THE CHARACTERISATION OF PRODUCTION TRAITS AND TECHNOLOGICAL QUALITY TRAITS OF PORK IN BM BREED, DIVIDED BY POLYMORPHISM HAL GENE ALLELE

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Abstract

The aim of our experiment was to evaluation of phenotype manifestation of various combinations of HAL gene's alleles. This manifestation was evaluated on selected rearing and slaughter indicators and on selected indicators of technological quality of meat in group of pigs of white meat breed. In experiment were placed 151 pigs of white meat breed, 75 boars and 76 gilts. In Laboratory of Institute of Genetics and Animal Breeding of MZLU in Brno were made DNA analysis. Group of pigs was divided into three subgroups. First subgroup was created by 60 pigs of genotype (NN). Second subgroup of pigs was created by 76 pigs of genotype (Nn). Third group was created by 15 pigs of genotype (nn). These three subgroups was statistically interpreted and compared by two factorial analysis of dissipation. In average daily gains in rearing, we found out statistically significances differences between sexes of watched groups of pigs on level $P < 0.01$. In number of feed days, we found out statistically significances differences between sexes of pigs on the same level. In the indicator of proportional share of valuable meaty parts from weight of slaughter half in kilograms we found out statistically highly significances differences between nn and NN genotypes of HAL gene on level $P< 0.001$. In the indicator of thickness of back fat in cm we found out statistically highly significances differences between nn and NN genotypes of HAL gene on level $P< 0.01$. In the indicator of proportional share of weight of leg from weight of slaughter half in kg, we discovered statistically highly significances differences between nn and Nn genotypes on level $P< 0.001$ and between nn and NN genotypes on level $P< 0.001$. In indicators of pH_1 - log molc.(H^+) in MLT, unbound water and color of meat at 520nm in MLT, we discovered statistically highly significances differences between genotypes of HAL gene between group nn genotype and Nn genotype on level $P< 0.001$, between group nn genotype and NN genotype on level $P < 0.001$ and between group Nn genotype and NN genotype on level $P < 0.001$. From results of experiment follows that the pigs of NN genotype reached better values of fattening indicators. Pigs of nn genotype reached better results in slaughter indicators. This group presents animals with worst parameters of technological quality. This is a demonstration of stress perceptiveness of pigs.

Key Words: Technological quality of meat, stress perceptiveness, slaughter value, fattening parameters

Introduction

Increased sensitivity of pigs on stress and losses in pigs breeding is a consequence of breeding intensification and intensive breeding of pigs on mass type. But the main problem is an occur of abnormality of meat (PSE, PSS) post mortem. This is why we pay attention to the selection of pigs with respect to stress sensitivity for their inclusion in the breeding or breeding program.

DVOŘÁK, TESAŘOVÁ (1992) investigated that the highest gains showed individuals resulting from mating of NN x NN genotypes. Individuals from mating of nn x NN genotypes showed lower gains and thickness of back fat.

WITTMANN (1993) found out, significantly higher gains nad higher proportional share of valuable meaty parts in HAL^+ animals as in HAL^- animals.

McPHEE (1994) discovered, that nn genotypes have lower feed consumption, lower gains and lower back fat thickness than Nn and NN genotypes. Lower increases, and the thickness of back fat found in pigs with NN genotypes also in Germany, the authors [4].

DOVČ (1996) followed the effect of RYR1 gene on the fattening properties of 2,403 pieces of five different breeds of pigs and analyzed the average daily gain in periods of growth from 30 - 60 kg, 60 - 100 kg and 30 - 100 kg, feed intake and feed conversion during the three periods, the average thickness of back fat in 100 kg measured by ultrasound. Statistical evaluation revealed a significant effect of RYR1 genotypes for certain fattening characters: animals with nn genotypes had compared with NN and Nn, higher age at reaching 30, 60 and 100 kg live weight and therefore lower daily gains (statistically substantiating only breed Landrase the period from 30 - 60 kg). The average thickness of back fat in 100 kg was high significantly lower (P = 0,0017) only in Landrase breed.

Material and Methods

The aim of our experiment was evaluation of phenotype manifestation of various combinations of HAL gene's alleles. This manifestation was evaluated on selected rearing and slaughter indicators and on selected indicators of technological quality of meat in group of pigs of white meat breed.

Experiments were made at the station of fattening and carcass value in Nitra. Biological material was fatted and monitored during the period from 30 to 100 kg live weight. Pigs were slaughtered upon completion of test period and than slaughter indicators were evaluated. Indicators of physical and technological meat quality were assessed and evaluated in the biochemistry laboratory KŠZ SPU in Nitra.

In experiment were placed 151 pigs of white meat breed, 75 boars and 76 gilts. In Laboratory of Institute of Genetics and Animal Breeding of MZLU in Brno were made DNA analysis. Group of pigs was divided into three subgroups. First subgroup was created by 60 pigs of genotype (NN). Second subgroup of pigs was created by 76 pigs of genotype (Nn). Third group was created by 15 pigs of genotype (nn). These three subgroups was statistically interpreted and compared by two factorial analysis of dissipation.

Animals were slaughtered at the slaughter weight of 100 kg and carcass dissection was done. Indicators of carcass value and meat quality characteristics of these data evaluated under the current methodology.

Monitored subgroups of pigs:

Subgroup of NN genotype n.1	75
Subgroup of Nn genotype n. 2	76
Subgroup of nn genotype n. 3	15
Subgroup of boars	75
Subgroup of gilts	76

Monitored fattening indicators:

- average daily gain during the test (kg)
- average consumption of ME per 1 kg gain during the test in MJ

Monitored slaughter indicators and indicators of carcass dissection:

- proportional share of valuable meaty parts from weight of slaughter half (%)
- proportional share of weight of leg from weight of slaughter half (%)
- MLT in cm^2
- averaged thickness of back fat in cm

Monitored indicators of meat quality:

- pH1 – log molc. (H+) v MLT
- unbound water (%)
- color of meat at 520nm in MLT

Detecting of pH values

We used a portable battery acidometer IP-109 with the combined microcapillary electrode to measure the current values of acidity.

Unbound water

We used 50 ± 0,1 g of muscle from MLT since 24 to 48 hours from slaughter of pigs. Muscles were hung in special pockets of synthetic material in fridge at temperature of 4-6 °C. Weight loss was expressed in %.

Color of meat at 520 nm in MLT

We defined it using of movement Spekol – 11 with attachment R 45/0 at wavelength 520 nm. Color of meat was shown in % of remission.

Results

Average daily gain in rearing

All monitored group of hybrid pigs reached an average daily gain of 710.350 g with the variability of 10.455 %. Boars had average daily gain higher (730.850 g) with the variability of 10.022 %, and gilts had lower (690.120 g) with the variability 10.147 %. The highest average daily gain achieved genotype NN (726.700 g) with the variability of 11.049 %, the second highest gain had genotype of nn (706.670 g) with the variability of 9.784 %. Group of genotype Nn had the lowest average daily gain (698.170 g) with variability of 9.821 %. In the correlation interrelationship of monitored indicators were determined significant differences of ADG in rearing in g with feed days $r = -0{,}981^{++}$, with average consumption of feed mixture per 1 kg of gain in kg was $r = -0{,}345^{++}$ a with average consumption of metabolized energy per 1 kg of gain in kg was $r = -0{,}345^{++}$.

Average consumption of ME per 1 kg of average daily gain in rearing in MJ

Monitored group achieved consumption of metabolizable energy per 1 kg of ADG 34.403 MJ with the variability of 11.542 %. Boars had consumption of 34,376 MJ/kg metabolizable energy with the variability of 11,346 %, gilts had consuption higher (34,439 MJ/kg) with the variability of 11,281 %. Group 3. achieved consumption of metabolizable energy of 39,978 MJ/kg with variability of 13,552 %, group 2. (Nn) 40,004 MJ/kg with variability of 11,156 % and group of genotype NN 41,005 MJ/kg with variability of 11,533 %. In the correlation interrelationship of monitored indicators were determined significant differences of average consumption of metabolized energy per 1 kg of ADG in rearing with ADG $r = -0{,}345^{++}$, with feed days $r = 0{,}345^{++}$, with average consumption of metabolized energy per 1 kg of ADG in rearing $r = 1{,}000^{++}$, with average thickness of back fat $r = 0{,}242^{++}$, with MLT area in cm^2 $r = -0{,}248^{++}$.

Percentage proportional share of valuable meaty parts from weight of slaughter half in kilograms

Monitored groups of hybrid pigs had proportional share of valuable meaty parts of 48,292 % with variability of 5,839 %. Gilts reached a higher proportional share of valuable meaty parts of 48.470% with the variability of 6.158 % boars a slightly lower value of 48.112 % with the variability of 5.510 %. Group of genotype nn achieved the largest proportional share of valuable meaty parts of 50.924 % with the variability of 5.848 %, group of genotype Nn value of 48.286% with the variability of 6.188 % and group of genotype NN value of 47.643 % with the variability of 4.490%. In the correlation interrelationshipof monitored indicators were determined significant differences of percentage share of valuable meaty parts from weight of slaughter half in kilograms with MLT area in kg $r = 0{,}526^{++}$, with percentage share of weight of leg from weight of slaughter half in kg $r = 0{,}710^{++}$, with average thickness of back fat in cm $r = -0{,}550^{++}$, with average weight of back fat $r = -0{,}545^{++}$, with pH$_1$-log molc.(H$^+$) in MLT $r = -0{,}204^{+}$.

Percentage share of weight of leg from weight of slaughter half in kg

All followed a group of hybrid pigs reached share of weight of leg from weight of slaughter half of 19.612 % with the variability of 7.944 %. In boars the value was less (19.546 %) with the variability of 8.513 % and gilts had the value slightly larger than average (19.676 %) with the variability of 7.395 %. The order of genotypes was as follows: group of genotype NN 19.331 % with the variation of 5.587 %, group genotype Nn 19.538 % with the variability of 8.973 % and a group of genotype nn 21.112% with the variability of 6.453 %. In the correlation interrelationship of monitored indicators were determined significant differences of monitored indicator percentage share of weight of leg from weight of slaughter half in kg with percentage share of weight of valuable meaty parts from weight of slaughter half in kilograms r = $0,710^{++}$, with MLT area in cm^2 r = $0,435^{++}$ and with average weight of back fat in cm r = $-0,548^{++}$, with pH_1-log molc. (H^+) in MLT r = $-0,204^{+}$.

MLT area in cm^2

This indicator achieved value of 37.025 cm^2 in monitored group of hybrid pigs with the variability of 12.899 %. Gilts reached a higher value of that parameter (37.436 cm2) with the variability of 12.747 % and boars 36.608 cm^2 with variability of 13.046 %. The largest MLT area was in group of genotype nn (37, 580 cm^2) with the variability of 14.944 %, the group of genotype Nn achieved a lower value (37.483 cm^2) with variability of 12.045 % and group of genotype nn achieved the lowest value (36.305 cm^2) with the variability of 13.414 %. In the correlation interrelationship of monitored indicators were determined significant differences of MLT area in cm^2 with average consumption of feedstuff per 1 kg of ADG in rearing r = $-0,248^{++}$, with average consumption of metabolized energy per 1 kg of ADG in rearing r = $-0,248^{++}$, with percentage share of weight of valuable meaty parts from weight of slaughter half in kilograms r = $0,526^{++}$, with percentage share of weight of leg from weight of slaughter half in kg r = $0,435^{++}$, with average weight of back fat in kilograms r = $-0,309^{++}$ and with average thickness of back fat in cm r = $-0,332^{++}$.

Average thickness of back fat in cm

Monitored group of hybrid pigs achieved value of 2, 713 cm with variability of 14, 080 %. Gilts had a thickness of back fat 2, 724 cm with variability of 13,493 % a boars 2,702 cm with variability of 14,752%. Group of genotype NN had the most rough back fat (2,781 cm) with variability of 10,967 %, group of genotype Nn had thickness of back fat 2,719 cm and group of genotype nn had the thinnest bach fat (2,412 cm) with variability of 19,853 %. In the correlation interrelationship of monitored indicators were determined significant differences of monitored indicator average thickness of back fat in cm with average consumption of metabolized energy per 1 kg of ADG in rearing r= $0,242^{++}$, with average consumption of feedstuff per 1 kg of ADG in rearing r= $0,242^{++}$, with percentage share of weight of leg from weight of slaughter half in kg r= $-0,511^{++}$, with percentage share of weight of valuable meaty parts from weight of slaughter half in kilograms r = $-0,550^{++}$, with average weight of back fat in kilograms r = $0,643^{++}$ and with MLT area in cm^2 r = $-0,332^{++}$.

pH1-log molc.(H+) in MLT

Whole of monitored group of hybrid pigs achieved pH1 value of 6,115 in MLT with variability of 6,132 %. Boars achieved pH_1 value 6,138 in MLT with variability of 5,785 % a gilts 6,092 with variability of 6,500 %. Group of genotype NN reached pH_1 value of 6,328 in MLT with variability of 4,237 %, group of genotype Nn reached pH_1 value of 6,069 in MLT with variability of 5,271 % and group of genotype nn reached pH_1 value of 5,493 with variability of 3,534 %. In the correlation interrelationship of monitored indicators were determined significant differences of pH_1-log molc.(H^+) in MLT with percentage share of weight of valuable meaty parts from weight of slaughter half in kilograms r = $-0,263^{++}$, with percentage share of weight of leg from weight of slaughter half in kg r = $-0,204^{+}$, with unbound water r = $-0,566^{++}$ and with color of meat at 520 nm in MLT r = $-0,345^{++}$.

Unbound water

This indicator reached value of 6,954 in whole of monitored group of pigs with variability of 41,661 %. Gilts achieved the highest value (7,336) with variability of 37,888 % and boars value of 6,567 with variability of 45,380 %. Group of genotype nn had the largest unbound water (11,421) with variabilty of 16,266 %, group of genotype Nn had lower unbound water (7,544) with variability of 32,763 % and group of genotype NN had the lowest unbound water (6,344) with variability of 37,778 %. In the correlation interrelationship of monitored indicators were determined significant differences of unbound water with pH1-log molc.(H+) in MLT r = -0,566++ and with color of water at 520 nm in MLT r = 0,415++.

Color of meat at 520nm in MLT

In the monitored group reached the color of meat at 520 nm in the MLT value of 27.152% with the variability of 17.455 %. Boars reached lower value of the variable (26.999) with the variability of 15.616 % and gilts 27.302 with variability of 19.152 %. The 3rd group reached the greatest value (33.447) with the variability of 16.967 % and the 2nd group reached value of 27.789 with variability of 14.641 %. The 1st group reached value of 24.770 with the variability of 14.017 %. In the correlation interrelationship of monitored indicators were determined significant differences of color of water at 520 nm in MLT with pH1-log molc.(H+) in MLT r = -0,345++, with unbound water r = 0,415++.

The significance of differences between genotypes HAL gene, sex and their interactions in the production variables.

In indicator of average daily gains in rearing, we found out statistically significances differences between sexes of watched groups of pigs on level $P < 0.01$. We found out no statistically significances between genotypes of HAL gene. In interaction between genotypes and sexes were no statistically significances. Error trial was found out of

5091,792. We found out statistically significances at P < 0,05 in indicator of average consumption of metabolizable energy per 1kg of ADG in rearing between sexes. We also found out no statistically significances between genotypes of HAL gene. In interaction between genotypes a sex statistically significance was not found out. Error trial was found out of 21,045. In the experiment was found out no statistically significance between sexes in indicator of proportional share of valuable meaty parts from weight of slaughter half in kilograms. Between genotypes of HAL gene was found high statistically significances between groups nn and Nn genotypes of HAL gene on level of P < 0,05, between groups of genotype nn and Nn on level of P < 0,05 and between groups of genotype nn and genotype NN on level of P < 0,001. In interaction between genotypes a sex statistically significance was not found out. Error trial was found out of 7,269. In the indicator of proportional share of weight of leg from weight of slaughter half in kg, we discovered no statistically significances between sexes of pigs. Between nn and Nn genotypes of HAL gene we found high statistically significances on level of P< 0,001 and between nn and NN on level of P < 0,001. In the interaction between genotypes a sex statistically significance was not found out. Error trial was found out of 2,235. In indicator of MLT area in cm^2 were found out no statistically significances between sexes of monitored groups of pigs. We found out no highly significances differences between genotypes of HAL gene. In interaction between genotypes a sex statistically significance was not found out. Error trial was found out of 22,433. In the indicator of thickness of back fat in cm we found out no significances differences between sexes of monitored groups of pigs. Between genotypes of HAL gene was found high statistically significances between groups nn and Nn genotypes of HAL gene on level of P < 0,05 and between groups nn and NN on level of P < 0,01. In interaction between genotypes a sex statistically significance was not found out. Error trial was found out of 0,139. In the indicator of pH$_1$ - log molc.(H$^+$) in MLT we found out no statistically significances differences between sexes of monitored groups of pigs. Between genotypes of HAL gene was found high statistically significances between groups nn and Nn genotypes of HAL gene on level of P < 0,001, between groups nn and NN on level of P < 0,001 and groups Nn and NN on level of P < 0,001. In interaction between genotypes a sex statistically significance was not found out. Error trial was found out of 8,561E-02. We found out no statistically significances differences in the indicator of unbound water between sexes of monitored groups of hybrid pigs. Betweengenotypes of HAL gene was found high statistically significances between groups nn and Nn genotypes of HAL gene on level of P < 0,001, between groups nn and NN on level of P < 0,001 and between groups of Nn and NN on level of P < 0,001. In interaction between genotypes a sex statistically significance was not found out. Error trial was found out of 4,9. We found out no statistically significances differences in the indicator of color of meat at 520 nm in MLT between sexes of monitored groups of hybrid pigs. Between genotypes of HAL gene was found high statistically significances between groups nn and Nn genotypes of HAL gene on level of P < 0,001, between groups nn and NN on level of P < 0,001 and between groups of Nn and NN on level of P < 0,001. In interaction between genotypes a sex statistically significance was not found out.

Discussion

DVOŘÁK and TESAŘOVÁ found, that individuals from dominant homozygote NN x NN breeding had highest gain in contrast with individuals from crossbreeding nn x NN, which showed lower gain and lower thickness of back fat. Our results confirmed only lower thickness of back fat at heterozygote eventually in recessive homozygote of Large White. This result was in accorded with results of above-mentioned authors.

In contrast to WITTANN (1993) we did not find higher gain at HAL$^+$ animal, but higher percent of cenné mäsité časti was confirmed at HAL$^+$ animal in our experiment. We found that recessive homozygote nn has lower feed consumption, lower gain and lower average thickness of back fat that Nn and NN likewise as McPHEE (1994). MATTHES an SCHWETIN (1995) found lower gains and thickness of back fat at swine with nn genotype in Germany.

FISHER and MELLET (1997) observed in experiments 59 crossbreeds of L x LW. In period from 27 to 86 kg average daily gain and number of days until achievement of slaughter weight were found for genotype nn higher gain (756 g.day^{-1}) and by that less days required for achievement of slaughter weight in contrast with our results, where we recorded higher growth intensity at NN genotype. The result was not significant.

PARK (1998) achieved similar results as our experiment. They found that swine of nn genotype had significant lower gain than NN (by over 67 g) in experiment with 499 hugs and 196 brood sow of LW, L and D breed in Korea. Significant differences were between breeds in number of days needs for achievement weight 30 and 90 kg, where individuals of NN genotype achieved final weight rather by over 5,1 days than individuals of nn genotype.

Conclusion

From achieved results in experiment results that swine from dominant homozygote group reached slightly more values of fattening traits. Recessive homozygote achieved better results in butcher traits and together they presenting group with worse parameters of meat technological quality traits. It can be expression of swine higher stress sensibility. Heterozygote group from observed groups presenting average from all traits and we reached that conclusion based on the findings, that into rearing we should assign homozygote and also heterozygote with unchanged meat quality.

Results from this experiment showed, that recessive homozygote group achieved the best results in parameters of butcher traits whereas dominant homozygote and heterozygote achieved the best results in fattening traits and in meat traits quality meat. We could advised only dominant homozygote individuals for selection.

Next development of swine breeding in the Slovakia will go toward increasing economic efficiency and improving meat quality. We need to improve the quality of nutrition, to tighten selection and widen modern stabling technology and feeding all swine category.

Table 1. The single statistics of productive performance in BM pigs

Trait		**NN**	**Nn**	**nn**	**CS**	**Boars**	**Gilts**
	n	**60**	**76**	**15**	**151**	**75**	**76**
Average daily gain (g)	x	726,700	698,170	706,670	710,350	730,850	690,120
	s	80,292	68,566	69,139	74,270	73,243	70,027
	sx	10,366	7,865	17,852	6,044	8,457	8,033
	v%	11,049	9,821	9,784	10,455	10,022	10,147
MJ ME/Kg	x	41,005	40,004	39,978	40,399	39,404	41,382
	s	4,729	4,463	5,418	4,663	4,470	4,668
	sx	0,610	0,512	1,399	0,379	0,516	0,535
	v%	11,533	11,156	13,552	11,542	11,346	11,281
Valuable meat parts (%)	x	47,643	48,286	50,924	48,292	48,112	48,470
	s	2,139	2,988	2,978	2,820	2,651	2,985
	sx	0,276	0,343	0,769	0,230	0,306	0,342
	v%	4,490	6,188	5,848	5,839	5,510	6,158
Thigh portion (%)	x	19,331	19,538	21,112	19,612	19,546	19,676
	s	1,080	1,753	1,362	1,558	1,664	1,455
	sx	0,127	0,139	0,351	0,127	0,192	0,167
	v%	5,587	8,972	6,451	7,944	8,513	7,395
Longissimus muscle area (cm^2)	x	36,305	37,483	37,580	37,025	36,608	37,436
	s	4,870	4,515	5,616	4,776	4,776	4,772
	sx	0,629	0,518	1,450	0,389	0,551	0,547
	v%	13,414	12,045	14,944	12,899	13,046	12,747
Average backfat thickness (cm)	x	2,781	2,719	2,412	2,713	2,702	2,724
	s	0,305	0,393	0,479	0,382	0,399	0,368
	sx	0,039	0,045	0,124	0,031	0,056	0,042
	v%	10,967	14,454	19,859	14,080	14,752	13,493
pH1 – log molc. (H+) **v MLT**	x	6,328	6,069	5,493	6,115	6,138	6,092
	s	0,268	0,320	0,194	0,375	0,355	0,396
	sx	0,035	0,037	0,050	0,031	0,041	0,045
	v%	4,237	5,271	3,534	6,132	5,785	6,500
Colour of meat	x	24,770	27,789	33,447	27,152	26,999	27,302
	s	3,472	4,069	5,675	4,740	4,216	5,229
	sx	0,448	0,467	1,465	0,386	0,487	0,600
	v%	14,017	14,641	16,967	17,455	15,616	19,152
Free water (%)	x	5,090	7,544	11,421	6,954	6,567	7,336
	s	1,923	2,472	1,858	2,897	2,980	2,780
	sx	0,248	0,284	0,480	0,236	0,344	0,319
	v%	37,778	32,763	16,266	41,661	45,380	37,888

Table 2. Mean squares (MS) of two-factor analyses of fattening performance and carcass traits in BM pigs

Trait		**Gender** **A** $F_A = 1$	**Combina-tions of HAL gene's alleles** $F_B^{B} = 2$	**Interaction** **AB** $f_{AB} = 1$	**Error trial** **e** $f_e = 53$	**Statistical significance**
Average daily gain (g)	MS	50417,24	11583,174	1717,836	5091,792	
	F	9,902**	2,275	0,007		
MJ ME/Kg	MS	116,005	23,507	8,038	21,045	
	F	5,512*	1,117	0,382		
Thigh portion (%)	MS	0,218	19,35	0,395	2,235	0:1*** 0:2***
	F	0,097	8,656***	0,177		
Average backfat thickness (cm)	MS	4,416E-03	0,81	2,232E-02	0,139	0:1* 0:2**
	F	0,032	5,813**	0,16		
Longissimus muscle area (cm^2)	MS	72,807	22,996	47,673	22,433	
	F	3,246	1,025	2,125		
Valuable meat parts (%)	MS	0,378	64,76	3,396	7,269	0:1** 0:2***
	F	0,052	8,909***	0,453		
pH_1 -log molc. (H^+) v MLT	MS	2,243E-02	4,308	3,531E-03	8,561E-02	0:1*** 0:2*** 1:2***
	F	0,262	50,317***	0,041		
Free water (%)	MS	6,642	261,74	0,657	4,9	0:1*** 0:2*** 1:2***
	F	1,355	53,412***	0,134		
Colour meat	MS	1,193	481,352	12,132	16,409	0:1*** 0:2*** 1:2***
	F	0,073	29,335***	0,739		

Table 3. The correlations of fattening performance and carcass traits by BM pigs

Trait	1	4	5	7	8	9	10	11	12
Average daily gain (g)		++ -0,345	- 0,071	- 0,056	- 0,041	- -0,013	- 0,129	- -0,127	- -0,075
MJ ME/Kg	++ -0,345		- -0,078	++ 0,242	++ -0,248	- -0,121	- -0,094	- -0,009	- -0,018
Thigh portion (%)	- 0,071	- -0,078		- 0,050	++ 0,435	++ 0,710	+ -0,204	- 0,045	- 0,136
Average backfat thickness(cm)	- 0,056	++ 0,242	++ -0,511		++ -0,332	++ -0,550	- 0,050	- -0,064	- -0,084
Longissimus muscle area (cm^2)	- 0,041	++ -0,248	++ 0,435	++ -0,332		++ 0,526	- 0.022	- 0,009	- -0,091
Valuable meat parts (%)	- -0,013	- -0,121	++ 0,710	++ -0,550	++ 0,526		++ -0,263	- 0,102	- 0,094
pH_1 - log molc. (H^+)v MLT	- 0,129	- -0,094	+ -0,204	- -0,050	- 0,022	++ -0,263		++ -0,566	++ -0,345
Free water (%)	- -0,127	- 0,009	- 0,045	- -0,064	- 0,009	-0,102	++ -0,566		++ 0,415
Colour meat	- -0,075	- -0,018	- 0,136	- -0,084	- -0,091	- 0,094	++ -0,345	+ 0,415	

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