CONNECTION BETWEEN GLUTATHIONE PEROXIDASE ACTIVITY AND CARCASS TRAITS IN RABBITS

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Abstract - Relationship between glutathione-peroxidase activity of blood plasma, red blood cell haemolysates and 10.000 g supernatant fraction of liver homogenate and some carcass traits of rabbits was investigated. The carcass traits were estimated by CT method and determined after slaughtering.
The correlation between the above mentioned parameters was different depending on the tissue where the enzyme activity was measured. The results also suggest that the selection, oriented to the improvement of dressing traits, as genetic effect could independently influence the dressing traits and glutathione-peroxidase activity.

INTRODUCTION

Slaughter percentage is one of the most important trait of meat rabbit put on the market. Its heritability is considerable high, however, techniques to measure this trait are either destructive (i.e. the evaluated animal can not be used for breeding any more) or expensive (e.g. computer tomography), so any different solution would be preferable.
Glutathione peroxidase is a selenium dependent enzyme (ROTRUCK et al, 1973) which is of major importance for protection of tissues against oxidative damage.
A genetic variation in glutathione-peroxidase activity has been suspected previously in pigs (STOWE and MILLER, 1985), and chicken (CUNNINGHAM et al, 1987). A slight correlation between glutathione-peroxidase acitivity and growth rate was also reported in the case of chicks (LA VORGNA and COMBS, 1982) and pigs (LINGAAS et al, 1991).
Previous investigations of our group directed to the glutathione-peroxidase (GSHPx) enzyme activity as a possible selection marker for rabbit breeding demonstrated slight negative phenotypic correlation between dressing percentage and enzyme activity of erythrocytes in New Zealand White (NZW) rabbits (MEZES et al., 1994).
The purpose of present study was to give further and more detailed data on the relationship between enzyme activities and dressing traits. It was to provide evidence that the demonstration of phenotypic relationship was also possible in the case of Pannon White (PW) rabbits, which represents another breed.

MATERIAL AND METHODS

Experimental animals

Pannon White bucks were selected on the basis of their average L-value-average surface of the m. longissimus dorsi between the 2nd and 3rd, and 4th and 5th lumbal vertebrae detected and measured by CT (SZENDRÓ et al, 1992) - as minus (lowest) and plus (highest) ones. These were applied at insemination of randomly chosen does of the same breed. Among the male progenies the selection was repeated to obtain a second generation of plus bucks. The method of selection is described by SZENDRÓ et al (1996). Number of progenies born at the same time from minus sel, plus$_1$ sel and plus$_2$ sel bucks mated to randomly chosen does can be seen in Table 1.
Broilers were slaughtered after 24 hours fasting and measured for dressing traits using the method proposed by BLASCO et al. (1993) at body weight between 2780 and 2785 grams.
Blood and liver samples for the enzyme activity determination were taken at the same time.

Table 1 : Number of parents and progenies in the different groups

Progeny groups	Bucks	Does	Progenies
minus sel	4	13	21
plus$_1$ sel	5	12	15
plus$_2$ sel	5	12	14

Determination of enzyme activity

Glutathione peroxidase (E.C. 1.11.1.9) activity was measured in blood plasma, red blood cells 1:9 haemolysate and 10.000 g supernatant fraction of liver 1:9 homogenate. Blood plasma was separated by centrifugation at 1500 rpm, 4 °C for 10 minutes. Erythrocytes were haemolyzed by a nine-fold dilution with redistilled water. Liver samples (1 g) were homogenized in 9 ml of 0.9 % NaCl, centrifuged and 10.000 g supernatant was used.

Blood plasma and RBC haemolysate protein content was determined by the biuret method (GORNALL and BARDAWILL, 1949), and liver homogenate protein as described by LOWRY et al (1952). Glutathione-peroxidase activity was measured in the presence of reduced glutathione and cumene-hydroperoxide as substrates using an end-point direct assay (MATKOVICS et al, 1988). The enzyme activity was expressed in units reflecting the oxidation of reduced glutathione in nmoles per minute at 25 °C and was calculated to the protein content.

Correlation, variance and regression analysis methods were used to evaluate phenotypic relationships and the effect of the selection (SNEDECOR and COCHRAN, 1976).

RESULTS AND DISCUSSION

Phenotypic correlation

Linear phenotypic correlations between glutathione peroxidase activity and dressing traits were evaluated. Three of the total studied dressing traits have significant correlation with the blood plasma enzyme activity, 5 with the erythrocytes, 1 with the liver enzyme activity respectively, as presented (traits without any significant correlation are not shown) in table 2.

Calculation of genetic correlations were not possible because of the small number of full and half sibs between the progenies.

Table 2 : Correlations between carcass traits and enzyme activities measured in different tissues

	inedibles	carcass	dressing%	forepart	hinds	meat on loin	meat on hind
blood serum	0.08	-0.04	-0.06	-0.01	-0.26*	0.29**	-0.31**
erythrocytes	0.27*	-0.33**	-0.36***	0.32**	-0.32**	0.01	-0.07
liver	0.36***	-0.06	-0.21	-0.01	-01	-0.04	-0.02

Symbols *, ** and *** denote significant correlation at P<0.1, P<0.05 and P<0.01

Effect of selection

Selection caused at least 2% difference (P<0.05) in the dressing percentage between the minus sel and plus$_2$ sel progenies. Carcass, intermediate and hind part weights were increased with 35, 22 and 12 grams, respectively in the above mentioned order as it have been reported earlier by ROMVARI et al. (1994).

Considering the moderate correlation between enzyme activity and dressing traits if some part of this would be determined genetically successful selection for any one of them should cause change of the other at the same degree. Therefore analysis of variance was performed on the enzyme activity values at progenies of the three types of previously selected bucks. The results are shown on Table 3.

A weak but significant difference was found between the different progeny groups only in the blood serum enzyme activity. Since minus sel and plus$_1$ sel progenies did not differ significantly those were contracted and the analysis was repeated. These results were 3.04 ± 0.91 and 2.56 ± 0.50 at the minus sel and plus$_1$ sel progenies, as well as plus$_2$ sel group, respectively, which differ significantly at P<0.1 level.

Therefore supposedly some genetic effect, in this case perhaps selection could stay behind moderate negative correlation between blood serum GSHPx enzyme activity and hind's weight and meat on hind in rabbit. Nevertheless, the results are not conclusive because the difference between minus and plus groups was

expected to be greater to the one between plus$_1$ sel and plus$_2$ sel groups. By the other hand, selection based on "meat on loin" (L-value) which is however positively correlated with blood serum enzyme activity.

Table 3 : Glutathione peroxidase activities (U/ g protein content) at the different groups of progenies (mean ± S.D.)

PROGENY GROUPS	TISSUE		
	blood serum	erythrocytes	liver
minus sel	2.93 ± 0.47^a	2.55 ± 0.61	11.77 ± 2.07
plus$_1$ sel	3.19 ± 0.79^a	2.52 ± 0.60	11.94 ± 2.66
plus$_2$ sel	2.56 ± 0.50^b	2.32 ± 0.53	11.00 ± 1.06

a and b in the same column denote statistical significance at P<0.1

Since the enzyme acitivities of RBC haemolysate and 10.000 g supernatant of liver homogenate did not differ among the selected groups to ascertain whether values at any one of the pair of traits studied can be dependent on the other regression analysis were performed.
Regression equations returned from these analyses are :

- meat on the hind (dkg) = 38.2 - 0.6 * blood plasma enzyme activity
- dressing percentage (%) = 64.3 - 0.71 * erythrocyte enzyme activity
- fore part's weight (dkg) = 41.4 -0.84 * erythrocyte enzyme activity
- weight of inedibles (dkg) = 31.5 + 0.5 * liver enzyme activity.

At all of the cases the effect of the enzyme activity as independent variable on the carcass traits as dependent variable was proved to be significant. This can be explained on the way that enzyme activity is a base process influenced by rather unknown possibly mainly environmental factors so that its change causes changes at the carcass traits in turn.

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