

## **Growth rate and carcass quality in relation to *GH/MspI* and *GH/HaeII* PCR-RFLP polymorphism in pigs\***

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The objective of this study was to investigate the effect of two single nucleotide polymorphisms in growth hormone (GH) gene on performance traits in pigs. The animals (n= 320) belonged to four groups of commercial crosses being the progeny of crossbred Polish Landrace × Polish Large White sows and Polish Landrace, Polish Large White, Duroc or Pietrain boars. Genotypes of growth hormone gene (*GH*) were established with PCR-RFLP technique using *MspI* and *HaeII* endonucleases. The *GH/MspI* and *GH/HaeII* genotypes were found significantly related to the weight of ham, weight of ham meat and ham content of carcass. Moreover, nearly significant differences between *GH/MspI* genotypes were found for mean fat thickness (from five measurements), fat thickness at lower back (point K2) and over the loin, and for loin eye height. The results presented allow to assume that near the analysed mutation the QTLs for performance traits in pigs are located.

**KEY WORDS:** carcass / gene polymorphism / growth hormone / pig

The „candidate gene” approach is purposeful when a gene is known to function in such a way that it may explain genetic variation in traits of interest. It is well known that growth hormone (GH) is one of the most important factors for growth and development of animal cells. Porcine GH is synthesized as 190-amino acid peptide and secreted pulsatile by acidophilic or somatotropic cells of the anterior pituitary [Kato *et al.* 1990]. The GH gene (*GH*) is assigned to pig chromosome 12 [Thomsen *et al.* 1990, Yerle *et al.* 1993, Chowdhary *et al.* 1994]. GH has long been known to have a significant beneficial effect on carcass quality in pigs. Treating pigs with exogenous porcine GH improves daily live weight gain, feed efficiency and lean content of carcass [Chung

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and Etherton 1986, Etherton *et al.* 1986]. Comparison between pig lines selected for live weight gain and backfat thickness showed correlation of both high growth rate and low backfat thickness with higher blood GH level [Rindberg Lund-Larsen and Bakke 1975, Althen and Gerrits 1976]. Because of physiological importance of GH the *GH* gene was the objective of several studies as the candidate gene for performance traits in farm animals [Zwierzchowski *et al.* 2002, Ge *et al.* 2003]. The effect of *GH* variants on performance traits in pigs have been reported, among others, by Casas-Carrillo *et al.* 1997, Knorr *et al.* 1997, Krenkova *et al.* 1999, Pierzchała *et al.* 1999, Cheng *et al.* 2000, and Putnova *et al.* 2001].

The goal of the pig industry is to produce the high quality, lean pork. The most economically important traits are sow fertility, growth rate, feed conversion, meat content of carcass, as well as meat quality. Growth process and cell proliferation in animals are regulated by multitude of physiological pathways among which the somatotrophic axis plays a key role. Thus the differences in frequency of restriction sites identified as GH gene polymorphisms may explain growth rate and carcass composition differences occurring between pigs.

In this study we tried to evaluate the effect of the porcine *GH/MspI* and *GH/HaeII* polymorphisms on growth rate and carcass quality in commercial pig crosses.

### Material and methods

The pigs belonged to four commercial lines obtained by crossing of purebred boars (Polish Landrace, Polish Large White, Duroc, Pietrain) with crossbred (Polish Landrace × Polish Large White) sows. Eighteen growth rate and carcass quality traits were measured in a total of 320 animals.

Polymorphism of growth hormone gene (*GH*) was identified with PCR-RFLP using primers and procedure of Kirkpatrick [1992]: *MspI* within second intron (A – 284 and 222 bp, B – 222, 147 and 137 bp) and *HaeII* within the second exon (A – 506 bp, B – 173 and 333 bp). Considered was also the effect of *RYR1* genotype.

Statistical analysis using the least squares (SAS Institute Inc., Cary, USA) was performed to find significant differences between *GH* genotypes in 18 recorded traits of performance. The following model was used:

$$Y_{ijklm} = \mu + G_i + B_j + S(B)_{jk} + R_l + (GB)_{ij} + (GR)_{il} + \beta(wc_{ijklm} - \underline{wc}) + e_{ijklm}$$

where:  $Y_{ijklm}$  – trait measured on *ijklm*-th animal;

$\mu$  – overall mean;

$G_i$  – effect of *i*-th genotype (*GH/MspI* = 1,2,3; *GH/HaeII* = 1,2,3);

$B_j$  – effect of *j*-th breed of a sire (j = 1, 2, 3, 4);

- $S(B)_{jk}$  – nested effect of  $j$ -th sire within the  $k$ -th breed;  
 $R_l$  – effect of  $l$ -th *RYR1* genotype ( $l = 1, 2, 3$ );  
 $(GB)_{ij}$  – effect of interaction  $i$ -th genotype  $\times$   $j$ -th breed;  
 $(GR)_{il}$  – effect of interaction  $i$ -th genotype  $\times$   $l$ -th *RYR1* genotype;  
 $\beta$  – regression coefficient on cold carcass weight;  
 $e_{ijklm}$  – random effect.

### Results and discussion

AA, AB, and BB frequencies of *GH/MspI* were found 3.8, 28.4 and 67.8%, and of *GH/HaeII* – 22.2, 50.6, and 27.2%, respectively (figures not tabulated).

Within *GH/MspI* locus (Tab. 1) higher values for loin eye height, weight of ham, weight of ham meat, and ham content of carcass were found significantly ( $P < 0.05$ ) associated with genotype BB, while higher mean fat thickness (from five measurements) and backfat thickness at point K2 nearly significantly ( $P < 0.1$ ) with AA genotype.

Within *GH/HaeII* locus (Tab. 2) higher values of weight of ham and weight of ham meat ( $P < 0.05$ ) as well as ham content of carcass ( $P < 0.01$ ) were found associated with genotype AA. There were no differences for fatness related to *GH/HaeII* genotypes.

QTL mapping performed by Korwin-Kossakowska *et al.* [2001] within the Polish Pig Genome Mapping Project provides information on localization of genes affecting fat deposition (abdominal fat) on chromosome 12 near the microsatellite markers S0083 and S0090. These microsatellites are linked to *GH* gene [Larsen *et al.* 1995, Rohrer *et al.* 1994, 1996, Archibald *et al.* 1994, Korwin-Kossakowska *et al.* 1999]. Studies performed by Arbona *et al.* [1988] demonstrated that pigs selected for increased growth rate had higher basal plasma GH concentration than unselected pigs, whereas in a study by Saleri *et al.* [2001] growth rate in pigs was significantly correlated not with GH, but with insuline-like growth factor I (IGF-I) and insuline-like growth factor-binding proteins (IGFBP2 and IGFBP3) secretion. Casas-Carrillo *et al.* [1997] found association of neither *GH/DdeI*, nor *GH/HaeII* genotype with growth rate and selected carcass traits in pigs.

Associations of another two *GH* variants with pig performance traits were analysed by Knorr *et al.* [1997] in two resource families – Wild boar  $\times$  Pietrain (W  $\times$  P) and Meishan  $\times$  Pietrain (M  $\times$  P). Significant associations between eight carcass fatness traits and *GH/HinPII* and *GH/ApaI* variants were found only in family M  $\times$  P. This corroborates the results of Larsen *et al.* [1995] who also could not find such relations in W  $\times$  P pigs. In our earlier study on the reference family Zlotnicka Spotted  $\times$  Polish Large White [Pierzchala *et al.* 1999], as well as in that performed by Krenkova *et al.* [1999] similar relations between *GH/HaeII* genotype and fat and meat deposition traits were found. Moreover, Krenkova *et al.* [1999] showed the unfavourable effect of both AA *GH/MspI* and AA *GH/HaeII* genotypes on mean fatness and leanness of carcass, while

Table 1. Least-squares means (LSM) and their standard errors (SE) for performance errors across three C-14004 genotypes in 2012

Trait	C-14004						C-14004					
	2012			2013			2012			2013		
	LSM	SE	D.F.	LSM	SE	D.F.	LSM	SE	D.F.	LSM	SE	D.F.
Daily live weight gain (g)	576	15	15	576	6	6	576	576	5	576	576	5
Rectal temperature (°C)	1.76	0.17	1.76	0.07	1.76	0.07	1.67	0.06	1.67	0.06	1.67	0.06
Rectal temperature (°C)	1.55	0.17	1.55	0.07	1.71	0.07	1.71	0.06	1.71	0.06	1.71	0.06
Rectal temperature and over-back - E1 (°C)	1.91	0.21	1.91	0.09	1.85	0.09	1.74	0.07	1.74	0.07	1.74	0.07
Rectal temperature and over-back - E2 (°C)	1.66	0.20	1.66	0.08	1.91	0.08	1.74	0.07	1.74	0.07	1.74	0.07
Rectal temperature and over-back - E3 (°C)	1.66	0.20	1.66	0.07	1.7	0.11	1.61	0.10	1.61	0.10	1.61	0.10
Rectal temperature over-loan (°C)	1.64	0.21	1.64	0.09	1.59	0.09	1.61	0.08	1.61	0.08	1.61	0.08
Rectal temperature over-head (°C)	1.21	0.21	1.21	0.09	1.98	0.09	1.89	0.07	1.89	0.07	1.89	0.07
Height of hump (cm)	6.17	0.25	6.17	0.25	6.50	0.11	6.63	0.09	6.63	0.09	6.63	0.09
Width of hump (cm)	9.61	0.26	9.61	0.26	9.65	0.11	9.71	0.09	9.71	0.09	9.71	0.09
Water content of hump (%)	50.76	1.71	50.76	1.71	53.71	0.56	53.77	0.47	53.77	0.47	53.77	0.47
Water content of hump (°C)	74.45	1.81	74.45	1.81	75.26	0.49	76.17	0.41	76.17	0.41	76.17	0.41
Shale of hump in summer (%)	11.95	0.41	11.95	0.41	11.30	0.17	11.69	0.15	11.69	0.15	11.69	0.15
Weight of hump without bone (g)	9120	701	9120	701	9819	137	9971	106	9971	106	9971	106
Weight of hump containing fat (g)	1714	179	1714	179	1650	51	1644	49	1644	49	1644	49
Weight of hump (g)	11014	709	11014	709	11369	170	11615	109	11615	109	11615	109
Weight of hump bones (g)	11327	47	11327	47	1147	18	1179	13	1179	13	1179	13
Weight of hump muscle (g)	8191	211	8191	211	8491	118	8671	99	8671	99	8671	99

Table 1. Least squares means (LSM) and their standard errors (SE) for performance and carcass traits GM/HaeII genotypes in 2002

Trait	GM/HaeII				Difference between genotypes (P)			
	GM		Hae		GM-Hae		GM-Hae	
	LSM	SE	LSM	SE	LSM	SE	LSM	SE
Daily live weight gain (g)	585	11	571	6	576	9		
Pecudinae (front) measurement (cm)	1.71	0.09	1.71	0.07	1.71	0.10		
Back fat thickness (cm)	1.76	0.09	1.76	0.07	1.76	0.10		
Pecudinae subcutaneous fat (cm)	1.71	0.11	1.81	0.04	1.76	0.11		
Pecudinae subcutaneous fat (cm)	1.80	0.10	1.80	0.04	1.87	0.11		
Pecudinae subcutaneous fat (cm)	1.77	0.11	1.60	0.11	1.61	0.16		
Pecudinae variation (cm)	1.69	0.11	1.57	0.09	1.61	0.17		
Pecudinae over shoulder (cm)	1.85	0.11	1.94	0.09	1.81	0.11		
Height of thorax (cm)	6.88	0.11	6.64	0.11	6.66	0.15		
Width of thorax (cm)	9.74	0.11	9.56	0.11	9.59	0.15		
Measurement of frame (kg)	51.11	0.10	51.56	0.09	53.19	0.17		
Measurement of frame (kg)	75.65	0.11	75.87	0.09	75.21	0.09		
Shape of frame (cm)	11.91	0.11	11.76	0.11	11.96	0.16	0.04	0.16
Shape of frame (cm)	100.7	1.61	97.7	1.26	98.10	1.77		0.16
Weight of frame (kg)	17.0	0.11	16.1	0.11	16.1	0.10		
Weight of frame (kg)	117.60	1.61	119.11	1.26	111.00	1.60		0.04
Weight of frame (kg)	11.7	0.11	12.1	0.11	11.6	0.15		0.04
Weight of frame (kg)	18.7	1.50	18.76	1.17	17.8	1.65		0.16

in the study of Pierzchała *et al.* [1999] the respective unfavourable effect was found of only AA *GH/HaeII*, the AA *GH/MspI* loci affecting both traits positively. Relation between carcass quality and both *GH/MspI* and *GH/HaeII* loci is evident also from the present results (Tab. 1 and 2). Significant and positive effect of BB *GH/MspI* genotype was found on ham weight, and especially on ham meat weight, as well as nearly significant on ham content of carcass, and backfat thickness. Positive effects on ham weight, ham meat weight, and ham content of carcass were also found of AA *GH/HaeII* genotype.

As far as *GH/MspI* locus is concerned, the present results partially corroborate those reported by Křenková *et al.* [1999], but are opposite to our earlier data [Pierzchała *et al.* 1999]. Considering *GH/HaeII* locus, differences between genotypes point out to trends opposite to those obtained by us earlier, as well as presented recently by Kurył *et al.* [2003]. Importance of this region of genome for carcass performance traits in pigs was also mentioned by Geldermann *et al.* [2003] where several QTLs were localized on chromosome 12, and especially near the *GH* gene [Yue *et al.* 2003].

The results obtained in several studies on the relationship between *GH* gene variants and carcass traits, sometimes slightly opposite to each other cannot, so far, be definitely summarized, but there is enough evidence that the linkage of analysed *GH* gene variants with other mutation (causal) is highly probable.

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## Tempo wzrostu i cechy jakości tuszy świń w powiązaniu z restrykcyjnym polimorfizmem PCR-RFLP genu hormonu wzrostu – *GH/MspI* i *GH/HaeII*

### Streszczenie

Celem badań było określenie zależności między cechami użytkowymi świń a polimorfizmem genu hormonu wzrostu (*GH*). Materiał badawczy stanowiły zwierzęta pochodzące z krzyżowania knurów czystych ras (pbz, wbp, Duroc, Pietrain) z lochami mieszańcowymi (wbp × pbz). Analizą objęto 18 cech tempa wzrostu i jakości tuszy 320 zwierząt.

Istotne zależności między analizowanymi genotypami *GH/MspI* i *GH/HaeII* odnotowano dla masy szynki, masy mięsa szynki oraz udziału masy szynki w tuszy (%). Ponadto stwierdzono bliskie istotności zależności między genotypem *GH/MspI* a średnią grubością słoniny z pięciu pomiarów, grubością słoniny mierzoną na krzyżu w punkcie K2, grubością słoniny okrywającej pośladkowiec oraz wysokością oka pośladkowiec. Prezentowane wyniki wraz z wcześniejszymi doniesieniami potwierdzają tezę, że w rejonie chromosomu 12 obejmującym *locus GH* znajdują się QTLs, które istotnie wpływają na poziom cech użytkowych świń.