

The effect of colipase gene (*CLPS*) polymorphism on selected carcass traits in Polish Large White and Polish Large White × Polish Landrace fatteners

Hanna Jankowiak

Department of Pig Breeding, University of Technology and Life Sciences in Bydgoszcz*,
Mazowiecka 28, 85-084 Bydgoszcz, Poland

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The study covered 30 purebred Polish Large White (PLW) and 30 crossbred PLW × Polish Landrace (PLW × PL) fatteners, free of *RYRI*^T gene and reared under standard conditions. The pigs were slaughtered at a mean live body weight of 105 kg and their carcasses were evaluated according to the reference method of Walstra and Merkus. The relationship was studied between selected carcass quality traits and the colipase (*CLPS/Ddel*) genotype. Within PLW fatteners the animals of *AB* genotype showed a significantly thicker backfat than those of genotype *AA* (3.33 vs. 2.87 cm). Within crossbreds, meat content of loin was significantly higher in *AB* than in *AA* pigs (53.70 and 50.02%, respectively).

KEY WORDS: carcass quality / colipase gene / gene polymorphism / pigs

Quantitative traits of animal carcasses (e.g. fat and lean meat content) are polygenic ones, and require the estimation of single genes' role. Searching for quantitative trait *loci* (QTLs) responsible for carcass and meat quality in pigs revealed the region of chromosome 7 containing genes of major histocompatibility complex (MHC) as well as genes influencing backfat thickness and meat marbling [Rothschild *et al.* 1995]. In that region the colipase gene (*CLPS*) was identified by Baskin and Pomp [1998] and later considered a candidate gene for QTL affecting carcass fatness in pigs [Demeure *et al.* 2003].

Colipase (*CLPS*) is a required co-factor for lipase and is a key regulator of dietary lipid metabolism. The enzyme is synthesized in pancreas as a preprocolipase, secreted

*Former University of Technology and Agriculture.

from pancreas as a procolipase which is activated by trypsin [Erlanson-Albertsson 1992]. CLPS reverses inhibition of triacylglycerol lipase by bile salts, restoring the ability to digest dietary lipids [Baskin and Pomp 1998, Brockman 2000]. Because of its important effects on lipid metabolism CLPS is an attractive candidate gene especially within the QTLs for fat deposition.

The aim of this study was to identify the polymorphism of colipase gene (*CLPS/DdeI*) in purebred Polish Large White and Polish Large White × Polish Landrace crossbred fatteners and to assess the significance of relationship expected to exist between the *CLPS/DdeI* genotype and carcass quantitative traits.

Material and methods

Sixty fatteners of two genetic groups, free of *RYRI^T* gene were analysed. One group included 30 purebred Polish Large White (PLW) pigs, while the second 30 PLW × Polish Landrace (PLW × PL) crossbreds (F_1), with 1:1 gilts to castrated males ratio in each group. All animals were reared and fattened under standard conditions. Blood samples were withdrawn from *vena cava anterior* to test-tubes containing EDTA*K₂, and then frozen down to, and kept at -20°C until required. The *CLPS* genotypes were identified with PCR-RFLP using *DdeI* restriction enzyme [Baskin and Pomp 1998]. The fatteners were slaughtered at a mean body weight of 105 kg.

After 24 h cooling the left carcass-sides were evaluated. Backfat thickness was measured at five points: over the shoulder, over the last rib, and over the I, II and III sacral vertebra. Carcass-sides were evaluated according to Walstra and Merkus [1996]. Four cuts: ham, loin, shoulder and belly were dissected into meat, skin with subcutaneous fat, intermuscular fat, and bones. Lean content of carcasses was determined according to equation:

$$\% \text{ lean} = \text{sum of meat weight in dissected cuts (kg)} / \text{carcass side weight (kg)} \times 1.3.$$

In order to evaluate the results the computer programme STATISTICA 5.5 PL [2000] was used. Differences between groups across *CLPS/DdeI* genotypes were defined using the single-factor analysis of variance and their significance was identified with the Duncan test.

Results and discussion

Table 1 shows the frequency of particular genotypes and alleles of the *CLPS/DdeI* gene. In both breed groups (PLW and PLW × PL) allele *A* was more frequent than allele *B* (0.70 and 0.30 vs. 0.77 and 0.23, respectively).

Two genotypes – *AA* and *AB* – were identified within populations tested. Determined was also the number of homo- and heterozygous genotypes of *CLPS* gene (Tab. 1) Within the PLW animals genotype *AB* was more frequent (0.60) than genotype *AA* (0.40). These frequencies differ from those reported for PLW gilts by Blicharski *et al.* [2004] where the most numerous were animals of *AA* genotype (n=208) and the

least those of genotype *BB* (n=6). In the group of crossbreds considered in the present study the frequency of *AA* genotype (0.53) was found higher than that of genotype *AB* (0.47). In the study by Kurył *et al.* [2001] on fatteners upgraded with 50% of Pietrain breed most of animals appeared heterozygous (n=63) while the least numerous were homozygotes *BB* (n=10).

Within the animals studied no pigs of *BB* genotype were found, so the detailed analysis of the effect of *CLPS* genotype on some carcass quality traits was rather difficult.

Table 1. Frequency of genotypes and alleles of the *CLPS/DdeI* gene in PLW and PLW × PL fatteners

Breed group		Genotypes			Alleles	
		<i>AA</i>	<i>AB</i>	<i>BB</i>	<i>A</i>	<i>B</i>
PLW	number	12	18	-	0.70	0.30
	frequency	0.40	0.60	-		
PLW × PL	number	16	14	-	0.77	0.23
	frequency	0.53	0.47	-		

PLW – Polish Large White; PL – Polish Landrace.

Table 2. Backfat thickness, loin eye area and lean meat content of carcass as related to *CLPS/DdeI* genotype in PLW and PLW × PL fatteners

Trait		Genotype			
		<i>AA</i>	<i>AB</i>	<i>AA</i>	<i>AB</i>
		PLW		PLW × PL	
Backfat thickness (cm)					
over shoulder	mean	2.87 ^B	3.33 ^A	3.39	3.24
	SD	0.39	0.44	0.46	0.53
over last rib	mean	1.58	1.87	2.12	2.22
	SD	0.30	0.43	0.28	0.28
over sacrum I	mean	1.72	2.07	2.54	2.61
	SD	0.50	0.57	0.36	0.41
over sacrum II	mean	1.08	1.42	1.72	1.80
	SD	0.45	0.53	0.19	0.35
over sacrum III	mean	1.75	2.09	2.49	2.54
	SD	0.52	0.60	0.34	0.45
mean from 5 measurements (cm)	mean	1.80 ^b	2.15 ^a	2.46	2.49
	SD	0.35	0.46	0.24	0.31
Loin eye area (cm ²)	mean	41.75	44.56	40.46	42.16
	SD	6.25	4.61	4.74	5.06
Lean content of carcass (%)	mean	56.03	53.85	50.82	52.45
	SD	4.01	3.54	3.23	3.23

^{aA...} Within breed groups means for individual traits bearing different superscripts differ significantly at: small letters – $P \leq 0.05$; capitals – $P \leq 0.01$.

PLW – Polish Large White; PL – Polish Landrace.

Significant effect of the colipase genotype was shown as regards traits linked to carcass fatness (Tab. 2). The widest diversity was observed within PLW animals. Significant differences were shown for backfat thickness measured over the shoulder and for the mean from five measurements. Animals of *AB* genotype showed the thicker backfat (3.33 cm over the shoulder and 2.15 cm for mean) than *AA* animals (2.87 cm and 1.80 cm, respectively, $P \leq 0.01$ and $P \leq 0.05$). In crossbreds backfat thickness found in particular points of measurement does not allow to conclude about any significant relations between the *CLPS* gene polymorphism and traits studied; all evaluated traits showed similar values in both groups.

Kurył *et al.* [2001], Blicharski *et al.* [2004] and Jankowiak [2005] reported a trend of higher carcass fatness in *BB/CLPS* than in *AA/CLPS* pigs. In Pietrain \times (PLW \times PL) crossbreds the backfat measured over sacrum I and III was found significantly thicker in *BB* than in *AA* genotype animals by Kurył *et al.* [2001] and Jankowiak [2005]. However, Blicharski *et al.* [2004] reported in PLW gilts an insignificant relation between *CLPS BB* genotype and carcass fatness.

The basic parametre of the carcass lean content is loin eye area. The *CLPS* genotype was not found related to any difference in that trait in the whole population studied (Tab. 2). Moreover, insignificant differences were identified for lean content of carcass. No relations between the colipase genotypes and carcass lean content of PLW pigs were reported by Blicharski *et al.* [2004].

Table 3. Parametres of loin and ham as related to *CLPS/DdeI* genotype in PLW and PLW \times PL fatteners

Trait		Genotype			
		<i>AA</i>	<i>AB</i>	<i>AA</i>	<i>AB</i>
		PLW		PLW × PL	
Loin					
weight (kg)	mean	7.29 ^b	8.09 ^a	7.17	7.23
	SD	1.02	0.98	0.50	0.76
lean content (%)	mean	54.59	53.57	50.02 ^b	53.70 ^a
	SD	3.78	4.05	4.52	4.10
backfat content (%)	mean	28.96	30.52	33.98 ^a	30.20 ^b
	SD	4.66	4.58	4.60	3.91
Ham					
weight (kg)	mean	9.57	10.27	9.48	9.40
	SD	0.85	1.05	0.64	0.44
lean content (%)	mean	72.03	69.66	66.39	67.76
	SD	4.05	3.17	3.02	3.23
backfat content (%)	mean	17.39	18.83	21.84	20.66
	SD	3.87	3.33	2.32	2.60
intermuscular fat content (%)	mean	1.80	2.06	2.13	2.40
	SD	0.53	1.76	1.33	2.07

^{aA...} Within breed groups means for individual traits bearing different superscripts differ significantly at: small letters – $P \leq 0.05$; capitals – $P \leq 0.01$.

PLW – Polish Large White; PL – Polish Landrace.

Table 3 shows the weight of two basic cuts (loin and ham) and their tissue composition. Within PLW group a significantly higher weight of loin was found in animals of *AB* (8.09 kg) than of *AA* (7.29 kg) *CLPS* genotype. The effect of *CLPS* gene polymorphism was identified on lean content and backfat content of loin in crossbreds, where lean content was higher in *AB* (53.70%) than in *AA* (50.02%) fatteners ($P \leq 0.05$). Simultaneously, higher backfat (with skin) content of loin was found in *AA* (33.98%) than in *AB* (30.20%) crossbreds ($P \leq 0.05$).

Individual colipase genotypes identified in this study did not significantly differentiate the weight and tissue content of ham: differences found between pigs of different *CLPS* genotypes were not confirmed statistically. In the report by Blicharski *et al.* [2004] on PLW gilts no significant effect of the *CLPS* gene polymorphism on weight of ham (without fat and skin) was observed (8.58 kg in *BB*, 8.56 kg in *AA*, and 8.49 kg in *AB*).

Summarizing the results presented here one can conclude that the colipase gene polymorphism affects certain important traits connected with fatness and lean content of carcass in PLW and PLW \times PL pigs. There is a high probability that the effect of *CLPS/DdeI* gene polymorphism is significantly determined by breed. In this study higher differentiation of carcass traits values as related to *CLPS/DdeI* genotype was shown within the purebred PLW pigs than within PLW \times PL crossbreds.

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Hanna Jankowiak

Wpływ polimorfizmu genu kolipazy (*CLPS*) na cechy jakości tuszy świń rasy wielkiej białej polskiej i mieszańców rasy wielkiej białej polskiej z polską białą zwislouchą

Streszczenie

Badaniom poddano tuczniki wolne od *RYR1^T* (genu wrażliwości na stres), z których 30 należało do rasy wielkiej białej polskiej (PLW), a 30 było mieszańcami F_1 ras wielkiej białej polskiej z polską białą zwislouchą (PLW \times PL). Zwierzęta utrzymywano w ujednoliconych warunkach i ubijano przy masie ciała około 105 kg. Tusze dzielono na półtusze i wybrane wyřeby, które dysekowano zgodnie z metodyką referencyjną Walstry i Merkusa, stosowaną w krajach Unii Europejskiej. Oceniono wybrane cechy tuszy na tle genotypu genu kolipazy (*CLPS/Ddel*). Wykazano istotny wpływ polimorfizmu tego genu na niektóre cechy związane z otluszczeniem i umięśnieniem badanych tuczników. W obrębie rasy PLW osobniki o genotypie *AB* charakteryzowały się istotnie grubszą słoniną na łopatce (3,33 cm) niż osobniki *AA* (2,87 cm). W obrębie mieszańców PLW \times PL wyższą zawartość mięsa ($P \leq 0,05$) stwierdzono w polędwicy heterozygot niż homozygot *AA*.