



Estimating dominance effects and inbreeding depression of carcass traits in Pannon White rabbits

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ABSTRACT

Authors analyzed the slaughter records of 527 Pannon White rabbits. These records were collected in the course of three experimental slaughters conducted in 2013, 2014 and 2015, respectively. The examined traits were: weight of thigh fillet (THIGHW), dressing out percentage (DoP) (calculated as the ratio of the chilled carcass weight and live body weight at slaughter), hind part percentage (HIND%) (compared to the reference carcass) and weight of perirenal fat (FATW). Genetic parameters were estimated using basic and extended (with dominance effects) single trait animal models using the REML procedure. Inbreeding depressions for the examined traits were determined by the BLUP procedure. Applying the basic model, heritability estimates were moderate for THIGHW (0.18 ± 0.07), DoP (0.19 ± 0.06) and for HIND% (0.23 ± 0.07). On the contrary, high heritability was estimated for FATW (0.68 ± 0.08). Extending the models with dominance effects the heritabilities did not change except for FATW (0.59 ± 0.16). According to these results the estimated dominance effects were practically zero for THIGHW, DoP and HIND% and moderate for FATW (0.16 ± 0.06). Concerning inbreeding depression 10% increase of the inbreeding coefficient resulted in severe decrease (-24.4 g) for THIGHW. DoP and HIND% were less sensitive for inbreeding depression (-0.06% and -0.02%). On the contrary, similarly to THIGHW, FATW showed substantial inbreeding depression (-2.88 g). Presenting inbreeding depressions as the percentages of the mean values of THIGHW, DoP, HIND% and FATW, the received values were 6.2%, 9.8%, 5.2% and 17.1%, so the largest depression was observed for FATW.

Keywords: slaughter traits, genetic parameters, inbreeding depression

INTRODUCTION

Rabbit meat is considered as a high-quality meat due to its favorable properties (low fat- and cholesterol, high protein - and polyunsaturated fatty acid (PUFA) content). The world's rabbit meat production has an increasing trend, and the annual output is about 1.400.000 tons. One element for improving the quality and keeping the growing production level is an indirect selection of the carcass traits. The indirect selection is based on the performances of the progeny and the collaterals, so it cannot spread in practice. In the 1980's Szendrő *et al.* (1988) reported their progeny test experiences, so, it is subservient to use indirect selection to improve the carcass traits. The University of Kaposvár had been using this type of selection since 1990, based on Computer Tomography (CT) measurements. Szendrő *et al.* (2015 a, 2015 b) summarized this worldwide unique selection method and their 25 years experience in breeding. Thus, the

first goal of the selection is improving the slaughter output, with the continuous genetic evaluation of the measured traits by Comuter Tomography. The performances of the rabbits are evaluated with sample slaughters at the University of Kaposvár's experimental farm. During the last 12 years, selection was based on the estimated BLUP (Henderson, 1975) breeding values for the selection criteria traits. Although the favorable properties of BLUP methodology are well known for a long time (Kennedy et al., 1988) one side effect of BLUP based selection can be that the inbreeding level of the selected population can quickly be increased (Kristensen and Sorensen, 2005). Another interesting issue is that although BLUP selection has been applied in rabbit breeding for decades generally the so-called simplified models are applied which means that genetic effects are limited to additive genetic effects and non-additive genetic effects are ignored. The main reason for this phenomenon is that including dominance effects in animal models requires large computing capacity and a large proportion of full sibs (Miształ, 2001). Based on these facts, the purpose of this study is, to estimate the genetic parameters of the carcass traits due to the sample slaughters in the past few years and examining the inbreeding depression. The resulting parameters can be interfered with indirect selection work and the pairing system used to improve the efficiency of the slaughter performance.

MATERIAL AND METHODS

The analysis was conducted in 2013, 2014 and 2015. In these years, we choose 180 growing rabbits annually in April from the Pannon White breed on the experimental farm of the University. The rabbits were slaughtered in the Olivia Inc. slaughterhouse (Lajosmizse) and the carcasses were dissected according to the World Rabbit Science Association (WRSA) recommendations as described by *Blasco és Ouhayoun* (1996). The examined traits were as follows: weight of the hind leg meat (THIGHW), dressing out percentage (DoP%) (chilled carcass yield/slaughter weight*100), the hind part ratio (HIND%) (compared to the reference carcass) and the weight of the perirenal fat (FATW). We present the measured statistical characteristics in *Table 1*. Due to the fact, that we had several data losses from different kinds of reasons, we evaluated 527 carcass data of the growing rabbits.

Table 1.

Descriptive statistics of the analyzed traits

Trait	Number of records	Minimum	Maximum	Mean	SD
CC (g)	527	1329	2223	1741	153
THIGH (g)	527	289	517	396	38.6
DoP% (%)	527	53.6	66.5	61.5	1.66
HIND% (%)	527	35.4	45.4	38.8	1.23
FATW (g)	527	3	44	16.8	6.93

CC: Chilled carcass; THIGHW: weight of thigh fillet; DoP%: dressing out percentage; HIND%: Ratio of hind part compared to the reference carcass; FATW: weight of perirenal fat

There were 3828 individuals in the total pedigree of the animals. Because of the small number of records, we examined the characteristics with a single trait model according to REML method, using the VCE6 software (Groeneveld et al., 2008).

To determine the inbreeding coefficient we used the PEDIG software (Boichard, 2007). The structure of the applied model was the following:

$$y = Xb + Za + e$$

Where: y = vector of observations, b = vector of the environmental effects, a = vector of the additive genetic effect. X and Z , in this order: environmental effects, occurrence matrix of the additive genetic effect. The supplemented models estimated the amount of the dominance effects, so we added a Wd component to the model (d = vector of the dominating effects). The characteristics of the applied animal model are given in Table 2.

Table 2. Structure of the applied animal models

Factor	Type	Levels
Animal effect	Random	3828
Sex	Fixed	2
Chilled carcass (CC)	Covariate	1
Year-month (of slaughter)	Fixed	3
Inbreeding coefficient (F)	Covariate	1
Family variance	Random	396970

Chilled carcass (CC); F: inbreeding coefficient

For the dressing out percentage and the ratio of the hind part traits, the chilled carcass (as a covariant) was not included in the animal model.

RESULTS AND DISCUSSION

The estimated heritability values (h^2) and the amount of the dominating effects (d^2) for the traits are in Table 3.

Table 3. Estimated genetic parameters of the analyzed traits

Trait	h^2 (base model)	h^2 (supplemented model)	d^2 (supplemented model)
THIGHW (g)	0.18±0.07	0.18±0.09	0.003±0.005
DoP% (%)	0.19±0.06	0.19±0.08	0.012±0.011
HIND% (%)	0.23±0.07	0.23±0.07	0.019±0.016
FATW (g)	0.68±0.07	0.59±0.16	0.16±0.06

THIGHW: weight of thigh fillet; DoP%: dressing out percentage; HIND%: ratio of hind part compared to the reference carcass; FATW: weight of perirenal fat

Only the perirenal fat showed significant h^2 value and meaningful dominance effect from the examined traits (Table 3). Similarly to this finding Garreau et al. (2008) and Larzul et al. (2005) also reported high heritability (0.64 and 0.64) for perirenal fat weight analyzing French rabbit populations. For the other traits, the heritability values were moderate, while the estimated dominance effects were statistically zero. According to previous slaughters in the same breed, Nagy et al. (2006) got similar results to the

current range (0.20-0.57) to heritability, but in that study, the weight of the hind leg meat showed the highest heritability value (0.57 ± 0.11). In connection to the results, it should be noted, that the amount of the rated database was under 1000 in both cases, so the values have to be treated with reservations, especially to dominance effects French and Belgian authors *Larzul et al.* (2005) and *Varewyck et al.* (1986) reported about higher heritability values for the dressing out percentage (0.55 and 0.70). Concerning the influence of dominance for carcass traits unfortunately no similar studies are available to compare our results. *Table 4* shows the amount of the inbreeding depression for the traits.

Table 4.

**Estimated inbreeding depression of the analyzed traits
(per 10% increase of the inbreeding coefficient)**

Trait	Inbreeding depression
THIGHW (g)	-24.4
DoP% (%)	-0.06
HIND% (%)	-0.02
FATW (g)	-2.88

THIGHW: Weight of hind leg meat; DoP%: Dressing out percentage; HIND%: Ratio of hind part to reference carcass; FATW: Weight of perirenal fat

Because of the closed population structure and the relatively small number of the Pannon white rabbits, it represents increasing inbreeding, nevertheless *Szendrő et al.* (2015b) and *Nagy et al.* (2010) reported about a slight inbreeding coefficient (5.5%) in does and bucks which were born in 2007, thanks to the pairing system. In this study, the mean of the inbreeding coefficient was 10.2% individually. Although this value is significant, the continuous selection can decrease its negative effects. According to the results of *Table 4.*, the possible pairing should consider inbreeding especially to hind leg meat. Contrary to our findings in a similar study carried out analyzing the Pannon Large rabbit population *Nagy et al.* (2013) reported significant inbreeding depression for average daily gain (-0.57 g/10% increase of inbreeding coefficients) while no inbreeding depression was found concerning thigh muscle volume. Regarding inbreeding depression, it also has to be considered that fast inbreeding especially when done repeatedly is much more harmful than the slow increase of the population's inbreeding level. *Chai et al.* (1969) performed close inbreeding reaching an average inbreeding coefficient of 80% so the substantial inbreeding depression obtained for body weight at the age of 10 weeks is not surprising. However, in real animal breeding programs, this kind of mating schedule is simply not applied. *Ferraz et al.* (1992) studied a rabbit population where the level of average inbreeding was about the same as in our case and similarly to *Chai et al.* (1969) they also reported substantial inbreeding depression for 10-week old body weight. Generally, carcass traits are not liable to inbreeding depression due to the lack of dominance effects. Looking the results in *Tables 3. and 4.* it is clear that among the analyzed traits the magnitude of the dominance effects was the only substantial for the weight of the perirenal fat, so it is not surprising that compared to the phenotypic means of the trait the highest inbreeding depression was also observed for this trait.

CONCLUSIONS

The Pannon white breed is suitable for the sequence of CT selection, due to its carcass properties and genetic parameters. It is also capable of improving these traits in the future. The traits- except for the perirenal fat- were not influenced by the dominance effects. The pairing should be optimized making possible maximizing genetic response while maintaining inbreeding applying Gencont software (*Dagnachew and Meuwissen, 2014*).

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