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GENETIC PARAMETERS OF CARCASS TRAITS IN PANNON WHITE RABBITS BASED ON COMPUTER TOMOGRAPHY AND TEST SLAUGHTER

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1.INTRODUCTION

In rabbit selection programmes there are three directions improving productivity Improving reproductive traits is important in the case of maternal lines, while improving growth rate and carcass and meat quality traits is important in the case of the paternal lines . For instance of the multi-purpose lines the aim of the selection for improving the total litter traits and growth traits together (Khalil and Saef, 2008). The most important carcass traits are the m. Longissimus Dorsi, thigh and fat, because these parameters significantly influence the carcass quality. But these carcass traits are hardly measured on live animals, so new technical tools such as ToBEC /Total Body Electrical Conductivity/, CT /Computer Tomography/) are involved in the selection work by researchers to improve the efficiency of the selection. The Pannon white is a sintetic breed, selected using by CT methodology from 1992. Selection based on in vivo CT measurements, decreasing the generation intervall through increasing the selection response of the examined traits. Although the heritability of thigh muscle weight determined by slaughter is high (0.57) (NAGY *et. al*.,2006b), while the heritability of thigh muscle volume determined by CT is low (0.19-0.21) (GYOVAI et al., 2008, 2012; NAGY *et al*. (2010). Favourable genetic correlation was found between the thigh muscle volume and the hind part to reference carcass% traits, reported by NAGY *et al*. (2010).

The aim of the present study is to analyse the genetic parameters of different carcass traits in 11 weeks old Pannon White rabbits in order to evaluate the efficiency of in vivo CT (Computer Tomography) measurements.

2.MATERIALS AND METHODS

The research was based on 316 records of 11 weeks old Pannon White rabbits. The animals were born and reared at the experimental rabbit farm of the Kaposvár University. Growing rabbits were housed in fattening cages (2-3 rabbits per cage). After weaning at 5 weeks of age all rabbits were fed *ad libitum* a commercial pellet and water was offered *ad libitum* from nipple drinkers. Animals were chosen random in order to represent the Pannon White population as much as possible. The CT scanning of the rabbits was performed at the Institute of Diagnostic Imaging and Radiation Oncology (Kaposvár University) using Siemens Sensation Cardiac CT. After the CT investigation rabbits were slaughtered at the average body weight of 2,82 kg and the dissection was performed according to WRSA recommendation (BLASCO and OUHAYOUN, 1996). The examined traits (total body volume determined by CT; muscle weight of the hind leg determined by dissection; muscle volume of the hind leg determined by CT; fat volume of the hind leg determined by CT; fat volume of the whole body determined by CT; muscle volume of the whole body determined by CT) were evaluated with the REML using bivariate models. The applied software was VCE 6 (Groeneveld et al., 2008).

Table 1: The considered factors for the examined traits

Factor	Level	Type of factor	Traits	
			hlm_sl (g)	all CT based
Animal	3418	A	x	x
Year-month	2	F	x	x
Sex	2	F	x	x
Body weight before slaughter	1	C	x	-
total body volume	1	C	-	x

F: fixed effects; A: additive genetic effects; R: random effect; C: covariant; hlm_sl = muscle weight of the hind leg determined by dissection

The examined traits were evaluated with the REML procedure in order to estimate heritability and genetic correlation coefficients. Because of the small dataset the genetic correlations were estimated with bivariate models.

The applied softwares were PEST (Groeneveld, 1990) (used only for data coding) and VCE 6 (Groeneveld et al., 2008). The applied linear model was:

$$y = Xb + Za + Wc + e$$

The model was:

$\mathbf{y} = \mathbf{Xb} + \mathbf{Za} + \mathbf{e}$

where $\mathbf{y}$ = vector of observations, $\mathbf{b}$ = vector of fixed effects, $\mathbf{a}$ = vector of random animal effects, $\mathbf{e}$ = vector of random residual effects, $\mathbf{X}$ and $\mathbf{Z}$ incidence matrices relating records to fixed and animal effects, respectively.

3.RESULTS AND DISCUSSION

Descriptive statistics for the CT measured and test slaughter data are shown in Table 2.

Table 2: Descriptive statistics of the examined traits

Trait	N	Mean	Standard deviation	Minimum	Maximum
bw (g)	316	2825	243	2284	3992
tvol_ct (cm^3)	316	2566	219	2145	3304
hlm_sl (g)	316	400	39.2	306	517
hlm_ct (cm^3)	316	422	40.3	319	539
hlf_ct (cm^3)	316	64.8	22.6	16	140
tf_ct (cm^3)	316	88.3	260	83	549
tm_ct (cm^3)	316	1557	140	1169	2036

tw = live body weight before slaughter; tvol_ct = total body volume determined by computer tomography; hlm_sl = muscle weight of the hind leg determined by dissection; hlm_ct = muscle volume of the hind leg determined by computer tomography; hlf_ct = fat volume of the hind leg determined by computer tomography; tf_ct = fat volume of the whole body determined by computer tomography; tm_ct = muscle volume of the whole body determined by computer tomography

Because the genetic correlations were estimated with bivariate models for all traits several heritability estimates were obtained. However, these estimates did not differ substantially, therefore only one stimate is presented for all traits.

The estimates of heritability and genetic correlation coefficients can be seen in Table 3.

Table 3: Estimate of heritability (diagonals) and genetic correlation (off-diagonals).

	hlm_sl (g)	hlm_ct (cm^3)	hlf_ct (cm^3)	tf_ct (cm^3)	tm_ct (cm^3)
hlm_sl (g)	0.44±0.11	0.94±0.07	-0.34±0.16	-0.13±0.17	0.16±0.22
hlm_ct (cm^3)		0.50±0.10	-0.59±0.13	-0.56±0.11	0.67±0.21
hlf_ct (cm^3)			0.58±0.11	0.96±0.02	-0.56±0.11
tf_ct (cm^3)				0.61±0.12	-0.96±0.03
tm_ct (cm^3)					0.28±0.10

tw = live body weight before slaughter; tvol_ct = total body volume determined by computer tomography; hlm_sl = muscle weight of the hind leg determined by dissection; hlm_ct = muscle volume of the hind leg determined by computer tomography; hlf_ct = fat volume of the hind leg determined by computer tomography; tf_ct = fat volume of the whole body determined by computer tomography; tm_ct = muscle volume of the whole body determined by computer tomography

As expected the examined traits had moderately high or high heritabilities. The fat related traits showed higher values compared to the muscle related traits. The heritability of the CT-based total body fat volume (cm^3) and the heritability of the CT-based hind leg fat volume (cm^3) showed higher values (0.61, 0.58) compared to the CT-based hind leg muscle volume (cm^3) (0.50) and total body muscle volume (cm^3) (0.28). NAGY *et al.* (2006b) reported higher values in the case of the heritability of the thigh muscle weight determined by slaughter, while GYOVAI et al., (2008, 2012) and Nagy *et al.*, (2010) reported lower heritability values of the thigh muscle volume determined by CT. The fat and muscle related traits showed negative genetic correlations as expected. Because of the small datasets the estimated standard errors were large especially for the estimated genetic correlations. This obtained values should be treated with caution. Nevertheless it could be noted that the fat and muscle related traits showed negative correlations as expected.

4.CONCLUSIONS

The weight and volume of the hind leg is basically the same trait thus the CT based selection currently performed at the Kaposvár University has high potential for improving the thigh muscle weight.

5.SUMMARY

The investigation was based on 316 records of 11 weeks old Pannon White rabbits. CT data and test slaughter results were analysed. The rabbits were reared at the experimental rabbit farm of Kaposvár University. CT scanning of the animals was carried out by using Siemens Sensation Cardiac CT. The rabbits were slaughtered at 11 weeks of age at the average body weight of 2.82 kg. The main traits that were obtained in the analysis were the following: total body volume determined by CT (tvol_ct, cm^3), muscle volume of the whole body determined by CT (tm_ct, cm^3), fat volume of the whole body determined by CT (tf_ct, cm^3**)**, muscle volume of the hind legs determined by CT (hlm_ct, cm^3), fat

volume of the hind legs determined by CT (hlf_ct, cm^3); live body weight before slaughter (bw, g), weight of hind legs (hl_sl, g). The examined traits were evaluated with the REML using bivariate models, contained year-month and sex as fixed effects and body weight before slaughter and total body volume as covariates. The applied softwares were PEST (GROENEVELD, 1990) (used only for data coding) and VCE 6 (GROENEVELD, 2008). The heritability of the tf_ct and the heritability of the hlf_ct were higher (0.61, 0.58), compared to the hlm_ct (0.50) and the tm_ct (0.28), respectively. The fat and muscle related traits showed negative genetic correlations: between hlf_ct and hlm_ct was negative and high (-0.59); between tf_ct and tm_ct was negative and high (-0.96); between hlm_sl and hlf_ct was negative and moderate (-0.34), respectively. Most of the examined traits had moderately high or high heritabilities. The fat related traits showed higher values compared to the muscle related traits. Because of the small datasets the estimated standard errors were large especially for the estimated genetic correlations. Thus the obtained values should be treated with some caution.

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