

A relationship between genotypes at the *GH* and *LEP* loci and carcass meat and fat deposition in pigs

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The aim of this study was to characterize the polymorphism of *GH* and *LEP* genes in selected pig breeds reared in Poland and to analyse the relation between the *GH* and *LEP* genotypes and carcass meat and fat deposition. The tests covered a total of 305 animals of the following breeds and lines: Pietrain (P), Złotnicka Spotted (ZS), Polish Landrace (PL), Torhyb [P × (PL × Polish Large White)], Stamboek (Dutch Landrace × Dutch Large White) and Pig Improving Company (PIC) pigs.

The frequency of particular variants of porcine *LEP* and *GH* genes proved to be dependent on breed or line. An association between genotypes at loci *LEP* and *GH* and carcass traits was analysed on a material comprising 115 Torhyb, 44 Stamboek and 56 PIC pigs. The genotype at loci *LEP* and *GH* affected the value of particular carcass traits, but what traits were affected and what was the level of significance depended on the line. Genotype *TT* at locus *LEP* proved more advantageous for decreasing both fat weight and fat content of ham in PIC pigs than genotype *CT*. Moreover, genotypes *AA* at locus *GH/HaeII* and *BB* at locus *GH/MspI* were the least advantageous for weight of ham and ham meat when compared to the remaining genotypes at these loci. The same genotypes at the *GH* locus increased carcass length. It is concluded that a knowledge of *LEP* and *GH* genotypes might be useful for improving several traits determining carcass quality in some pig breeds and lines.

KEY WORDS: carcass quality / *GH* / *LEP* / meat / pig

Meat and fat deposition are important traits in pig production that show a quantitative variation within populations. A quantitative trait is controlled by several or many genes (QTLs), which may contribute to the phenotype to a different extent, and be affected also by environmental factors. Comprehensive genetic linkage maps have been

developed for the pig and on this basis and data from resource populations, several genome regions were discovered, which comprise QTLs affecting body composition [Malek *et al.* 2001a, 2001b – a review]. The identification of genes and the causal polymorphisms affecting the traits was the main aim of these studies. The effect of the polymorphism of those genes on a trait is evaluated on the basis of differences in a trait level observed between animals of different genotypes at individual *loci*. Several candidate genes have been selected as affecting carcass fat deposition, among them genes encoding leptin (*LEP*) and the growth hormone (*GH*). Leptin is a hormone secreted by adipocytes and involved in the regulation of feed intake and energy balance in animals [Remesar *et al.* 1997, Xie *et al.* 1999]. The expression and secretion of leptin is highly correlated with body fat mass and adipocyte size. A mutation in the leptin gene is responsible for the profoundly obese phenotype of the *ob/ob* mouse [Zhang *et al.* 1994]. Neuenschwander *et al.* [1996] were the first to report a partial cDNA sequence for pig leptin. Next, Ramsay *et al.* [1998] reported the full length coding region of porcine leptin gene. Moreover, they showed that relative levels of porcine leptin in the sera from obese pig were approximately by 306% higher than those present in sera from contemporary, crossbred pig. Seven polymorphisms in the pig leptin gene (*LEP*) were described [Stratil *et al.* 1997, Jiang and Gibson 1999, Kennes *et al.* 2001] and evaluated for association with economically important production traits in Yorkshire, Landrace and Duroc pigs [Kennes *et al.* 2001], as well as in Duroc, Hampshire, Landrace and Large White pigs [Jiang and Gibson 1999]. A significant difference was noticed in the frequency of *LEP* alleles between the high- and low-fat groups of pigs. A significant effect was observed of the *T/C* polymorphism at nucleotide 3469 in the *LEP* gene on the per cent of backfat and dissected lean in shoulder, loin and ham of Large White pigs [Jiang and Gibson 1999], on the mean daily weight gain in Landrace pigs [Kennes *et al.* 2001, Kulig *et al.* 2001] and on lean meat content (%) in Landrace pigs [Kulig *et al.* 2001].

An association between variants at locus *GH* in the pig and its carcass quality has been analysed in several studies [Nielsen *et al.* 1995, Knorr *et al.* 1997, Křenková *et al.* 1998, Pierzchała *et al.* 1999]. However, conflicting data indicate that the relationship between the *GH* genotype and carcass traits has not yet been fully clarified.

The objective of the present study was to evaluate, on the basis of selected pig breeds raised in Poland, the frequency of the *T/C* polymorphism at nucleotide 3469 of the *LEP* gene as well as of the *HaeII* and *MspI* polymorphisms in exon 2 and intron 2 of the *GH* gene. The effect of these polymorphisms on the carcass fat and meat deposition was also evaluated.

Material and methods

The study covered a total of 249 unrelated animals of the following breeds and lines: Pietrain (P, n=30), Zlotnicka Spotted (ZS, n=30), Polish Landrace (PL, n=30), Torhyb line [P × (PL × Polish Large White), n=115] and Stamoboek line (Dutch Large White × Dutch Landrace, n=44). The animals were kept at the AGRO-WRONIE farm,

Wronie near Toruń, Poland. Moreover, Pig Improving Company (PIC, n=56) pigs, coming from PROVIMI Polska (Czapelki n/Chełmno) were included.

From all animals blood samples were drawn into test-tubes containing K₂EDTA which then were kept at -20 or, for longer storage, at -70°C. Slaughtered were Thorhyb, Stamboek and PIC pigs; those from the first two lines at a live body weight of 105 kg, while from the latter – at 95 kg. Their right carcass sides were dissected according to the Pig Progeny Testing Stations procedure. Apart from dissection, the meat content of carcasses was estimated with the USG procedure and presented as UFOM (%). Carcass traits examined in this study are shown in Table 3.

Both maintenance and feeding were similar for P, ZS, PL, Torhyb and Stamboek pigs coming from AGRO-WRONIE farm.

Genomic DNA was isolated according to Kawasaki [1990] or Kanai *et al.* [1994]. The following PCR/RFLP polymorphisms of the genes were determined: *GH/HaeII* in exon 2 and *GH/MspI* in intron 2 [Kirkpatrick 1992]; *LEP/HinfI* in exon 2 [Stratil *et al.* 1997]. The *RYRI/HinP1* genotypes were identified using sequence of primers according to Fujii *et al.* [1991].

A statistical analysis was performed to compare meat deposition traits between pigs of different genotypes with reference to individual *GH* and *LEP* genes, using the least squares method of the GLM procedure (SAS 8.2) – [2001] according to the following model:

$$Y_{ijkl} = \mu + sex_i + RYRI_j + G_k + \beta (CS_{ijkl} - \overline{CS}) + e_{ijkl}$$

where:

- Y_{ijkl} – trait measured on *ijkl*-th animal;
- μ – overall mean;
- sex_i – effect of sex;
- $RYRI_j$ – effect of *RYRI* genotype ($j = CC, CT, TT$);
- G_k – effect of a particular genotype at the *GH* or *LEP* locus ($k = AA, AB, BB$);
- β – linear regression coefficient for cold carcass weight;
- CS_{ijkl} – cold carcass weight of *ijkl*-th individual included as covariable;
- \overline{CS} – mean for cold carcass weight;
- e_{ijkl} – random error.

Results and discussion

Polymorphism in *LEP* and *GH* genes

The frequency of genotypes at the *LEP* and *GH* loci is shown in Table 1. The T3469C polymorphism, identified with enzyme *Hinf*I, was detected in exon 2 of the *LEP* gene. Three *LEP/Hinf*I genotypes were observed within the breeds tested, but genotype *CC* occurred only in PL pigs. Stratil *et al.* [1997], Kulig *et al.* [2001] and Kennes *et al.* [2001] also reported a low frequency of allele *C* in Duroc, Landrace, Yorkshire, Large White, Pietrain, Hampshire, Czech Meat Pig, and Black Pied Preštice pigs. It is interesting to note, that Chinese Erhualian pigs [Jiang and Gibson 1999] and Meishan pigs [Stratil *et al.* 1997] appeared monomorphic as regards allele *C*. A relatively high frequency of allele *C* (0.09-0.47 depending on population) was observed in Large White pigs by Jiang and Gibson [1999].

Two or three genotypes were observed as regards the mutation recognized with *Hae*II endonuclease in exon 2 of gene *GH*. Genotypes *GH/Hae*II and *GH/Msp*I were not defined for some ZS, P and Torhyb pigs due to the atypical pattern of electro-

Table 1. Frequency of genotypes at loci *LEP* and *GH* in selected pig breeds and lines kept in Poland*

Breed/line	Total number of animals	Number and frequency of genotypes at loci								
		<i>LEP</i>			<i>GH/Hae</i> II			<i>GH/Msp</i> I		
		TT	TC	CC	AA	AB	BB	AA	AB	BB
P	30	30 0%	0 0%	0 0%	0 0%	11 37%	19 63%	6 20%	17 57%	7 23%
ZS	30	26 87%	4 13%	0 0%	10 36%	16 57%	2 7%	1 4%	14 48%	14 48%
PL	30	24 80%	4 13%	2 7%	1 4%	22 73%	7 23%	1 3%	4 13%	25 85%
Torhyb	115	81 70%	34 30%	0 0%	13 12%	67 58%	35 30%	16 15%	51 46%	43 39%
Stamboek	44	38 86%	6 14%	0 0%	0 0%	24 55%	20 45%	5 11%	37 84%	2 5%
PIC	56	35 63%	21 37%	0 0%	16 28%	26 46%	14 26%	2 4%	17 30%	37 66%

*Genotypes *GH/Hae*II and *GH/Msp*I were not defined for some tested P, ZS and Torhyb pigs because of atypical PCR/RFLP pattern.

phoretic separation of the PCR products digested with restriction endonucleases. This may suggest the presence of another point mutation(s) within the sequence of the *GH* gene being amplified and recognized by restriction endonucleases used in this study. A sequencing analysis of those PCR products will be performed in a further study. No homozygotes *AA* appeared in the Pietrain and Stamboek pigs.

Three genotypes at locus *GH/Msp*I were found within the breeds and lines analysed

but, in ZS, PL, Stamboek and PIC pigs a very low frequency ($\leq 5\%$) was observed for one of homozygous genotypes. The absence of one of the homozygous genotypes has been described in several commercial lines of pigs as regards most genes examined in studies on the relationship between genotype and carcass quality traits [Stratil *et al.* 1997, Kennes *et al.* 2001, Kulig *et al.* 2001].

A relationship between the *LEP* and *GH* genotypes and carcass traits

Certain earlier studies [Leach *et al.* 1996, Kurył *et al.* 2002] showed that both sex and *RYRI* genotype proved to have a significant effect on carcass quality. Therefore, both were included here in the statistical model. The frequency of the *RYRI* genotypes in the three pig lines chosen for an analysis of the relations between genotypes at loci *GH* and *LEP* and carcass quality traits is shown in Table 2. All three possible *RYRI* genotypes were present within the Torhyb line, whereas the Stamboek and PIC pigs appeared to be free of genotype *TT*. The significance of differences between *RYRI* genotypes within particular carcass traits is shown in Table 3.

In Torhyb pigs significant ($P < 0.05$ and $P < 0.01$) differences were observed (Tab. 3) for a majority of carcass traits between genotypes *TT* and *CC* or *CT*. Between genotypes *CC* and *CT* only few significant differences were found within the Torhyb, Stamboek and PIC pigs.

***LEP* gene.** In the Torhyb line, dressing percentage, meat content of ham and weight of tenderloin appeared to be significantly ($P \leq 0.05$) higher in animals of genotype *TC* at nucleotide 3469 in the *LEP* gene sequence than in *TT* homozygotes. In turn, a significantly higher values of meat weight and meat content of ham, and a lower fat weight and fat content of ham were observed in PIC pigs of *TT* than of *TC* genotype (Tab. 4). These differences observed between different pig breeds may indicate that mutation T3469C in the *LEP* gene, being a silent mutation not affecting the leptin amino acid sequence, may not be the causal mutation as regards differences in the carcass traits observed in this study between *LEP* genotypes. On the other hand, Pietrain pigs ap-

Table 2. Frequency of genotypes at locus *RYRI* in Torhyb, Stamboek and PIC pigs

Line	Number of animals	Number and frequency of genotypes <i>RYRI</i>		
		CC	CT	TT
Torhyb	115	36 31.3%	60 52.2%	19 16.5%
Stamboek	44	37 84.1%	7 15.9%	0 0%
PIC	56	33 58.9%	23 41.1%	0 0%

Table 3. Significance of the effect of genotypes at locus *RYR1* on carcass traits in the Turkyb, Stamboek and PIC pigs

Trait	Line				
	Turkyb			Stamboek	PIC
	CC:CT	CC:TT	CC:TT	CC:CT	CC:CT
Rit thickness (cm)					
over the shoulder	ns	*	*	*	ns
at the 1st rib	ns	ns	*	ns	*
at 5x7x7x point I	ns	*	***	*	ns
at 5x7x7x point II	ns	*	*	ns	ns
at 5x7x7x point III	ns	ns	ns	ns	ns
mean from the 5 measurements	ns	*	**	ns	ns
Ham					
weight of ham with shank (kg)	ns	***	***	ns	ns
weight of ham without shank (kg)	*	**	***	ns	ns
weight of meat (kg)	*	***	***	ns	ns
content of meat (%)	**	***	***	ns	ns
weight of fat with skin (kg)	ns	***	***	ns	ns
content of fat with skin (%)	*	***	***	ns	ns
Weight of tenderloin (g)	ns	***	***	*	ns
Eye-muscle area (cm ²)	*	***	***	**	**
Lean meat content of carcass (%)	*	***	***	nt	nt
Meat content of carcass (UFOM %)	nt	nt	nt	ns	*
Carcass length (cm)	nt	nt	nt	ns	ns

ns – not significant; nt – not tested; *P<0.05; **P<0.01; ***P<0.001.

Table 4. Least squares means (LSM) and their standard errors (SE) for carcass quality traits as affected by genotype at the *LEP* locus in Turkyb and PIC pigs

Line	Carcass trait	LEP genotype: stamboekide 3469					
		TT			TC		
		n	LSM	SE	n	LSM	SE
Turkyb	dressing percentage	81	79.88 ^a	0.34	34	80.78 ^a	0.30
	meat content of ham (%)	81	72.09 ^a	0.30	34	73.46 ^a	0.38
	weight of tenderloin (g)	81	346.8 ^a	10.8	34	369.3 ^a	11.9
PIC	weight of ham meat (kg)	35	6.88 ^a	0.97	21	6.56 ^a	1.25
	meat content of ham (%)	35	73.40 ^a	0.49	21	71.18 ^a	0.63
	weight of ham fat (kg)	35	1.37 ^a	0.04	21	1.76 ^a	0.05
	fat content of ham (%)	35	16.92 ^a	0.43	21	19.11 ^a	0.56

^{a,b} Within rows means bearing different superscripts differ significantly at: small letters – P<0.05; capital letters – P<0.01.

peared to be monomorphic as regards *LEP^T* allele (Tab. 1). This could suggest that *TT* genotype may be more advantageous for decreasing fat deposition in the carcass than genotype *TC*. The relation between the *LEP* genotype and carcass traits, observed in PIC pigs, seems to confirm this suggestion. Due to the metabolic function of leptin one may also assume that a higher value of meat deposition traits (meat content of ham), observed in the present study in animals of one of the *LEP* genotypes (comparing to the other genotypes) resulted from a lower fat thickness or lower fat content of ham.

Jiang and Gibson [1999] identified four polymorphisms in the porcine leptin gene and suggested a possible association between the polymorphism at nucleotide 3469 (*C/T*) and fat thickness in pigs. They observed a highly significant difference ($P=0.0017$) in the frequency of alleles *C* and *T* between Large White pigs selected for the highest or lowest ultrasonic backfat thickness. However, that relation, observed in one group of Large White pigs, was not confirmed on other group of animals of the same breed obtained from the same population. Kennes *et al.* [2001], identified three more polymorphisms in the porcine *LEP* gene. They analysed the effect of the *LEP* gene mutations, as well as that at 3469 nucleotide, on growth rate and backfat thickness in Duroc, Landrace and Yorkshire pigs (39, 102 and 40 animals, respectively). In Landrace pigs an association was observed between polymorphism A2845T (intron 2) and total feed intake ($P=0.0061$) and between polymorphism T3469C (exon 2) and mean daily live weight gain ($P=0.0078$).

Mutations in the leptin gene lead to defective leptin production and cause a recessively inherited early onset obesity in mice [Zhang *et al.* 1994]. In humans, two families have been described with a genetic deficiency in leptin level, but mutations in the translated part of the *LEP* gene could not explain the high prevalence of obesity [Mammés *et al.* 2000 – a review]. Hager *et al.* [1998] and Mammés *et al.* [2000] identified polymorphisms in the 5' untranslated region of the human *LEP* gene causing a lower leptin concentration associated with common obesity phenotypes. It is known that leptin mRNA levels are higher in adipose tissue obtained from obese than from lean pigs – Robert *et al.* [1998], McNeel *et al.* [2000].

Taking into consideration the results of the present study and those presented in literature one may conclude that further studies are needed in order to identify the porcine *LEP* gene mutation(s) in its regulatory region. This type of gene mutation may affect the leptin mRNA level as well as the concentration of leptin in circulating blood what results in an increased fat deposition in pig carcass.

GH gene. Within Torhyb pigs only the weight of tenderloin appeared to be related to the *GH/MspI* genotype. The highest weight was observed in pigs of *AA* genotype. This confirms the results of an earlier study by Pierzchała *et al.* [1999] who demonstrated that genotype *AA* at locus *GH/MspI* was the most advantageous as regards eye muscle area. In the present report no relation was observed in Torhyb pigs between carcass quality traits and the *GH/HaeII* genotype.

In Stamboek pigs no significant differences were observed between genotypes *AB* and *BB* at locus *GH/HaeII* in the value of any carcass trait being considered in

the present study. The highest weight of ham with and without shank and weight of ham meat was observed for PIC pigs of genotype BB at *locus GH/HaeII* (difference significant compared to animals of AA genotype at this *locus*). As regards carcass length significant differences were observed between both homozygous genotypes at this *locus*. No significant differences were observed between heterozygotes and both homozygous genotypes as regards traits presented in Table 5.

Out of the 44 Stamboek pigs examined 37 were of genotype AB at *locus GH/MspI*. Therefore, the effect of any genotype at this *locus* was not analysed for this line. The comparison of carcass traits between BB and AB pigs at *locus GH/MspI* was performed on PIC pigs; the analysis did not include the two animals of AA genotype. The genotype at *locus GH/MspI* affected the same carcass traits as did the genotype at *locus*

Table 5. Least squares means (LSM) and their standard errors (SE) for carcass quality traits of Todyb and PIC pigs differing as regards genotype at the *GH/HaeII* and *GH/MspI* loci

Line	Carcass trait		<i>GH/HaeII</i> locus			<i>GH/MspI</i> locus		
			AA	AB	BB	AA	AB	BB
Todyb	Weight of tenderloin (kg)	LSM	ns	ns	ns	368.3 ^{ab}	366.2 ^a	343.5 ^b
		SE				11.3	10.1	9.9
PIC	Weight of ham with shank (kg)	LSM	10.37 ^a	10.63 ^{ab}	10.83 ^b	ns	10.89 ^a	10.48 ^b
		SE	0.13	0.10	0.13		0.12	0.09
	Weight of ham without shank (kg)	LSM	9.04 ^a	9.33 ^{ab}	9.60 ^b	ns	9.30 ^a	9.17 ^b
		SE	0.13	0.10	0.14		0.12	0.08
	Weight of ham meat (kg)	LSM	6.49 ^a	6.82 ^{ab}	7.00 ^b	ns	7.08 ^a	6.62 ^b
		SE	0.37	0.13	0.09		0.13	0.09
	Carcass length (cm)	LSM	79.63 ^a	77.14 ^{ab}	75.23 ^b	ns	75.46 ^a	78.40 ^b
		SE	1.16	0.87	1.28		1.11	0.77

ns – not significant, ns – not estimated.

^{aa} Within rows and *loci*, means bearing different superscripts differ significantly at: small letters – P≤0.05; capital – P≤0.01.

GH/HaeII. Weight of ham with or without shank, as well as weight of ham meat, were significantly higher in PIC pigs of genotype AB at *locus GH/MspI* than in BB pigs. The *GH/MspI* polymorphism affected also the length of the carcass which in BB animals was about 3 cm longer than in those of genotype AB.

The results reported by Nielsen *et al.* [1995] indicated the differences existing in transcriptional activity between *GH* gene variants (TATA-box alleles), what may eventually cause higher GH plasma concentration and higher growth rate. However, they established neither a direct cause nor the effect of relationship between *GH* gene polymorphism and trait value. Knorr *et al.* [1997] analysed an association between *GH* variants (*HinPI* and *ApaI*) and quantitative traits within wild boar × Pietrain and

Meishan × Pietrain families. In the latter family eight traits related to fatness were significantly related to *GH* genotype, while in the wild boar × Pietrain family no such significant associations were found. It was concluded that *locus GH* should be further investigated in commercial breeds so as to determine its value for marker-assisted selection programmes. In an earlier study by Pierzchała *et al.* [1999] performed on F₂ castrated males ([Polish Large White × Zlotnicka Spotted] × [Polish Large White × Zlotnicka Spotted]) the *GH/HaeII* and *GH/MspI* genotypes, as well as *HaeII-MspI* haplotypes, differed significantly as regards lean meat content of carcass and several traits related to carcass fat deposition. The effect of *GH* genotype on selected carcass traits was confirmed in this study (weight of ham with or without shank). This indicates that polymorphism in exon 2 and intron 2 of the porcine *GH* gene, identified with *HaeII* and *MspI* enzymes, respectively, might be useful for improving the carcass quality of some pig breeds or lines.

The differences in the value of carcass traits observed between genotypes depend on the range of gene polymorphism in an individual breed. The absence of one of the homozygous genotypes renders it difficult or impossible to draw definite conclusions. The value of a given trait, observed in one of the homozygous genotypes and in heterozygotes, might sometimes give an erroneous indication as to the trait level in representatives of the remaining homozygote. The absence of one of the homozygous genotypes has been described in several commercial lines of pigs [Kulig *et al.* 2001, Cieślak *et al.* 2002, Kurył *et al.* 2002] and refers to a majority of genes examined in studies on relationship between genotype and quantitative traits. Thus, it is difficult to make a correct evaluation of the effect of genotype on a given trait within a single breed or line (both homozygous genotypes are not available). Comings and MacMurray [2000] reviewed the accumulating evidence that what is known as “molecular heterosis” is common in humans and may occur in up to 50% of all gene associations. Molecular heterosis occurs when a heterozygote for a specific genetic polymorphism shows a significantly greater or lesser (positive and negative heterosis, respectively) level of a given quantitative trait than homozygotes for either allele. Moreover, Comings and MacMurray [2000] have presented several examples in which heterosis was sex-specific. Another problem observed when evaluating the effect of a particular gene polymorphism on carcass quality is connected with the *RYR1* genotype which should always be defined (and included into statistical model) for pigs used as experimental material for analysing the effect of any gene on carcass traits. Moreover, the highly significant effect of genotype *TT* on a trait level, observed for example in Torhyb pigs in this study, may disguise the effect, which the gene examined may in fact have.

The results presented here lead to the conclusions given below.

The frequency of particular variants of the porcine genes *LEP* and *GH* depends on breed and line. The genotype at the *LEP* and *GH loci* affects the value of particular carcass traits, but the level of significance differs between pig breeds or lines; Genotypes *AA* at *locus GH/HaeII* and *BB* at *locus GH/MspI* are the least advantageous for carcass meat deposition traits when compared to the remaining genotypes at these *loci*.

In some pig lines the *GH* genotype affects carcass length.

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Zależność między genotypami GH i LEP a cechami mięsności i otłuszczenia tuszy świń

Streszczenie

Celem badań była charakterystyka polimorfizmu genów hormonu wzrostu (*GH*) i leptyny (*LEP*) świń ras i linii hodowanych w Polsce oraz ocena jego wpływu na mięsność i otluszczenie tuszy. Częstość występowania poszczególnych genotypów *GH* i *LEP* określono łącznie u 305 świń następujących ras i linii: pietrain (P), złotnicka pstra (ZS), pbz, Torhyb [P × (pbz × wbp)], Stamboek (holenderska landrace × holenderska wielka biała) i PIC, stwierdzając jej zróżnicowanie zależnie od rasy lub linii. Zależność między genotypami *GH* i *LEP* a cechami tuszy analizowano niezależnie dla 115 osobników linii Torhyb, 44 linii Stamboek i 56 linii PIC. Stwierdzono zróżnicowanie w poziomie niektórych cech tuszy zależnie od genotypu *GH* lub *LEP*, przy czym nie każda zależność występująca wśród świń jednej linii znalazła potwierdzenie w innej. I tak, wśród świń PIC genotyp *TT* względem *locus LEP* okazał się korzystniejszy dla zmniejszenia masy i zawartości tłuszczu w szynce (a tym samym zwiększenia masy i zawartości w niej mięsa) w stosunku do genotypu *CT*. Z kolei wśród świń Torhyb wyższą zawartość mięsa w szynce stwierdzono dla genotypu *CT* niż *TT*. Ponadto genotypy *AA* względem *locus GH/HaeII* oraz genotypy *BB* względem *locus GH/MspI* okazały się najmniej korzystne dla masy szynki i mięsa szynki w porównaniu z innymi genotypami względem tych *loci*. Genotypy te natomiast wiązały się ze zwiększoną długością tuszy. Autorzy wnioskują, że znajomość genotypów *GH* i *LEP* może być przydatna w selekcji ukierunkowanej na poprawę jakości tuszy świń, zależnie od rasy lub linii.