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CROSSBREEDING EFFECTS ON CARCASS TRAITS AT 12 WEEKS OF AGE IN PANNON AND DANISH WHITE RABBITS AND THEIR RECIPROCAL CROSSES

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ABSTRACT

Carcass traits of 105 growing rabbits, which consists of 57 straightbred and 48 crossbred, produced from two purebreds (Pannon White, PW and Danish White, DW) as well as their reciprocal crosses were compared. The experiment was carried out at the rabbit farm of the University of Kaposvar. The aim of the study was to evaluate the crossbreeding effects (i.e. direct, maternal additive and heterotic effect) for carcass traits of rabbits slaughtered at 12 weeks of age. Dressing out percentage based on the ratio of hot carcass (with head, liver, kidneys, heart, lungs, perirenal fat) weight to live weight after 24-hour fasting of PW, DW, PW x DW and DW x PW were: 58.0, 55.9, 58.5 and 57.5%, respectively. Tests of significance revealed that breed group (BG) and sex (S) had no effect on the majority of the carcass traits except on slaughter weight ($P \leq 0.01$). No significant differences were found in BG x S interaction for all traits. Breed of sire (SB) and dam (DB) had no influence on all carcass traits investigated except that for SB on the percentage of the head. However, SB x DB had significant effect only on the perirenal fat ($P \leq 0.05$). Direct heterosis was significant ($P \leq 0.05$) for perirenal fat, which was negatively signed. Direct and maternal additive effects were almost insignificant on carcass traits disregarding direct additive effect on the percentage of gastrointestinal tract and the head and on dressing out percentage (in favour of PW; $P \leq 0.05$); as well as the maternal effect ($P \leq 0.05$) on (kidneys + heart + lungs) in favor of DW. Examining crossbreeding results it could be recommended that the offspring of PW bucks and DW does the dressing out percentage and the total edible parts improved, while the percentage of perirenal and scapular fat decreased compared to purebred rabbits.

Key words: rabbits, carcass traits, heterosis, direct and maternal additive effect.

INTRODUCTION

The main purpose of crossing is to improve carcass traits and to combine different characteristics which are advantageous in the crossed breeds (i.e. complementarities) WILLHAM and POLLAK (1985). Diversity generated among breeds may result in greater non-additive genetic activity in crosses originating from breeds selected for different criteria. Non-additive genetic effect is an important factor in meat production, due to the opportunities to combine stocks that complement each other or interact favourably. This allows development of mating combinations for rapid growth and other important economic traits (MARKS, 1995). This made possible to estimate the crossbreeding parameters, which have a great importance for modern poultry breeding. The question is that this non-linearity how can be can be approximated by linear models and what extent. Furthermore, the linear model adopted for the estimation of the genetic group does not contain the genotype x environment interaction, which might be important as well. Dickerson models also do not contemplate the various kinds of epistatic effects as a part from the non-additive genetic effects. All these motives forced us to conclude that these considerations must be in mind in subsequent analyses devoted for estimating unbiased crossbreeding effects.

The aim of the present study was to estimate crossbreeding effects (i.e. breed group, direct and maternal additive effect and direct heterosis) as well as some non-genetic effects (sex and breed group x sex interactions) on carcass traits of two European rabbit breeds (Pannon White and Danish White) slaughtered at 12 weeks of age.

MATERIAL AND METHODS

This experiment was carried out at the rabbit farm of the University of Kaposvar with Pannon White (PW) and Danish White (DW) rabbits. The selection program of PW launched in 1988. Priorities of selection are the weight gain and the carcass traits (SZENDRŐ *et al.*, 1998). The performance of DW has been followed since 1994 (JENSEN, 1983). The main emphasis of selection is placed on the improvement of growth rate and vitality. Rabbits were housed in closed buildings in flat deck wire-mesh cages. Ventilation was provided through windows, at both long sides of the rabbit house, which was complemented with ventilators when required. Commercial pellet (10.3 MJ DE/kg, crude protein: 17.5%, crude fat: 3.6%, crude fibre: 12.5%) was fed *ad lib*. Drinking water was available continuously from nipples.

Does were inseminated artificially using fresh, diluted sperm parallel to GnRH treatment. Does were mated first at 18 weeks of age and regularly on the 11th day after parturition. Suckling rabbits were weaned at 5 weeks of age and they were slaughtered at 12 weeks of age after 24h fasting from feeds only. Carcass data were obtained on a total number of 105 growing rabbits of straightbred (57) and crossbred (48), originated from two purebreds (Pannon White /PW/ which was selected for daily weight gain and carcass traits and Danish White /DW/ which was selected for improving growth rate and vitality) as well as their reciprocal crosses. Rabbits of each breed groups were chosen randomly, (47 PW x PW; 10 DW x DW; 8 PW x DW and 40 DW x PW) from the experimental animals. Rabbits were slaughtered and dissected according to the method of BLASCO *et al.* (1993). Body weight before and after fasting, blood, head, offals (full gastrointestinal tract), liver, giblets, kidneys, heart, lungs, perirenal fat, scapular fat, carcass (hot carcass with head), fore-, intermediate- and hind-parts of carcass were measured. Dressing out percentage was calculated as carcass/live weight x 100.

Mixed model Least Squares and Maximum Likelihood Computer Program PC version 2, LSMLMW (HARVEY, 1990) was used for analyzing the data. Significance levels are reported at the $P \leq 0.05$ and $P \leq 0.01$ levels. The linear fixed model adopted for the analysis included the effects of breed groups, BG (4 classes); sex (males and females); as well as the interactions between BG x S. Parts of the carcass were taken in the model as a percentage to body weight after fasting. The basic form of the general linear mathematical model is:

$$Y = X\text{ß} + e$$

Where;

Y = an observational column vector of body weight records.

X = Incidence matrix of zeros and ones which relating records to the appropriate fixed effects for a given trait i.

ß = the vector of unknown fixed effects and for trait i.

e = The vector of random residual effect for trait i.

Crossbreeding effects (direct additive G^i; Additive maternal G^m; direct heterotic H^i effects) on different traits were derived applying a selected set of linear contrasts on breed groups' least squares means (DICKERSON, 1992).

Genetic parameter	Genotypes†				Divisor
	Straightbreds		Crossbreds		
	PW x PW	DW x DW	PW x DW	DW x PW	
Straightbred difference	1	-1	0	0	1
Direct heterosis	-1	-1	1	1	2
Direct additive	1	-1	1	-1	1
Maternal additive	0	0	-1	1	1

† Sire strain is denoted first and dam strain second.

PW = Pannon White and DW = Danish White.

The previous contrast statements quantify differences attributable to the aforementioned effects as follows:

The method of least squares analysis (i.e. using the residual error mean squares) was used for parameter estimation. In a general form, the expected Dickerson model value can be written for any genetic group as follows (WOLF *et al.* 1995):

$$\breve{G} = \mu + (\alpha_1 - \alpha_2)\, g + \delta_{12} h + (\alpha_1^M - \alpha_2^M)\, a^M$$

Where:

G = Least squares mean of the given genetic group G;

μ = General Least squares mean ("genetic background", reference value for remaining genetic effects);

α_i = proportion of genes in G from the ith source population (I = 1, 2);

g = direct additive effect (sire breed difference);

δ_{ij} = probability that at a randomly chosen locus of a randomly chosen individual of G one allele is from the ith (jth) source population and the other is from the jth (ith) source population (i,j = 1,2 and i < j);

h = direct heterotic effect and it includes part of the additive X additive interaction as well (WOLF *et al.* 1995);

α_i^M = proportion of genes in the dam population of G from the ith source population (i = 1, 2);

a^M = additive maternal effect

RESULTS AND DISCUSSION

Breed group (BG):

The variation among rabbit breeds and crossbreeding combinations of different origin for carcass traits is evident (RAO *et al.,* 1978; LUKEFAHR *et al.,* 1982; LUKEFAHR *et al.,* 1983; LOPEZ *et al.,* 1990; SZENDRO *et al.,* 1994). Least-squares means and standard errors for different carcass traits given in the percentage of the live weight are given in Table 1. Dressing out percentage of PW, DW, PW x DW and DW x PW were 58.0, 55.9, 58.5 and 57.5%, respectively (Table 1). BG had significant effect only on the percentage of blood ($P \leq 0.01$; Table 3). However, values of carcass traits are difficult to be compared objectively with those reported in literature because of the different initial weights, breeds, methods of slaughter and evaluations as well as the statistical model adopted. Dressing out percentage of PW x DW crosses was the highest, while the DW purebred was the lowest one (Table 1). However, these differences were statistically negligible at most cases. These results may indicate that crosses sired by PW were somewhat more valuable.

Breed group-Sex interactions:

The breed group x sex interactions were not significant (Table 3). These results may mean that it is correct to discuss the effects of sex or breed group on carcass traits separately.

Straightbred differences:

Results of Table 2 show that some carcass traits (percentage of head, hind part and dressing out percentage) of DW rabbits were statistically inferior ($P \leq 0.05$ or $P \leq 0.01$) to PW rabbits. The trend was generally reversed in favour of DW rabbits in case of blood and full gastrointestinal tract ($P \leq 0.05$ or $P \leq 0.01$). Similar results were reported by SZENDRŐ *et al.* (1989). These relatively low and insignificant differences between the two breeds could be explained by the environmental circumstances and feeding regime applied which could influence the ability of the selected breeds. The higher dressing out percentage of PW rabbits is related to the selection based on computerised tomography (SZENDRŐ *et al.*, 2004).

Heterotic effect (H^I):

Estimates of direct heterotic effect (H^I) calculated for carcass traits (%) are presented in Table 2. The examined traits showed generally insignificant direct heterosis except on perirenal fat when H^I was significantly negative ($P \leq 0.05$). LUKEFAHR *et al.* (1983) confirmed our results that proportion of fore and hind parts differed slightly between straightbreds and crossbreds. Results reported herein revealed that crossbreeding is associated with negative effect or has a little importance. Therefore, it is not expected to improve carcass traits through crossing the two considered breeds. Heterosis or hybrid vigour for a certain trait does exist when the average performance of crossbred progeny is superior to the average performance of the two parents. This means that the magnitude of non-additive (mainly dominance) is comparatively substantial. The amount of heterosis can vary practically, depending on the environment and on the populations being crossed. Theoretically, the magnitude of heterosis is inversely related to the degree of genetic resemblance between parental populations (Willham and Pollak, 1985) and it is expected to be proportional to the degree of heterozygosity of the crosses (Sheridan, 1981; Hill, 1982). However, negative direct heterosis, if any, might be attributable to directional dominance of genes affecting these traits. In this respect, Falconer (1989) showed that a cross between two base populations would show heterosis if they differ in the frequency of genes affecting a given trait. The same author also added that the negative sign of heterosis could be attributed in some cases to the nature of the measurement (i. e. if the trait is expressed in another way such as the reciprocal of the present the heterosis would be positive in sign) and may be also due the size of dataset.

Table 1. Least squares means and standard errors (± SE) for carcass traits as percentage of live weight.

	Breed group (BG)				**Sex (S)**	
Traits	**DW x DW**	**DW x PW**	**PW x DW**	**PW x PW**	**Male**	**Female**
No. of rabbits	10	40	8	47	56	49
Live weight. (g)	2749±72	2717±33	2677±76	2709±30	2693±39	2734±41
Blood %	8.6±0.7	7.0±0.3	5.9±0.7	6.3±0.3	6.8±0.4	7.1±0.4
Full int. %	15.8±0.7	14.4±0.7	14.5±0.3	14.3±0.3	14.7±0.4	14.9±0.4
Head %	4.8±0.2	5.0±0.1	5.2±0.1	5.1±0.1	5.1±0.1	4.9±0.1
Liver %	2.9±0.1	2.8±0.1	2.9±01	2.7±0.0	2.8±0.5	2.9±0.1
Kidneys + Heart +Lungs	4.6±0.2	4.4±0.1	4.8±0.2	4.3±0.1	4.5±0.1	4.5±0.1
Perirenal fat %	0.84±0.1	0.70±0.1	0.53±0.1	0.80±0.0	0.80±0.1	0.80±0.1
Scapular fat %	0.30±0.1	0.27±0.0	0.20±0.1	0.22±0.0	0.22±0.0	0.27±0.0
Fore part %	14.9±0.0	15.1±0.0	15.4±0.0	15.5±0.2	15.3±0.2	15.2±0.3
Intermediate part %	14.4±0.3	15.0±0.1	14.9±0.3	15.0±0.1	14.7±0.2	15.0±0.2
Hind part %	17.2±0.4	17.9±0.2	18.3±0.4	18.0±0.2	17.9±0.2	17.8±0.2
Dressing out percentage %	55.9±0.8	57.5±0.4	58.5±0.9	58.0±0.4	57.6±0.5	57.3±0.5

PW = Pannon White and DW = Danish White.

Direct additive effect (G^i):

Crossing does not only take advantage of traits with considerable non-additive genetic variations (i.e. dominance and epistasis), but also exploits differences in additive effects (i.e. differences in average performance between populations as a deviation from the overall mean) between populations (Ahmed, 2003). On the level of loci responsible for a given trait, complementarity between additive effect of genes occupying these loci play an important role in the manifestation of G^i. Contrasts of G^i on edible parts of carcass traits studied were negative and therefore in favour of PW, except that for liver, scapular and perirenal fat. However, most of these differences were insignificant.

Table 2. Crossbreeding genetic effects (Linear function ± S.E) for carcass traits.

Traits	Breed differences	Direct heterosis (H_{F1})		Direct additive effect	Maternal effect
	DW vs. PW	Units	%	DW vs. PW	DW vs. PW
Live body wt.	39.8±78.0	-32.7±56.9	-1.19	39.8±56.9	-39.7±83.0
Blood %	2.38±.72**	-0.96±0.52	-13.42	1.79±0.53**	-1.21±0.75
Full int.%	1.48±0.71*	-0.59±0.52	-3.98	0.70±0.51	0.09±0.75
Head %	-0.34±0.14*	0.14±0.10	3.03	-0.26±0.10*	0.18±0.14
Liver %	0.23±0.12	0.06±0.09	1.79	0.05±0.09	0.12±0.13
Kidneys + Heart + Lungs%	0.03±0.07	0.06±0.05	3.37	-0.01±0.12	0.29±0.17*
Perirenal fat %	0.05±0.12	-0.21±0.09*	-25.00	0.11±0.09	-0.18±0.13
Scapular fat %	0.08±0.06	-0.03±0.04	-9.62	0.07±0.04	-0.07±0.06
Fore- part %	-0.62±0.49	-0.01±0.36	0.33	-0.44±0.36	0.26±0.52
Interm.part %	-0.58±0.32	0.23±0.24	1.70	-0.25±0.24	-0.09±0.34
Hind-part %	-0.88±0.42*	0.49±0.31	2.84	-0.61±0.31	0.34±0.45
Dressing out percentage %	-2.10±0.92*	1.04±0.66	1.84	-1.54±0.66*	0.98±0.96

* = P ≤ 0.05; ** = P ≤ 0.01; Full int. = Full intestine; PW = Pannon White and DW = Danish White.

It could be concluded that these relatively low and insignificant differences between the selected population could be due to the previous selection for body weight and growth rate.

Table 3. F-ratio of least squares analysis of variance of factors affecting percentages of carcass traits.

S. O. V.	df	Live body wt.	Blood	Full int.	Head	Liver	Kidneys + Heart + Lungs	Perirenal fat	Scapular fat	Fore-part	Int.part	Hind-part	Dressing %
BG	3	0.17	4.60**	1.48	0.36	2.31	1.36	2.17	1.22	1.09	1.11	1.63	2.13
SB	1	1.05	1.27	1.76	6.85*	0.39	1.20	1.56	2.32	0.75	1.19	2.35	3.50
DB	1	0.97	0.38	2.39	26.6	3.69	3.72	0.99	0.01	0.37	0.99	0.65	0.46
SB x DB	1	3.12	0.67	1.34	1.46	0.48	1.08	5.26*	0.19	0.12	0.91	1.27	1.30
Sex (S)	1	0.51	0.33	0.19	0.41	0.33	2.33	2.21	1.70	0.18	1.74	0.12	0.14
BG x S	3	0.35	0.73	0.73	0.1	2.24	0.68	1.16	0.44	0.49	2.13	0.46	0.95
Remindar M. S.	97	43400.65	3.72	3.58	0.13	0.11	0.04	0.10	0.02	1.72	0.77	1.31	5.87

BG = Breed groups; SB = Sire-breed; DB = Dam-breed; Full int. = Full intestine; * = P ≤ 0.05 and ** = P ≤ 0.01.

Maternal additive effect (G^m):

Maternal effect (G^m) consists mainly from additive maternal and cytoplasmic-inheritance. However, the maternal effect herein is conceivably confounded with the reciprocal effect (i.e. sex linkage) since it is determined as the difference between the two reciprocal crosses. Sex linkage as an effect, is due to additive effects of the genes concerned with the trait and carried on the sex chromosomes. Denoting G^m in terms of complementarity effect, certain crosses may show much more G^m than others depending upon the extent to which the crossed populations differ in reproductive performance and in production characters. Therefore, this type of effect rely on the direction of the crossing (AHMED, 2003). In the scope of the present data, results in Table 2 demonstrated that effect of G^m on all carcass traits was not significant, except on kidneys + heart + lungs ($P \leq 0.05$). However, no trend could be detected for the effect of G^m on the carcass traits studied. These results may lead us to assume that both rabbit breeds of the present study could be used as a dam-line. In other words, the two selected populations of rabbit breeds do not complement each other or aggregate the responsible genes, regarding maternal effect and reproductive efficiency of the studied traits.

There was no evidence of positive heterosis, and maternal effects were negligible due to crossing between PW and DW rabbits for the examined carcass traits. The two selected breeds do not seem to complement each other or aggregate the responsible genes, regarding direct and maternal additive effects of the studied traits. This relatively low and non significant differences between the selected population of rabbit breeds could be due to the previous selection of body weight and growth rate they have been subjected for.

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