.8	326.0 B	104.9	1413.9 C	125.6	6827.3	405.8	106.3	983.5 B	116.8	7167.3	589.8 C	109.0	1372.6 C	123.7
2006	7141.1	83.1 D	101.2	1346.1 D	123.2	7258.0	312.2 C	104.5	1726.1 D	131.2	7122.6	295.3 A	104.3	1278.8 C	121.9	7143.0	-24.3 D	99.7	1348.3 D	123.3
2007	7607.1	466.0 DE	106.5	1812.1 E	131.3	7180.5 ab	-77.5 CD	98.9	1648.6 E	129.8	7689.5 a	567.0 A	108.0	1845.7 D	131.6	7589.1 b	446.2 DE	106.2	1794.5 E	131.0
2008	8125.2	518.1 E	106.8	2330.2 F	140.2	7649.2 AB	468.7 DE	106.5	2117.3 F	138.3	8076.5 A	387.0	105.0	2232.7 E	138.2	8192.7 B	603.6 E	108.0	2398.0 F	141.4
2009	8230.0	104.8	101.3	2435.0 G	142.0	8158.2	509.0 E	106.7	2626.3 G	147.5	8339.1	262.6	103.3	2495.3 F	142.7	8186.4	-6.3	99.9	2391.8 G	141.3
\bar{x}		347.9					375.2					356.5				341.7				

x_i-x_{i-1} – annual production progress – roczny postęp produkcyjny; x_i-x_0 – production progress in relation to the initial year (cumulative production progress) – postęp produkcyjny w stosunku do roku początkowego (kumulowany postęp produkcyjny); ** statistically significant effect at $P \leq 0.01$ – wpływ statystycznie istotny przy $P \leq 0.01$. Means marked with the same letters are statistically different – Średnie oznaczone tymi samymi literami różnią się statystycznie: A, B, C – at $P \leq 0.01$ – przy $P \leq 0.01$; a, b, c – at $P \leq 0.05$ – przy $P \leq 0.05$; with x_i-x_{i-1} differences between years are marked – przy x_i-x_{i-1} oznaczono różnice między latami; for x_i-x_0 , differences are indicated in relation to the initial year within the group – przy x_i-x_0 oznaczono różnice w stosunku do roku początkowego w obrębie grupy; mean differences between individual genotypes in *locus c.1178G>A* were determined – przy średnich oznaczono różnice między poszczególnymi genotypami w *locus c.1178G>A*.

^a until 2005 the Black-and-White name was used – do 2005 roku obowiązywała nazwa: czarno-biała.

Statistical analysis showed that the genetic variant of the polymorphic site and the year of analysis had a highly significant effect on the investigated traits. It was shown that for the entire population of cows milk yields were increasing year by year, while in the period of analysis average production progress and cumulative progress amounted to 347.9 kg and 2435.0 kg milk, respectively. The greatest annual production progress (523.9 kg) was recorded in 2005, when it was 108% yield from the previous year. Considering the analysed parameters in cows with the identified genetic variant at *locus c.1178G>A*, the greatest average annual production progress for milk yield (375.2 kg) was found for the AA homozygotes, whereas it was lowest (341.7 kg) for cows with the GG genotype. The greatest annual production progress of 589.8 kg milk was recorded in 2005 for the GG homozygotes. In turn, the AG heterozygotes had annual progress for that trait ranging from 101.9 to 108 %. Analysis of the level of the cumulative progress over the period of 2002–2009 for milk yield in cows varying in their genotypes in the investigated polymorphic site showed its greatest value amounting to 2626.3 kg milk in the AA homozygotes, followed by the AG heterozygotes (2495.3 kg) and the GG homozygotes (2391.8 kg). When investigating average milk yields of cows over the period of the study statistically significant differences were observed in 2007 and 2008 between the genotypes for the discussed parameter. The AA homozygotes were characterised by the lowest milk yields and differed from the other genotypes at the significance levels $P \leq 0.01$ and $P \leq 0.05$ in 2008 and 2007, respectively.

Table 2 presents results of the calculated production progress for the yield of fat in the years of 2002–2009 for the entire population of Polish Holstein-Friesian Black-and-White cows and in terms of division into genotypes at *locus c.1178G>A*. Statistical analysis showed a significant effect (at $P \leq 0.01$) of genetic variants at *locus c.1178G>A* and the year of the study on the investigated traits. In the period of analysis in the entire cattle population the average production progress for the yield of milk fat was 13.3 kg, while over several years the greatest value of this parameter (29.1 kg) was recorded for cows in 2007. Considering cumulative progress in 2009 production of this milk component increased by 38.8 % in relation to 2002. In terms of the division of cows into genotypes at *locus c.1178G>A* the greatest value (14.7 kg) of production progress for the yield of milk fat in the discussed period was found for cows with the AA genotype, followed by the GG (13.7 kg) and the AG genotype (12.1 kg). Only in 2004 and 2005 statistically significant differences were observed between the genotypes in terms of the yield of milk fat. In that period cows with the GG genotype were characterised by significantly higher production of milk fat in comparison to the AA homozygotes (at $P \leq 0.01$) and the AG heterozygotes (at $P \leq 0.05$). Moreover, in 2005 for that milking performance trait cows with the AG genetic variant differed ($P \leq 0.01$) from the AA homozygotes. When analysing cumulative production progress for the yield of fat its highest value (102.9 kg) in 2009 was recorded for the AA homozygotes, while it was lowest for the AG heterozygotes (85 kg), with the increase in milk fat production in relation to 2002 by 44.8% and 34.7%, respectively.

Statistical analysis showed the effect of genetic variants at *locus c.1178G>A* and the year of analysis on annual and cumulative production progress in the yield of milk protein (Table 3). For the entire population the average annual value of production progress for the production of milk protein was 11.2 kg and the calculated cumulative progress was 78.3 kg protein.

Table 2. Production progress for fat yield [kg] in the years 2002–2009 in the whole studied population of Holstein-Friesian Black-and-White cows^a and with regard to genotyping in *locus c.1178G>A*

Tabela 2. Postęp produkcyjny dla wydajności tłuszczu [kg] w latach 2002–2009 w całej badanej populacji krów rasy polskiej holsztyńsko-fryzyskiej odmiany czarno-białej^a, z uwzględnieniem podziału na genotypy w *locus c.1178G>A*

Year Rok **	Analysed population Badana populacja					Genotype – in <i>locus c.1178G>A</i> – Genotyp w <i>locus c.1178G>A</i>														
	\bar{x}	x_i-x_{i-1}	%	x_i-x_0	%	\bar{x}	x_i-x_{i-1}	AA **	x_i-x_0	%	\bar{x}	x_i-x_{i-1}	AG **	x_i-x_0	%	\bar{x}	x_i-x_{i-1}	GG **	x_i-x_0	%
2002	240.9	A		ABCD EFG		229.5 a			ABC Dab		245.3 a			ABC DEF		240.2	A		ABCD EFG	
2003	252.7	11.8 AB	104.9	11.8 A	104.9	244.5	15.0	106.5	15.0	106.5	244.8	-0.5 A	99.8	-0.5	99.8	256.4	16.2 AB	106.7	16.2 A	106.7
2004	272.3	19.6 BC	107.8	31.4 B	113.0	261.9 A	17.4 A	107.1	32.4 a	114.1	263.8 a	19.0 A	107.8	18.5 A	107.5	276.9 Aa	20.5 Ba	108.0	36.7 B	115.3
2005	280.5	8.2 C	108.0	39.6 C	116.4	257.5 AB	-4.4 AB	98.3	28.0 b	112.2	272.9 Ba	9.1	103.4	27.6 B	111.3	285.5 Aa	8.6 a	103.1	45.3 C	118.6
2006	282.9	2.4 D	103.0	42.0 D	117.4	283.6	26.1 B	110.1	54.1 A	123.6	279.3	6.4 B	102.3	34.0 C	113.9	284.7	-0.8 C	99.7	44.5 D	118.5
2007	312.0	29.1 DE	110.3	71.1 E	129.5	304.1	20.5	107.2	74.6 B	132.5	307.8	28.5 BC	110.2	62.5 D	125.5	314.4	29.7 CD	110.4	74.2 E	130.9
2008	329.3	17.3 E	105.5	88.4 F	136.7	326.7	22.6 C	107.4	97.2 C	142.3	323.0	15.2 C	104.9	77.7 E	131.7	332.6	18.2 D	105.8	92.4 F	138.5
2009	334.3	5.0	101.5	93.4 G	138.8	332.4	5.7 C	101.7	102.9 D	144.8	330.3	7.3	102.3	85.0 F	134.7	336.2	3.6	101.1	96.0 G	140.0
\bar{x}		13.3					14.7					12.1					13.7			

Explanations see Table 1 – Objaśnienia zob. tab. 1.

Table 3. Production progress for protein yield [kg] in the years 2002–2009 in the whole studied population of Holstein-Friesian Black-and-White cows^a and with regard to genotyping in *locus c.1178G>A*

Tabela 3. Postęp produkcyjny dla wydajności białka [kg] w latach 2002–2009 w całej badanej populacji krów rasy polskiej holsztyńsko-fryzyjskiej odmiany czarno-białej^a, z uwzględnieniem podziału na genotypy w *locus c.1178G>A*

Year Rok **	Analysed population Badana populacja					Genotype – in <i>locus c.1178G>A</i> – Genotyp w <i>locus c.1178G>A</i>														
	\bar{x}	$x_i - x_{i-1}$	%	$x_i - x_0$	%	AA **					AG **					GG **				
						\bar{x}	$x_i - x_{i-1}$	%	$x_i - x_0$	%	\bar{x}	$x_i - x_{i-1}$	%	$x_i - x_0$	%	\bar{x}	$x_i - x_{i-1}$	%	$x_i - x_0$	%
2002	193.0	A		ABCD EFG		185.9 Aa	A		ABC DEFG		195.2 A			ABC DEF		192.7 a	A		ABC DEF G	
2003	203.5	10.5 AB	105.4	10.5 A	105.4	199.8 a	13.9 AB	107.5	13.9 A	107.5	198.2 b	3.0 A	101.5	3.0	101.5	205.9 ab	13.2 AB	106.9	13.2 A	106.9
2004	223.6	20.6 BC	109.9	30.6 B	115.9	223.0	23.2 B	111.6	37.1 B	120.0	218.6 A	20.4 AB	110.3	23.4 A	112.0	225.9 A	20.0 BC	109.7	33.2 B	117.2
2005	237.1	13.4 C	106.0	44.1 C	122.8	227.5 A	4.5 C	102.0	41.6 C	122.4	231.1 B	12.5 BC	105.7	35.9 B	118.4	240.3 AB	14.4 C	106.4	47.6 C	124.7
2006	238.7	1.7 D	100.7	45.7 D	123.7	243.6 ab	16.1 C	107.1	57.7 D	131.0	238.0 a	6.9 CD	103.0	42.8 C	121.9	238.8 b	-1.5 D	99.4	46.1 D	123.9
2007	253.3	14.6 DE	106.1	60.3 E	131.2	242.5 Aa	-1.1 a	99.5	56.6 E	130.5	255.8 A	17.8 DE	107.5	60.6 D	131.0	252.6 a	13.8 DE	105.8	59.9 E	131.1
2008	268.5	15.2 E	106.0	75.5 F	139.1	251.9 AB	9.4 Da	103.9	66.0 F	135.5	267.6 A	11.8 E	104.6	72.4 E	137.1	270.4 B	17.8 E	107.0	77.7 F	140.3
2009	271.3	2.8	101.0	78.3 G	140.6	263.6	11.7 D	104.6	77.7 G	141.8	267.5	-0.1	99.9	72.3 F	137.0	273.5	3.1	101.1	80.8 G	141.9
\bar{x}		11.2					11.1					10.3					11.5			

Explanations see Table 1 – objaśnienia zob. tab. 1.

Analysis of annual production progress for the yield of milk protein in individual years showed its highest value irrespective of genotype in 2004. The percentage value of the yield of milk protein in relation to the previous year ranged from 109.7 for the GG homozygotes to 111.6 for the AA homozygotes. The greatest average annual production progress for this parameter (11.5 kg) was recorded for the GG homozygotes, while it was lowest (10.3 kg) in the AG heterozygotes. Cows with the AA, AG and GG genetic variants in the analysed period had cumulative production progress for the yield of milk protein amounting to 77.7 kg, 72.3 kg and 80.8 kg, respectively. In terms of the average yields of milk protein in individual years the greatest value of that trait was recorded for the GG homozygous cows. In turn, cows with the AA genotype at *locus c.1178G>A* had the lowest yield of milk protein (185.9 kg) in 2002, which most probably influenced the cumulative production progress in the investigated period.

DISCUSSION

The positive effect of the AA genetic variant on the yields of milk, milk fat and protein was reported by Parmentier et al. (2001). In turn, Renaville et al. (1997) recorded an advantageous dependence between the AA variant and the yield of milk and protein. Similar dependencies between the AA genotype at *locus c.1178G>A* and milk production were shown by Hori-Oshima and Barreas-Serrano (2004), Vargas et al. (2004) and Doosti et al. (2011). In contrast, opposite results were given by Oprządek et al. (2006), who reported the lowest milk yield in the 2nd lactations and the lowest yields of milk fat and protein in the 2nd and 3rd lactations for cows with the AA genotype.

A greater production progress and cumulative progress in the investigated period (except for production progress for milk yield in 2006 and 2009) were found for cows in this study in comparison to the active population. Yaeghoobi et al. (2011) showed that over a period of 10 years in primiparous Holstein cows the annual phenotypic trend for milk yield was 71.99 kg. In a study by Roman et al. (1999) conducted on Jersey cows it was found that annual changes in genetic progress for milk yield ranged from 36.8 to 41.0 kg/head. In turn, Neja et al. (2013) reported that in the period from 2001 to 2009 in Black-and-White cows and Polish Holstein-Friesian Black-and-White cows in Poland, covered by performance testing, the cumulative production progress for milk yield was 1423 kg. Results for analyses in the groups of animals varying in their genotype at *locus c.1178G>A* in comparison to the results published by KCHZ (2003, 2004, 2005) and PFHBiPM (2006, 2007, 2008, 2009, 2010) concerning the entire active population of cows in Poland and (apart from very few cases) showed in the cows included in this study greater milk yields as well as more advantageous annual and cumulative production progress in milk yields.

Analysis of results recorded in this study showed that a greater yield of milk fat, greater annual production progress (except for 2005 and 2009) as well as a more advantageous cumulative production progress in the investigated period for animals included in this study in comparison to the entire active population of cows in Poland, which productivity was presented in studies published by KCHZ (2003, 2004, 2005) and PFHBiPM (2006, 2007, 2008, 2009, 2010). In turn, Neja et al. (2013) reported that in the population of the investigated cattle breeds, i.e. Black-and-White and Polish Holstein-Friesian Black-and-White, in the

period of 2001–2009 cumulative production progress in the yield of milk fat was 57 kg. The value of this parameter in comparison to the results obtained in this study for the period of 2002–2009 was by 24.6 kg lower. A comparison of results for animals differing in their genotype at *locus c.1178G>A* to those for the entire active population of cows in the investigated period indicates that among the three genetic variants the least advantageous values of the analysed traits are found for the AG heterozygotes.

When comparing results calculated for the entire population of cows with those published by KCHZ (2003, 2004, 2005) and PFHBiPM (2006, 2007, 2008, 2009, 2010) for the entire active population in Poland we may state that for the animals analysed in this study for all the investigated traits higher values were recorded in 2006 (except for annual production progress in the yield of milk protein). In their study covering a 10-year period Yaeghoobi et al. (2011) stated in primiparous Holstein cows an annual phenotypic trend for the yield of milk protein of 1.4 kg. In turn, Neja et al. (2013) reported that in the active population of Black-and-White and Polish Holstein-Friesian cows in the period from 2001 to 2009 cumulative production progress for the yield of milk protein was 48 kg. A comparison of results for animals differing in their genotype at the analysed *locus* with those published by KCHZ (2003, 2004, 2005) and PFHBiPM (2006, 2007, 2008, 2009, 2010) for the entire Polish active population showed the most advantageous values of milk protein parameters for cows with the GG genotype.

CONCLUSION

Polish Holstein-Friesian Black-and-White cows with the AA genotype at *locus c.1178G>A* were characterised by the greatest annual production progress and cumulative progress for the yield of milk and the yield of milk fat. In turn, in terms of the yield of milk protein more advantageous values of calculated parameters were found for the GG homozygotes.

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Abstract. The aim of this study was to analyse the dependence between *PIT-1* gene polymorphism in exon 6 of bovine chromosome 1 (*c.1178G>A*) and the level of production progress in Polish Holstein-Friesian Black-and-White cows. The greatest annual production progress and cumulative progress for the yield of milk and milk fat was found for the AA homozygotes. For the yield of milk protein more advantageous values of calculated parameters were recorded for the GG homozygotes.

