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Relationship between parameters of the glucose tolerance test (GTT) in young sires and their estimated breeding value (EBV)

Vztah mezi parametry glukózového tolerančního testu (GTT) u mladých býků a odhadem jejich plemenné hodnoty

L. Panicke[1], R. Staufenbiel[2], E. Fischer[3]

[1]Research Institute for Biology of Farm Animals, Dummerstorf, Germany
[2]Free University Berlin, Institute of Veterinary Physiology, Berlin, Germany
[3]University of Rostock, Faculty of Agricultural and Environmental Sciences, Rostock, Germany

ABSTRACT: A high milk performance connected with sound health regarding metabolism and sufficient fertility in dairy cows depends on a well balanced distribution of energy in the body. The terms "type of turnover" and "type of deposition" embody two extremes of food energy preferably for milk production or for body composition. Insulin plays an outstanding role based on its central position in energetic metabolism. The function of insulin may be recorded by means of the intravenous glucose tolerance test (GTT). The reaction of insulin and glucose was investigated after infusion of 1 g glucose/kg$^{0.75}$ because of the probable genetic determination of the reactive ability. The coefficients of heritability range from $h^2 = 0.07 \pm 0.07$ to $h^2 = 0.20 \pm 0.12$. Investigating 52 sires the correlation coefficients amount to $r = -0.5$ for parameters of GTT and estimated breeding values (EBV) which is a closer relation than between pedigree breeding value (PBV) and GTT.

Keywords: cattle; glucose; blood; insulin; performance; breeding value

ABSTRAKT: Vysoká mléčná užitkovost spojená s pevným zdravím zahrnujícím správný metabolismus a uspokojivou plodnost dojnic závisí na dobře vyvážené distribuci energie v organismu. Výrazy „typ látkové výměny" a „typ ukládání" zahrnují dva extrémy přeměny energie krmiva v mléčnou produkci nebo v přírůstek hmotnosti. Inzulin hraje výjimečnou roli, která je založena na jeho ústřední pozici v energetickém metabolismu. Funkce inzulinu může být zaznamenána prostřednictvím intravenózního glukózového tolerančního testu (GTT). Reakce inzulinu a glukózy byla zkoumána po infuzi 1 g glukózy/kg^{0,75} s cílem zjistit pravděpodobnou genetickou determinaci schopnosti reagovat. Koeficienty heritability byly v rozmezí $h^2 = 0,07 \pm 0,07$ až $h^2 = 0,20 \pm 0,12$. Při vyhodnocení 52 otců byly korelační koeficienty pro parametry GTT a odhadnutá plemenná hodnota do –0,5, což je těsnější vztah než mezi plemennou hodnotou podle předků a GTT.

Klíčová slova: skot; glukóza; krev; inzulin; užitkovost; plemenná hodnota

INTRODUCTION

A high milk performance is related to stable and sound metabolism and sufficient fertility of dairy cows. It depends on a well balanced distribution of energy in the body. The terms "type of turnover" and "type of deposition" embody two extremes of food energy preferably for milk production or for body composition.

Insulin has a central position in the regulation of energy metabolism in cattle. There are close relations between the insulin as a controlling and glucose as a controlled parameter. The glucose level in the ruminant blood is kept almost constant at 35–55 mg glukose/100 ml for the undisturbed course of body functions (Kirchgessner, 1997). Glucose is needed for various performances in the cow metabolism. It is required for the synthesis of lactose, for the ATP-genesis in the glycolysis and tricarboxylic acid cycle, for the provision of NADPH and ribose in the pentosephosphate pathway and also for the genesis of glycerol for fat synthesis. Glucose is essential for the energetic functional ability of the nerve system (Gabel and Voigt, 2000). The glucose supply of the udder from endogenous and exogeneous sources can be regarded as a set point in the system of regulation of milk secretion

(Hagemeister and Voigt, 2000). Extensive investigations of Staufenbiel (1993) prove the balance between catabolism and anabolism particularly in the fat metabolism.

The measurement of the insulin reaction during the induced stressing of the metabolism is one possibility for the quantification of the cattle metabolic ability of reaction (Burkert, 1998). A stress situation takes place in the state of starvation induced by food deprivation (Gränzer *et al.*, 1983; Sejrsen *et al.*, 1984; Min *et al.*, 1993; Robinson *et al.*, 1994; Graml *et al.*, 1995; Schallenberger *et al.*, 1996; Müller *et al.*, 1997) or by the intravenous injection of hormones or metabolites like GRF, adrenaline, arginine, glucagon and glucose (Mackenzie *et al.*, 1988; Reinicke, 1993; Xing *et al.*, 1993; Løvendahl *et al.*, 1995; Burkert, 1998; Sørensen *et al.*, 2000).

The connection between the characteristics of endocrinologically controlled energy metabolism and the performance of cattle was repeatedly an object of scientific investigations particularly in the past ten years (Osmond *et al.*, 1981; Gränzer *et al.*, 1983; Sejrsen *et al.*, 1984; Flach *et al.*, 1985; Klindt, 1988; Mackenzie *et al.*, 1988; Kazmer *et al.*, 1991; Min *et al.*, 1993; Reinicke, 1993; Robinson *et al.*, 1994; Graml *et al.*, 1995; Schallenberger *et al.*, 1996; Løvendahl, 1997; Müller *et al.*, 1997; Oldenbroek *et al.*, 1997; Panicke *et al.*, 2000; Sørensen *et al.*, 2000). Blood has mainly been used as an investigative medium. Various spectrums of traits like the blood concentration of growth hormone, prolactin, somatotropin, thyroxines, TT3, TT4, free fatty acids, urea, glucose and insulin were considered in the investigations. Both male and female cattle were investigated. Breeding aspects are increasingly considered.

The investigations of Gränzer *et al.* (1983) and Schallenberger *et al.* (1996) were done with five to seven years old bulls in which the results from the progeny test were already known. Gränzer *et al.* (1983) found a higher decrease in the insulin concentration after food deprivation in the blood of bulls with a higher breeding value in comparison to bulls with a lower breeding value. Yet no clear connection between insulin values and breeding values was to be recognized. In the experiment of Schallenberger *et al.* (1996) the insulin levels before and after the stress test were positively correlated with the breeding values for milk yield. Graml *et al.* (1995) tested young and mature bulls. The insulin concentrations that were recorded in the starvation periods were negatively correlated with the breeding value for the milk yield, fat and protein concentration (–0.13 ... –0.56). Significantly lower insulin concentrations and higher glucose concentrations were proved in young bulls than in the blood of the mature ones. Sejrsen *et al.* (1984) registered an age-dependent change in the relations of the insulin and glucose concentration to the pedigree breeding values for the production of fat in young bulls. Whereas correlation coefficients 0.14 and 0.11 were calculated between the blood concentration at the start of the test and the breeding values of 3.5 months old bulls, the correlations of the same bulls at the age of seven months were about –0.14 and –0.07.

Løvendahl (1997) also pointed out the importance of the cattle age while evaluating GTT in four and nine months old bulls. He considered the time of testing as critical and demanded an age of at least six months. The significant dynamics of the relations of metabolism in the first week of life and in the course of rearing seems to declare the period around the twelfth months of life as the right moment for GTT in a young bull (Staufenbiel *et al.*, 2000).

Mackenzie *et al.* (1988) proved a connection between the insulin reaction and the predisposition for production in eight months old Friesian bulls. After an infusion of glucose, bulls with a higher pedigree breeding value for milk yield showed a more rapid decrease in the glucose concentration than less predisposed bulls. A comparable reaction was investigated by Xing *et al.* (1993) during GTT in six months old Friesian heifers. Reinicke (1993) calculated significant correlation coefficients for young cows (GTT 1st week p.p.) ranging from –0.3 to –0.6 between the parameters of insulin response and their first lactation record.

There are no continuous investigations with a wide spectrum of traits for cattle of different age classes or same and or similar animals over a period longer than five years. The present papers deal with the problems of experimentally comparable testing, the influence of the age and a differentiated spectrum of traits.

The aim of this paper was to investigate the effects of various factors on the results of the intravenous glucose tolerance test (GTT) and to clarify the connection with performance. The following aims for an additional contribution to the assessment of breeding bulls before the test are in process:

1. Derivation of suitable parameters for young sires to the indirect performance test.
2. Estimation of heritability coefficients and correlation coefficients to the EBV.
3. Calculation of the expected performance and estimation of its information increase.
4. Survey of the age at the time of testing.

MATERIAL AND METHODS

The intravenous glucose test (GTT) was carried out by Burkert (1998) at 6 breeding stations using 411 bulls of the German Holstein breed with the forms Black and White ($n = 329$) and Red and White ($n = 53$) and bulls of the Angler breed ($n = 29$). The GTT of the Black and White bulls was done in a way that representative animal numbers were distributed over the regarded age groups (Table 1).

Table 1. Number and age of Black and White bullsincluded in the glucose tolerance test

Age in years	1	2	3	4	> 4	Total
Number	74	56	82	63	54	329

Bulls receiving only water since their last feeding on the day before were injected 1 g glucose/kg$^{0.75}$ (40% glucose solution, body warm) within 1 to 3 minutes after positioning a closeable flexyle into the *v. jugularis* and taking a blood sample for determination of basic values. After the infusion of glucose 9 more blood samples were taken in intervals of 7 minutes to record of the glucose and insulin reaction. Besides the basic concentration of insulin (I0) and glucose (G0), the glucose half-life (GHWZ), the insulin area equivalent (IA) and the glucose area equivalent (GA) between each course of concentration and basic level and the quotient of the area equivalents IA/GA were determined for each animal. The animal effects for each parameter of GTT were estimated using PEST (Groeneveld *et al.*, 1993) on the basis of the values by Burkert (1998). The variance components for animal, residual and also coefficients of heritability were estimated using VCE 4.2 (Groeneveld, 1998). The estimation was carried out on the basis of the following single trait model:

$$y_{ijk} = \mu + st_i + lc_j + a_k + e_{ijk}$$

where: y_{ijk} – parameter of the k'th bull
μ – mean
st_i – i'th effect of the station and of the test day
lc_j – effect of the j'th age class (half-year of life)
a_k – random effect of the k'th bull
e_{ijk} – random residual effect

Results from the estimation of offspring's breeding values are so far available from 273 Black and White bulls tested in GTT. Correlation coefficients between the animal effects of the tested bulls and the offspring's breeding values (VIT Verden Germany) were calculated.

RESULTS AND DISCUSSION

The test parameters were transformed by logarithmic function because of not being normally distributed (Table 2). The estimated coefficients of heritability point to the genetic background of parameters of the glucose tolerance test. Coefficients from 0.12 to 0.20 were estimated for the parameters showing the concentration of glucose and degradation of glucose (Table 2). The measurements of insulin response led to a heritability coefficient from 0.07 to 0.20 whereas the basic concentration of insulin did not show any genetic determination. The half-life of glucose (GHWZ) and the maximum of insulin (IMAX1) depend on age (Figure 1). They reach their minimum or maximum in the 3rd year of age respectively.

The age of breeding sires at the time of the investigation affects the glucose tolerance test (GTT) considerably. No effect could be observed for the test station and the taking of samples except for test station 6. It may be concluded from this that there existed food supply which agreed with demand.

Investigating younger bulls, correlation coefficients between the GTT-parameters and the breeding values from the offspring's test up to 0.50 were obtained, whereas no significant correlations were found in older sires (Table 3). The calculated correlations for the bulls in their third half-year of life show that the glucose half-life and glucose area are suitable parameters for yield performance. Their repeatabilities were determined between $r = 0.5$ and $r = 0.7$ according to Burkert (1998).

The correlation coefficients shown in Tables 4 and 5 indicate the superiority of the parameter glucose half-life for the estimation of the predicted yield, although the glucose concentration is controlled by insulin. The controlled glucose concentration, which is phenotypically measured, suggests a closer connection with the estimated breeding value from the offspring's test than the controlling element. It also shows that the negative correlations of the GHWZ to the milk contents are lower than those of the PBV to milk quantity. The GHWZ varies in-

Table 2. Parameters of the glucose tolerance test in Black and White bulls (n = 329)

Parameter		absolute parameters			*logarithmus naturalis*			h^2	SE (h^2)
		mean	s	s (%)	mean	s	s (%)		
G0	(mmol/l)	4.2	0.6	13	1.43	0.14	9	0.12	0.10
GMAXI	(mmol/l)	11.7	0.9	7	2.45	0.07	3	0.18	0.10
GA		34.6	7.4	21	3.52	0.23	7	0.17	0.09
GHWZ	(min)	57.9	21.2	36	4.00	0.36	9	0.20	0.12
I0	(mU/ml)	14.0	8.2	59	2.50	0.53	21	0.00	0.00
IMAX1	(mU/ml)	130.6	70.1	54	4.72	0.57	12	0.07	0.07
IA		596.7	370.0	62	6.20	0.64	10	0.10	0.09
IA/GA		18.9	13.9	74	2.68	0.74	28	0.20	0.10

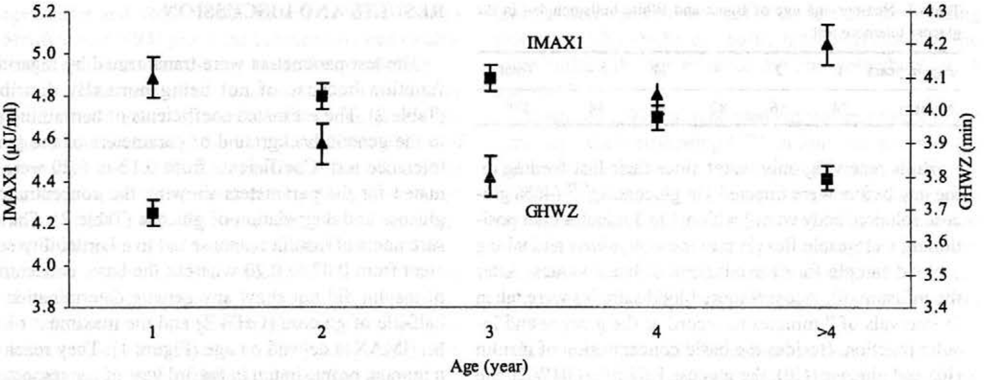

Figure 1. Effect of age on the glucose half-life (GHWZ) and the maximum of insulin (IMAX1)

Table 3. Correlations between the GTT-parameter glucose half-life and the offspring's breeding values of Black and White bulls according to the half-years of life (estimation of breeding value February 2000)

Half-year	*n*	Milk yield	Fat yield	Protein yield	RZM¹⁾
1	6	–0.12	0.07	–0.04	–0.02
2	24	–0.03	–0.21	–0.25	–0.25
3	28	–0.58**	**–0.48***	**–0.51****	**–0.54****
4	25	0.34	0.24	0.23	0.25
5	37	–0.22	–0.33*	–0.18	–0.21
6	45	–0.16	–0.11	–0.06	–0.08
7	35	0.02	0.15	0.12	0.14
8	28	0.13	0.14	0.14	0.15
9	24	0.02	–0.27	0.03	–0.04
≥10	21	0.08	0.38	0.14	0.20
Total	273	–0.10	–0.10	–0.05	–0.06

¹⁾RZM is a selection index combining the total breeding values of fat and protein yield with relative economic weights of 1 : 4

Table 4. Correlations between the parameters of GTT and the breeding value of bulls from the offspring's test (EBV) and the pedigree breeding values (PBV) (half-year of life 3; *n* = 28; estimation of breeding value February 2000)

Parameter	EBV				PBV	
	milk (kg)	fa (kg)	protein (kg)	RZM	protein (kg)	RZM
ln G0	–0.29	–0.18	–0.39*	–0.35	–0.04	0.15
ln GMAX1	0.10	0.04	–0.01	0.00	0.28	0.32
ln GA	–0.41*	–0.42*	–0.27	–0.34	–0.13	–0.29
ln GHWZ	–0.58**	**–0.48***	**–0.51****	**–0.54****	–0.11	–0.12
ln IA	0.18	0.34	0.18	0.23	–0.16	–0.14
PBV	0.73**	0.19	0.41*	0.26	–	–

Table 5. Correlations between the expected values of the GTT-parameters and selected breeding values of bulls (half-year of life 3; *n* = 28)

Breeding values (trait)	GTT-parameter			Pedigree breeding value	
	ln IA	ln GA	ln GHWZ	trait	RZM
Milk yield	+0.18	–0.41*	–0.58**	+0.73**	+0.50**
Fat yield	+0.34	–0.42*	**–0.48***	+0.19	+0.17
Protein yield	+0.18	–0.27	**–0.51****	+0.41*	+0.27
Fat content	+0.07	+0.14	+0.27	+0.68**	–0.43*
Protein content	–0.10	+0.42*	+0.41*	+0.63**	–0.62**
RZM	+0.23	–0.34	**–0.54****	+0.26	+0.26
RZS	–0.12	+0.18	+0.01	–	–0.41*
RZE	+0.03	–0.18	–0.38*	–	–0.02
RZG	+0.16	–0.28	–0.55**	–	+0.11

dependently with *r* around 0 to the breeding value somatic cell score (RZS). The correlation of $r = 0.4$ to the relative total breeding value for type (RZE) should not be regarded as overvalued. The total merit index (RZG) included RZM, RZE and RZS.

On the basis of the single and multiple linear and nonlinear regression between pedigree as well as GTT information and the estimated breeding value, an additional recommendation can be given before the start of the offspring's test to use various models with the GTT-parameters.

The correlation coefficients between the estimated (EBV) and the calculated breeding value (CBV) with respect to RZM of the bulls (Table 6) are similar for pedigree and GTT information with $r = 0.3$–0.4. The glucose half-life reaches $r = -0.5$ in the third half-year of life. In the interest of stability the glucose half-life and the glucose area (GA) were both included. Table 4 shows the

Table 6. Correlations between the estimated value and the relative breeding value for milk (RZM) of bulls on the basis of various sources of information and models

	Model	Correlation	
		half-year 2	half-year 3
1	mother RZM	+0.45	+0.22
2	father RZM	–0.16	+0.21
3	pedigree-RZM (P)	+0.35	**+0.26**
4	GA	-0.36	–0.34
5	GHWZ	-0.25	**–0.54**
6	GA + GHWZ	+0.36	+0.57
7	P + GA + GHWZ	+0.62	+0.64
8	P + GA + GA^2 + GHWZ + $GHWZ^2$	+0.65	**+0.68**
9	P + GA + GA^2 + GHWZ + $GHWZ^2$ reciprocal*	+0.45	+0.56

*regression coefficients between half-years 2 and 3 were exchanged

relative independent variation of pedigree and GTT information. It means that more information can be expected when both parameters are included. This is reflected in model 7 with $r = 0.64$. The nonlinear valuation gives further stabilisation to $r = 0.68$. The statistical loss of information caused by mistakes in the valuation of the examined life periods (model 9) decreases the correlation coefficients to $r = 0.45$ to 0.56. The time of investigation is important for the certainty of the results. Regarding the obtained correlations with $r = 0.65$ to $r = 0.68$, a certainty level $CL = r^2 = 0.4 \dots 0.5$ is possible. This result for the yield characteristics (Table 7) lies well above the pedigree information.

Sørensen *et al.* (2000) estimated a genetic correlation of 0.39 between the basal glucose concentration before GTT in nine months old female and male cattle and the later production of milk protein in heifers. The basal glucose concentration in the bulls' blood and the protein yield of their daughters were related with 0.34. The corresponding correlations between the maximum insulin concentration in the course of GTT and the milk protein production were about 0.22 and 0.13. Parameters of GTT were combined with the test results after an intravenous infusion of GRF and adrenaline to an "endocrine" index. A correlation (r_{IA}) of 0.40 and 0.26 was estimated between the index in nine months old female and male cattle and the milk protein production.

Table 7. Correlations between the predicted calculated breeding values (CBV), the pedigree breeding value (PBV) and the breeding values of bulls from the offspring's test with respect to selection traits (half-years of life 2 and 3; $n = 52$)

Selection traits	Breeding values (EBV)			
	milk (kg)	fat (kg)	protein (kg)	RZM
GA	–0.36**	–0.32*	–0.33*	–0.35*
GHWZ	–0.37**	-0.34*	-0.40**	-0.41**
CBV – milk (kg)	**0.83****	0.44**	0.71**	0.68**
PBV – milk (kg)	0.69**	0.35*	0.54**	0.52**
CBV – fat (kg)	0.53**	**0.68****	0.54**	0.60**
PBV – fat (kg)	0.33*	0.40**	0.19	0.26
CBV – protein (kg)	0.75**	0.45**	**0.72****	0.69**
PBV – protein (kg)	0.56**	0.27	0.45**	0.43**
CBV – RZM	0.71**	0.50**	0.68**	**0.67****
PBV – RZM	0.49**	0.24	0.31*	0.31*

The results from testing female cattle by Reinicke (1993) indicate the pubertal time periods. Results regarding the effect of the pubertal part of life on the performance in milk production, fertility and growth by Panicke (1994) may be underlined histologically by cell differentiation for the mammary gland by Falconer (1980), Pritchard *et al.* (1972) and Amir (1974), for the level of prolactin and growth hormone by Purchas *et al.* (1971) and for the hormone concentration during the prepubertal part of life by Day *et al.* (1986).

The expectations concerning the results from the sires tested in the 2nd and 3rd half-year of life are supported by the results of Reinicke *et al.* (1993) investigating 44 cows and their calves with $r = 0.41$, by Staufenbiel *et al.* (1999) and Panicke *et al.* (2000).

CONCLUSIONS

The contrary glucose and insulin reactions and their relations to the breeding values of the offspring's test are dependent on age. The estimated heritability coefficients point to a genetic determination of single parameters of the intravenous GTT. In the third half-year of life correlation coefficients around $r = -0.3$ to $r = -0.5$ are obtained for relations between the parameters glucose half-life and glucose area equivalent, respectively, and the breeding values from the offspring's test. The examined parameters glucose half-life and glucose area equivalent changed nonlinearly with the protein production. Physiological characteristics are to be optimised. They should not be maximized nor minimized. The protein yield is a suitable parameter of stability. The GTT-parameters vary in a relatively independent way in relation to the pedigree-breeding value. The additional information can improve the exactness of the young sires' indirect performance test to $r^2 = 0.5$. Important requirements are a standardized demand and animal-welfare appropriate environment of the companions in the shed as well as the time of investigation. If the so far achieved results are be confirmed, an additional recommendation for the valuation of the breeding bulls before the start of the test could be given. The test capacity could be extended or the costs for testing bulls could be lowered.

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Corresponding Author:

Prof. Dr. habil. Lothar Panicke, Research Institute for Biology of Farm Animals, Wilhelm-Stahl-Allee 2, 181 96 Dummerstorf, Germany
e-mail: panicke@fbn-dummerstorf.de

Comparison of preweaning growth traits of six beef cattle breeds in the Czech Republic

Růst telat od narození do odstavu šesti plemen masného skotu v České republice

J. ŘÍHA[2], V. JAKUBEC[1], J. GOLDA[2], I. MAJZLÍK[1]

[1]*Czech University of Agriculture, Prague, Czech Republic*

[2]*Research Institute for Cattle Breeding Ltd., Rapotín, Czech Republic*

ABSTRACT: In the years 1992 to 1998 six beef cattle breeds (Angus, Czech Pied, Hereford, Charolais, Limousin and Piemontese) were tested and the data on the following traits of calves were analyzed: birth weight, 120-day and 210-day weight and average daily gains (birth – 120 days, birth – 210 days and 120 – 210 days). The comparison of breeds and traits was based on the overall means (μ) and phenotypic standard deviations (σ_P). Both phenotypic parameters were obtained in the preceding analyses of these breeds by the generalized least squares method. The traits were analysed with respect to year of birth (1992–1998), herd, sex (male, female), calf number (single, twin), parity and sire. The phenotypic standard deviations of traits were transformed into genetic standard deviations (σ_G) by multiplication by the square root of the corresponding heritabilities. Genetic standard deviations were used to compare the genetic variability of breeds. The Hereford cattle showed the lowest overall means and a very low phenotypic and genetic variability in all traits. The variability was also very low in the Limousin for all growth traits. High overall means for all growth traits were recorded in the Charolais. The Piemontese exceeded the Charolais slightly in birth weight and the Czech Pied cattle showed a higher daily gain from 120 to 210 days than the Charolais. The Charolais had high standard deviations (phenotypic and genetic) with respect to all preweaning growth traits. Similar high standard deviations were also recorded in the Piemontese breed for weight at birth, 120 days and for the average daily gains from birth to 120 days and in the period of 120–210 days. In the 120-day and 210-day weights, and daily gains (birth – 120 days, birth – 210 days) a similar ranking of breeds was found. For the majority of traits the Piemontese breed showed average values. The other breeds (with the exception of Angus for the 120 day weight) were located above the average of the extremes. Theoretical frequency curves based on the normal distribution and the genetic standard deviations ($\mu \pm 3\sigma_G$) were used for comparing the weights from birth to weaning for three breeds representing the average and both extremes. Frequency curves for birth weight of Hereford and Charolais do not overlap, the Angus breed is in the middle of both these breeds. For the weights at 120 and 210 days differences between frequency curves are much less pronounced and show stronger overlapping between Hereford, Piemontese and Charolais breeds.

Keywords: beef cattle breeds; preweaning growth traits; breed comparisons

ABSTRAKT: V letech 1992 až 1998, tj. během sedmiletého období, bylo analyzováno šest plemen masného skotu, a to plemeno angus, české strakaté, hereford, charolais, limousin a piemontese se zřetelem na hmotnost telat při narození, ve 120 dnech, 210 dnech a denní přírůstky od narození do 120 dnů, od narození do 210 dnů, od 120 do 210 dnů. K porovnání plemen mezi sebou bylo použito obecných průměrů (μ) a fenotypových standardních odchylek (σ_P) sledovaných vlastností, získaných v předchozích analýzách těchto plemen metodou zobecněných nejmenších čtverců, přičemž byly zohledněny tyto faktory: rok narození telete, stádo, pohlaví, četnost vrhu, věk matky při narození telete a otec telete. Takto získané průměry byly použity ke srovnání užitkovosti analyzovaných plemen. Fenotypové standardní odchylky vlastností byly přeměněny na genetické standardní odchylky (σ_G) pomocí druhé odmocniny příslušných koeficientů heritability. Genetické standardní odchylky byly použity k porovnání genetické proměnlivosti mezi plemeny. Plemeno here-

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ford vykazovalo ve všech ukazatelích hmotnosti a růstu nejnižší průměry a velmi nízké standardní odchylky. Obdobně nízké standardní odchylky byly zaznamenány u plemene limousin, které jsou dokonce v některých případech nižší než u plemene hereford. Vysoké ukazatele hmotnosti a přírůstků byly zaznamenány u plemene charolais. Plemeno piemontese mělo nepatrně vyšší živou hmotnost při narození a český strakatý skot vyšší průměrné denní přírůstky od 120 do 210 dní než plemeno charolais. Plemeno charolais vykazovalo ve všech ukazatelích nejvyšší standardní odchylky s tím, že obdobně byly zaznamenány vysoké standardní odchylky u hmotnosti při narození, hmotnosti ve 120 dnech a v denních přírůstcích od narození do 120 dnů a od 120 do 210 dnů u plemene piemontese. Hmotnosti telat ve 120 a 210 dnech a přírůstky od narození do 120 a 210 dnů vykazovaly u sledovaných plemen shodnou tendenci. Nejblíže k průměru mezi extrémy se přibližuje plemeno piemontese, zatímco ostatní plemena (s výjimkou plemene angus v případě hmotnosti ve 120 dnech) se nalézají značně nad tímto průměrem. Křivky normálního rozdělení, spočívající na genetických standardních odchylkách ($\mu \pm 3\sigma_G$), byly použity pro porovnání ukazatelů hmotnosti pro tři plemena představující průměr a oba extrémy. Pro hmotnost při narození se pro plemena hereford a charolais křivky normálního rozdělení vůbec nepřekrývají. Plemeno angus se v hmotnosti při narození nalézá ideálně ve středu mezi oběma extrémními plemeny. V hmotnosti ve 120 a 210 dnech dochází k postupnému přechodu jednotlivých křivek normálního rozdělení od plemene hereford přes plemeno piemontese až po plemeno charolais.

Klíčová slova: masná plemena skotu; vlastnosti růstu od narození do odstavu; porovnání plemen

INTRODUCTION

The history of beef cattle production in the Czech Republic is relatively short. The first purebred animals (800 Polled Hereford heifers) were imported from Canada in 1974 and 1987. Larger imports of beef cattle breeds (Aberdeen Angus, Angus), Blonde d'Aquitaine, Galloway, Hereford, Highland, Charolais, Limousin, Piemontese, Salers and Simmental) were characteristic of recent years (since 1990). There is a very high variability between the mentioned breeds in two sets of traits: maternal performance and beef traits. Maternal performance includes the performance traits of the dam associated with reproduction (fertility and prolificacy) and rearing of its calves as well as those of its calves during fetal life (embryonic survival, prenatal growth and condition at birth) and until weaning (viability, growth and conformation). Beef traits concern mainly growth productivity of young cattle, after weaning and during fattening, and carcass utilization (growth rate, feed intake, feed efficiency, carcass composition and morphology, meat quality).

Beef production systems vary widely among countries because of differences in feed, climate, land resources and marketing situation. Profitable beef production depends on the wise use of all genetic and environmental resources available and on the development of marketing strategies that are in harmony with these resources. Efficiency of methods for using the genetic diversity of breeds, as stated by Dickerson (1973), is determined mainly by such factors as:

1. Size of breed differences in individual and maternal performance.
2. Magnitude of crossbred heterosis for individual, maternal and paternal performance.
3. Reproductive rate.
4. Importance of interactions of genetic components with management variables.

Identifying superior breeds would be simple if adequate life-cycle performance data were available on large representative samples of breed of potential interest. Comparisons would need to be made between cattle breeds raised under the same conditions and preferably over a range of conditions to evaluate the possibility of genotype × environment interactions. Unfortunately, such ideal comparisons require a large input of financial resources. In the Czech Republic most of the performance data recorded are restricted to one breed at a single location (herd). On the other hand, almost all beef breeds are kept in a lot of environmental situations. Beef cattle breeds are an important part of genetic resources available to change production potential. In contrast to slow changes associated with intrabreed selection, average differences between breeds or breed crosses can be exploited rapidly by capitalizing many years of cumulative change.

The main objective of the present study was the analysis and comparison of preweaning growth traits of important beef breeds in the Czech Republic representing different biological types.

MATERIAL AND METHODS

In the years 1992 to 1998, the following growth traits of the beef breeds Angus (n = 1 425), Czech Pied (n = 337), Hereford (n = 2 447), Charolais (n = 2 291), Limousin (n = 653) and Piemontese (n = 198) were recorded in the Czech Republic: birth weight, 120-day weight, 210-day weight and daily gains (birth – 120 days, birth – 210 days, 120 – 210 days). The data of the mentioned breeds were recorded in separate herds. On the other hand, almost all beef breeds were kept in a lot of environmental situations from lowlands to highlands, from foot-hills to mountains. Artificial insemination is rarely used in the herds.

In a preceding study the mentioned preweaning growth traits were analyzed by the generalized least squares method with respect to the following factors: year of birth, herd, sex (male, female), calf number (single, twin), parity and sire. For the beef breed comparison in the present contribution the following phenotypic parameter values, i.e. overall means (μ) and their standard deviations (σ_P), were used. Moreover, the genetic standard deviations (σ_G) were analyzed, too. The genetic standard deviations were obtained by multiplying the phenotypic standard deviations by the square roots of heritability (h). For all breeds the same estimates of heritability coefficients were used according to Ménnissier and Frisch (1992). The parameters for the breeds and traits are presented.

RESULTS AND DISCUSSION

Overall breed means and their phenotypic standard deviations estimated by the generalized least squares method (Jakubec *et al.*, 1999) are presented in Table 1. In the same table the averages of the 2 breeds with extreme values (minimum value and maximum one) are also given. The Hereford breed showed the lowest means and very low phenotypic standard deviations in all traits. Similar phenotypic standard deviations were found in the Limousin. High preweaning weights and growth parameters were recorded in the Charolais. A little higher birth weight was found in the Piemontese and higher daily gains were recorded in the Czech Pied and Angus cattle in the period from 120 to 210 days. Charolais had the highest phenotypic standard deviations of all analyzed breeds in all traits. Similarly, high phenotypic standard deviations for birth weight, 120-day weight and daily gains in the period birth – 120 days and 120–210 days resulted in the Piemontese. A high phenotypic variability of these two breeds indicates also a high genetic variability which is an important factor for achieving a high selection response. Preweaning growth traits are associated with two genetic effects, i.e. the individual effect (pre- and postnatal calf growth capacity) and the maternal effect (uterine environment, fertility, prolificacy, milk production, rearing qualities). Data presented in Table 1 and Figure 1 indicate that Hereford calves had the lowest birth weight (25.77 kg). Angus calves had medium birth weights, whereas almost identical maximum values (approx. 38 kg) were recorded in Piemontese and Charolais calves. Similar values at almost identical level were found in the Czech Pied and Limousin breeds (33.0 and 33.5 kg, respectively).

Birth weight is associated with calving difficulties. Calving difficulties are usually more frequent in breeds with high birth weights (Jakubec *et al.*, 1998). According to the reports from other countries the use of the Hereford and Angus breeds as dam breeds or dam crossbreds in commercial crossing and terminal rotation would also be advantageous in the Czech Republic. Genetic variability of calving difficulties depends also on the body size and muscling in premature and mature age. One has to be careful when using the Piemontese in purebreeding or crossbreeding due to its high birth weights, calving difficulties and strong muscling.

All the breeds showed a similar tendency in the 120-day weights and average daily gains from birth to 120 days. Piemontese and Angus were closest to the average of both extremes while Czech Pied and Limousin were considerably above this average. This tendency was also evident for the 210-day weight and the average daily gains from birth to 210 days. While the Piemontese and Angus showed similar averages in the 120-day weight, the ranking of breeds was changed in the 210-day weight. The Piemontese had again average weights, however the Angus calves showed the same level as the Limousin and Czech Pied not only in the 210-day weight but also in the average daily gain from birth to 210-days. The average daily gain in the period 120–210 days was lowest in Hereford cattle. The highest daily gain in this period was recorded for the Czech Pied and a medium daily gain for the Limousin breed.

Table 1. Least squares means ($\hat{\mu}$) and their phenotypic standard deviations (σ_P) for preweaning traits (kg)

Breed	Weight at						Average daily gains					
	birth		120 days		210 days		birth – 120 d		birth – 210 d		120 – 210 d	
	$\hat{\mu}$	σ_P	$\hat{\mu}$	σ_P	$\hat{\mu}$	σ_P	$\hat{\mu}$	σ_P	$\hat{\mu}$	σ_P	$\hat{\mu}$	σ_P
Czech Pied	33.38	3.15	156.21	28.98	252.34	42.55	1.024	0.239	1.043	0.201	1.068	0.341
Angus	30.92	3.30	145.89	28.70	245.97	36.80	0.958	0.237	1.024	0.174	1.112	0.314
Hereford	25.77	3.06	115.29	26.62	193.16	36.32	0.746	0.220	0.797	0.172	0.865	0.309
Charolais	37.64	4.92	166.22	32.00	258.66	43.00	1.070	0.264	1.049	0.204	1.030	0.378
Limousin	33.30	3.38	156.23	25.13	244.58	36.02	1.025	0.207	1.006	0.170	0.982	0.314
Piemontese	37.99	4.93	142.90	31.00	221.31	39.89	0.875	0.261	0.873	0.189	0.872	0.374
Average of extremes	31.88		140.76		225.91		0.908		0.922		0.948	

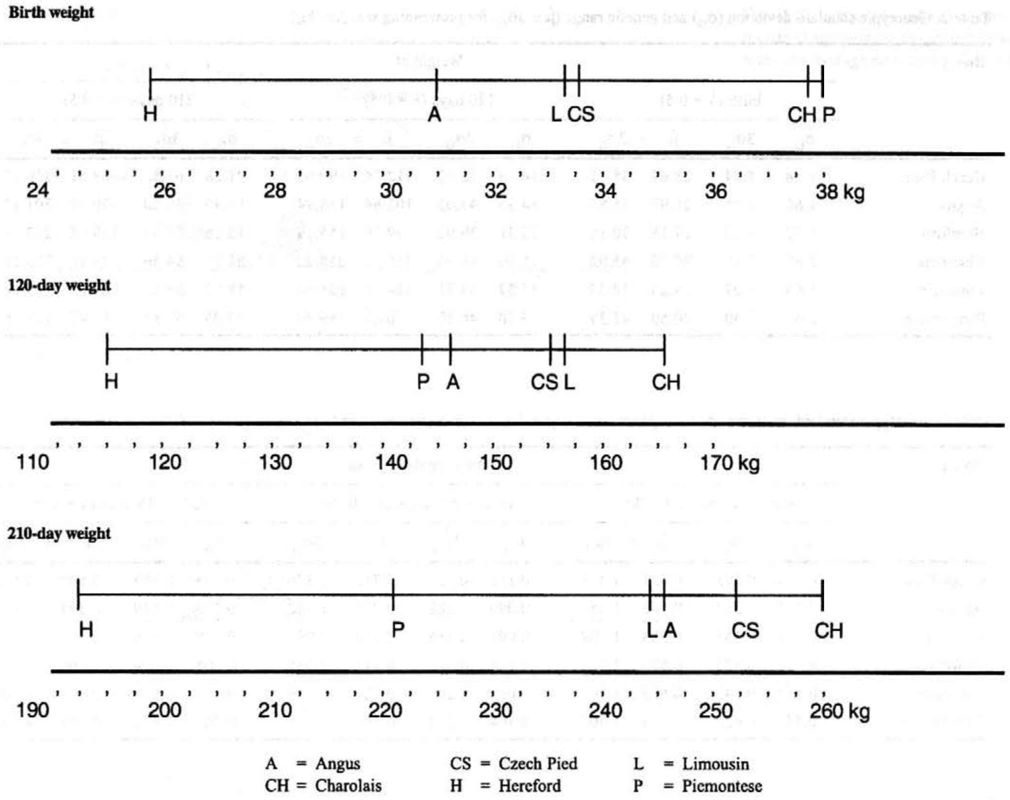

Figure 1. Comparison of preweaning weights

Genetic standard deviations (σ_G), triple values of these deviations ($3\sigma_G$) and genetic range (overall means ± 3 genetic standard deviations, $\mu \pm 3\sigma_G$) characterizing weights and preweaning daily gains from birth to weaning are presented in Tables 2 and 3. The genetic standard deviations were obtained by multiplying the phenotypic standard deviations by the square root of the heritability coefficient (h). Heritabilities for the preweaning traits of the beef breeds have not yet been estimated in the Czech Republic. Therefore the same adjusted heritabilities and their square roots for these traits were adopted from the review of Ménnissier and Frisch (1992). For all preweaning weights the value of $h = 0.5$ ($h^2 = 0.25$) and for all average daily gains the value of $h = 0.55$ ($h^2 = 0.30$) were used.

Genetic standard deviations are considered here as additive genetic standard deviations (σ_A). In reality they would be a little higher. The genetic standard deviation as a population parameter of an outbred population includes also components of dominance and epistatic variance. The genetic range for all preweaning traits ($\hat{\mu} \pm \sigma_G$) with the maximum and minimum performance can be taken from Tables 4 and 5. Table 4 is complemented by Figure 2.

From the Figure 2 is evident that the frequency curves of Hereford and Charolais for the birth weight do not overlap at all. The left half of the Angus frequency curve overlaps with the right half of the Hereford frequency curve and the right half of the Angus frequency curve overlaps with the left half of the Charolais frequency distribution. The Angus birth weight is placed in the centre between the two extreme breeds. The genetic range amounts to 10 kg in the Hereford and the Piemontese whereas the genetic range of the Charolais is 14.94 kg.

For the weights at 120- and 210-days the genetic frequency curves are only moderately shifted from Hereford to Piemontese and Charolais. So the values of Piemontese overlap to approximately 4 genetic standard deviations (from $+\sigma_G$ up to $-3\ \sigma_G$) with values of the Hereford cattle. The left part of the Charolais frequency curve reaches almost the mean of the Hereford frequency curve and up to $5\ \sigma_G$ into the frequency curve of the

Table 2. Genotypic standard deviation (σ_G) and genetic range ($\hat{\mu} \pm 3\sigma_G$) for preweaning weights (kg)

Breed	Weight at											
	birth (h = 0.5)				120 days (h = 0.5)				210 days (h = 0.5)			
	σ_G	$3\sigma_G$	$\hat{\mu} \pm 3\sigma_G$		σ_G	$3\sigma_G$	$\hat{\mu} \pm 3\sigma_G$		σ_G	$3\sigma_G$	$\hat{\mu} \pm 3\sigma_G$	
Czech Pied	1.58	4.74	28.64	38.12	14.49	43.47	112.74	199.68	21.28	63.83	188.51	316.17
Angus	1.65	4.95	25.97	35.87	14.35	43.05	102.84	188.94	18.40	55.20	190.77	301.17
Hereford	1.53	4.59	21.18	30.36	13.31	39.93	79.36	155.19	18.16	54.48	138.68	247.64
Charolais	2.46	7.38	30.26	45.02	16.00	48.00	118.22	214.22	21.50	64.50	194.16	323.16
Limousin	1.69	5.07	28.23	38.37	12.57	37.71	118.52	193.94	18.01	54.03	167.28	275.34
Piemontese	2.47	7.40	30.59	45.39	15.50	46.50	96.40	189.40	19.95	59.84	161.47	281.15

Table 3. Genotypic standard deviation (σ_G) and genetic range ($\hat{\mu} \pm 3\sigma_G$) for preweaning gains (kg)

Breed	Average daily gains											
	birth – 120 days (h = 0.55)				birth – 210 days (h = 0.55)				120 – 210 days (h = 0.55)			
	σ_G	$3\sigma_G$	$\hat{\mu} \pm 3\sigma_G$		σ_G	$3\sigma_G$	$\hat{\mu} \pm 3\sigma_G$		σ_G	$3\sigma_G$	$\hat{\mu} \pm 3\sigma_G$	
Czech Pied	0.131	0.393	0.631	1.417	0.111	0.333	0.710	1.376	0.188	0.564	0.504	1.632
Angus	0.131	0.393	0.565	1.351	0.096	0.288	0.736	1.312	0.173	0.519	0.593	1.631
Hereford	0.121	0.363	0.383	1.109	0.095	0.285	0.512	1.082	0.170	0.510	0.355	1.375
Charolais	0.145	0.435	0.635	1.523	0.112	0.336	0.713	1.385	0.208	0.624	0.406	1.654
Limousin	0.114	0.342	0.683	1.367	0.094	0.282	0.724	1.288	0.173	0.518	0.464	1.500
Piemontese	0.144	0.432	0.443	1.307	0.104	0.312	0.561	1.185	0.206	0.618	0.254	1.490

Table 4. Least squares means and genetic range of the breeds with the extreme and medium values for preweaning weights

Breed	Weight at								
	birth			120 days			210 days		
	$\hat{\mu} - 3\sigma_G$	$\hat{\mu}$	$\hat{\mu} + 3\sigma_G$	$\hat{\mu} - 3\sigma_G$	$\hat{\mu}$	$\hat{\mu} + 3\sigma_G$	$\hat{\mu} - 3\sigma_G$	$\hat{\mu}$	$\hat{\mu} + 3\sigma_G$
Hereford	21.18	25.77	30.36	79.36	115.29	155.19	13.68	193.16	247.64
Charolais	30.26	37.64	45.02	118.22	166.22	214.22	194.16	258.66	323.16
Angus	25.97	30.92	35.87						
Piemontese				96.40	142.90	189.40	161.47	221.31	281.15
Average of extremes		31.88			140.76			225.91	

Table 5. Least squares means and genetic range of the breeds with extreme and medium values for preweaning daily gains

Breed	Daily gains								
	birth – 120 days			birth – 210days			120 – 210 days		
	$\hat{\mu} - 3\sigma_G$	$\hat{\mu}$	$\hat{\mu} + 3\sigma_G$	$\hat{\mu} - 3\sigma_G$	$\hat{\mu}$	$\hat{\mu} + 3\sigma_G$	$\hat{\mu} - 3\sigma_G$	$\hat{\mu}$	$\hat{\mu} + 3\sigma_G$
Hereford	0.383	0.746	1.109	0.512	0.797	1.082	0.355	0.865	1.375
Charolais	0.635	1.070	1.523	0.713	1.049	1.385	0.406	0.030	1.654
Piemontese	0.443	0.875	1.307	0.561	0.873	1.185	0.254	0.872	1.490
Average of extremes		0.943			0.949			1.005	

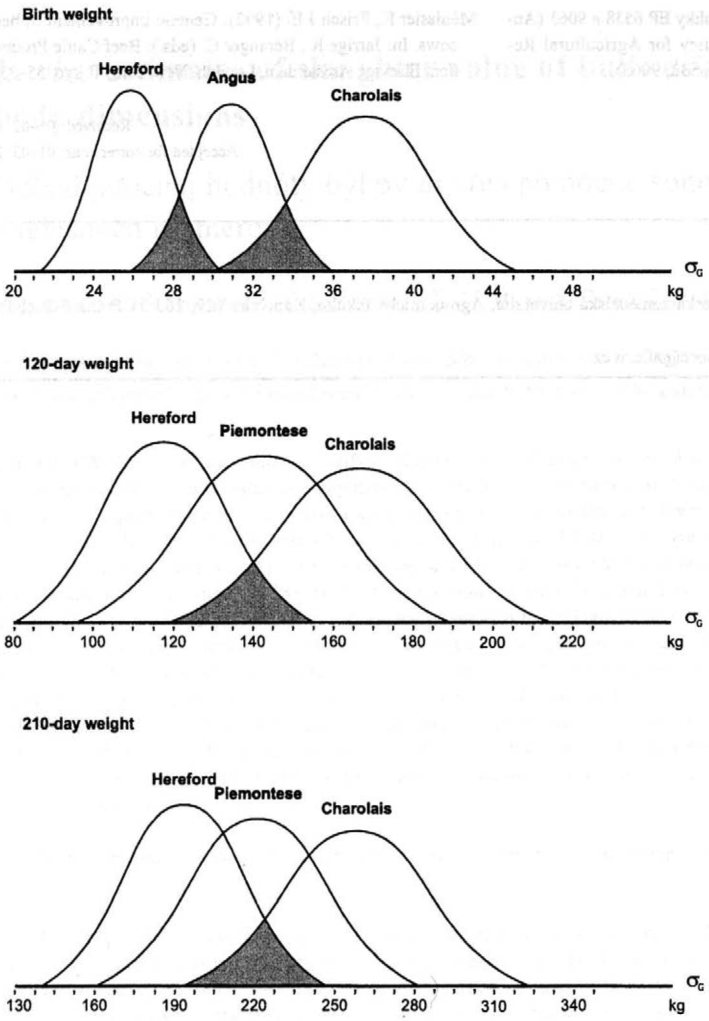

Figure 2. Frequency curves of three breeds characterizing minimum, maximum and average preweaning weights

120-day weight and up to 4 σ_G of the 210-days weight of the Piemontese cattle. For the 120-day and 210-day weights the Hereford shows the lowest genetic range and the Charolais the highest one. High differences were found in the genetic range for the 120-day and 210-day weights between Piemontese and Charolais. But the differences in the genetic range between Piemontese and Charolais on one hand and Hereford on the other hand were not as high for these traits as for the birth weight.

With respect to the fact that all average daily gain results are very similar to the corresponding weights from birth to 210 days the analysis of the frequency curves of daily gains for the Hereford, Angus, Piemontese and Charolais is not given here.

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Corresponding Author:

Prof. Ing. Václav Jakubec, DrSc., Česká zemědělská univerzita, Agronomická fakulta, Kamýcká 129, 165 21 Praha 6-Suchdol, Česká republika
Tel. +420 2 24 38 30 31, e-mail: jakubec@af.czu.cz

In vivo estimates of slaughter value of bulls using ultrasound and body dimensions

Odhad jatočnej hodnoty býkov *in vivo* pomocou sonografickej metódy a telesných rozmerov

P. Polák[1], K. Słoniewski[2], T. Sakowski[2], E. N. Blanco Roa[1], J. Huba[1], E. Krupa[1]

[1]*Research Institute of Animal Production, Nitra, Slovak Republic*

[2]*Institute of Genetics and Animal Breeding of the Polish Academy of Sciences, Jastrzębie, Poland*

ABSTRACT: This work was aimed at verifying the possibility of using ultrasound combined with body dimensions in *in-vivo* estimates of slaughter value in a population of beef bulls of the Slovakian Pied breed. The construction of suitable models of slaughter value estimates was another aim of our work. Slaughter value parameters were analyzed in 101 Slovakian Pied bulls. The animals were killed at an average age of 457 days and average weight of 486 kg; their lifetime average daily gain reached 1 011 g per animal and day. In each bull eighteen body dimensions were determined and tissue thickness was measured at five points by ultrasound. After killing and dissection warm carcass weight (WCW), weight of meat in the carcass (MCW) and weight of meat in the valuable cuts (WMVC) were determined. The highest coefficients of linear correlation were observed between weight before slaughter and all slaughter value indices ($r = 0.80–0.94$), tissue thickness on the last lumbar vertebra ($r = 0.47–0.49$), chest circumference ($r = 0.69–0.79$), central width of the pelvis (0.66–0.71), circumference of thigh (0.61–0.69) and chest width (0.52–0.56). These indices were used to construct linear models for assessing selected slaughter indices. The determination coefficients of these models for WCW, MCW and WMCV had the values of $R^2 = 0.92$, 0.86 and 0.79, respectively. The sonographic method combined with body dimensions showed to be suitable to estimate selected indices of slaughter value in live bulls of the Slovakian Pied breed.

Keywords: ultrasound; sonography; body dimensions; slaughter value; Slovakian Pied cattle

ABSTRAKT: Cieľom práce bolo overenie možností využitia sonografickej metódy kombinovanej s telesnými rozmermi ako metódy odhadu jatočnej hodnoty *in vivo* pre populáciu výkrmových býkov slovenského strakatého plemena a konštrukcia vhodných modelov pre odhad parametrov jatočnej hodnoty. Analyzované boli ukazovatele jatočnej hodnoty 101 býčkov slovenského strakatého plemena. Býky boli zabité v priemernom veku 457 dní pri priemernej hmotnosti 486 kg s priemerným denným celoživotným prírastkom živej hmotnosti 1 011 g. Pri každom býkovi bolo zmeraných 18 telesných rozmerov a sonograficky hrúbka tkaniva na piatich miestach tela. Po zabití a detailnej rozrábke sme zistili hmotnosť jatočného tela v teplom (HJTT), hmotnosť mäsa v jatočnom tele (HM) a hmotnosť mäsa 1. triedy (HM1T). Najvyššie koeficienty lineárnej korelácie sme zistili medzi hmotnosťou pred zabitím a sledovanými ukazovateľmi jatočnej hodnoty ($r = 0,80–0,94$), hrúbkou tkaniva na poslednom bedrovom stavci ($r = 0,47–0,49$), obvodom hrudníka (0,69–0,79), strednou šírkou panvy (0,66– 0,71), vinutým obvodom stehna (0,61–0,69) a šírkou hrudníka (0,52–0,56). Tieto ukazovatele boli použité na konštrukciu lineárnych modelov pre odhad vybraných jatočných ukazovateľov. Koeficienty determinácie takto zostrojených modelov mali hodnoty: pre HJTT $R^2 = 0,92$, pre HM $R^2 = 0,86$ a pre HM1T $R^2 = 0,79$. Sonografická metóda kombinovaná s telesnými rozmermi je aplikovateľná na odhad vybraných ukazovateľov jatočnej hodnoty na živých býkoch slovenského strakatého plemena.

Kľúčové slová: ultrazvuk; sonografia; telesné rozmery; jatočná hodnota; slovenský strakatý dobytok

INTRODUCTION

The first attempts leading to more exact estimates of slaughter value using instrumental equipment were performed in the USA in the 50ies. Temple *et al.* (1956, cit. Simm, 1983) were the first to use sonography for measuring slaughter indices in live animals. Turner *et al.* (1990) used fat thickness and MLTL (*musculus longissimus thoracis et lumborum*) area together with weight and testicular circumference to objectively check the slaughter value of 12-month-old Hereford bulls. They found a high correlation between the live weight of the animals, warm carcass weight and net slaughter weight. In the linear model the weight of the animals before killing sufficiently corresponded to the net slaughter weight. Adding of the other indices under observation increased the reliability of the model by 1%. Hamlin *et al.* (1995) determined the correlation between warm carcass weight and the MLTL area on the 12th–13th rib ($r = 0.51$) and fat thickness ($r = 0.33$), respectively. In Slovakia Demo *et al.* (1995) were the first to use ultrasound for slaughter value estimates. In cattle, experimental verification of sonography was set up at the Institute of Animal Breeding of the Research Institute of Animal Production (RIAP) in Nitra (Kmeť *et al.*, 1995). The first results obtained from a very small number of measurements suggested that the method would be employable under our conditions. Sakowski *et al.* (1996) used sonography in combination with body dimensions measured on digitized images to assess slaughter values. Sloniewski *et al.* (1996) observed muscle thickness at seven different body points of holsteinized Polish Black-and-White cattle and found high correlations between muscle thickness and slaughter value indices. They found the weight of animals before slaughter to have a dominant effect upon all slaughter value indices. What concerns sonographic dimensions the highest correlation with slaughter value indices was seen in muscle thickness behind the shoulder-blade and on the ischiadic bone. The authors used sonographic dimensions and body dimensions together with the weight before slaughter in models estimating the slaughter value of bulls; the determination coefficients ranged from 0.75 to 0.97.

Our work was aimed at the construction of suitable models for estimating slaughter value indices using ultrasound combined with body dimensions. Another aim of our work was to verify such a combined method as a method of estimating the slaughter value *in vivo* in a population of beef cattle of the Slovakian Pied breed.

MATERIAL AND METHODS

In this work the slaughter value parameters of 101 Slovakian Pied bulls were analyzed. The animals were killed at an average age of 457 days having an average weight of 486 kg and average lifetime weight gain of 1 011 g per animal and day.

Sonographic measurements were carried out at specific points 10 days before slaughter. Tissue thickness (muscle, subcutaneous fat and skin together) was measured on the shoulder-blade, behind the shoulder-blade, on the last thoracic and lumbar vertebra respectively as well as on the ischium. At each point four tissue measurements were done in order to eliminate measuring error. The arithmetic mean of four measurements at a given point was considered as thickness value. The instrumentation comprised an Aloka SSD 500 echocamera, a 3.5 MHz probe UST 5813 and the ECM-9 echocoupler.

Simultaneously with sonographic measurements the live weight of the animals was determined and 18 body dimensions were measured (height at withers, height of rump, diagonal length of the trunk, length of the chest, chest width behind the shoulder-blade, chest width on the last rib, depth of the chest, front width of the pelvis, central width of the pelvis, length of the pelvis, circumference of the metacarpus, chest circumference, circumference of thighs, circumference of the thigh, circumference of the waist, circumference of the cannon bone, shoulder width and width of the loins). Lydtin measuring staff, Wilckens callipers and a long and short measuring tape were used for body dimension measurements.

The animals were killed at the experimental slaughterhouse of the RIAP Nitra after 24h starvation. Immediately after slaughter WCW was determined. After 24h chilling and dissection of the right side of beef the weight of the basic tissues was determined. We obtained the MCW as the sum of meat from hind and rear carcass quarter multiplied by 2 and WMVC values as the sum of meat weight of the round, shoulder, loin and sirloin multiplied by 2. The data were processed by statistical analysis.

Statistical analysis was carried out at the Institute of Genetics and Animal Breeding of the Polish Academy of Sciences in Jastrzębie with the SAS 6.12 program package using the REG (SAS 1996 – 1) procedure. We started with calculations of the basic statistical variation parameters (arithmetic mean, standard deviation). Then the Pearson's coefficients of linear correlation between slaughter value indices and the body dimensions and sonographic dimensions, respectively, were determined. In order to construct the most suitable model of estimating selected slaughter value parameters (warm carcass weight – WCW, weight of meat in carcass – MCW and weight of meat in valuable cuts – WMVC) the Stepwise procedure (SAS 1996 – 2) was used. Sonographically measured tissue thickness at five different body points and 18 body dimensions entered the procedure. In this way slaughter weight, tissue thickness on the last thoracic vertebra, circumference of thigh, central width of pelvis, circumference of chest and chest width were included in the final models of selected slaughter value parameters.

Model equations for the slaughter value parameters:

$$y_i = a + b_1 x_{1i} + b_2 x_{2i} + b_3 x_{3i} + b_5 x_{5i} + e_i \quad (1)$$

$$y_i = a + b_1 x_{1i} + b_2 x_{2i} + b_5 x_{5i} + b_6 x_{6i} + e_i \quad (2)$$

$$y_i = a + b_1 x_{1i} + b_2 x_{2i} + b_3 x_{3i} + b_4 x_{4i} + b_5 x_{5i} + e_i \quad (3)$$

where:

y_i – dependent variables ($i = 1, \dots, 101$):
warm carcass weight – model (1)
weight of meat in carcass – model (2)
weight of meat in valuable cuts – model (3)
a – absolute member
b_1–b_6 – partial linear regression coefficients of the dependence of slaughter value parameters on the included properties (x_1–x_6), where the numeric subscript of the regression coefficient and of the independent variables (1–6) mark the following indices:
1 – weight before slaughter
2 – tissue thickness on the last thoracic vertebra
3 – circumference of thigh
4 – central width of pelvis
5 – chest circumference
6 – chest width
x_{1i} –x_{6i} – independent variables ($i = 1, \dots, 101$)
e_i – random errors, $N(0,\sigma_e^2)$, ($i = 1, \dots, 101$)

The equations were used to assess slaughter value indices from identical data. Slaughter value indices estimated in this way were compared with the data obtained at carcass dissection and the differences were tested by the paired *t*-test.

RESULTS AND DISCUSSION

The animals were slaughtered at an average age of 457 days, average weight of 486.4 kg and average lifetime weight gain of 1 011 g per animal and day. The mean WCW, MCW and WMCV values were 257.38, 185.80 and 100.42 kg, respectively, the dressing percentage reached 55.24%. Similar values of the fattening and slaughter traits were recorded by Kica *et al.* (1999) in purebred Slovakian Pied bulls.

Tissue thickness on the shoulder-blade, behind the shoulder-blade, on the last thoracic vertebra and on the ischiadic bone reached 60.75, 99.29, 73.41, 72.11 and 105.80 mm, respectively. The basic statistical variation values of the given slaughter value parameters and of tissue thickness as measured by ultrasound are given in Table 1.

Table 1. Basic statistical-variation values of selected slaughter value parameters and thickness of tissue layer as measured by ultrasound

	$\bar{x}$	S.D.
Weight before slaughter (kg)	486.38	30.23
Warm carcass weight (kg)	257.65	17.59
Weight of meat in carcass (kg)	185.80	13.42
Weight of meat in valuable cuts (kg)	100.42	8.28
Dressing percentage (%)	55.24	1.34
Tissue thickness on the shoulder-blade (mm)	60.75	4.41
Tissue thickness behind the shoulder-blade (mm)	99.29	8.22
Tissue thickness on the last thoracic vertebra (mm)	73.41	4.98
Tissue thickness on the last lumbar vertebra (mm)	72.11	4.81
Tissue thickness on the *ischium* (mm)	105.80	6.85

When generating the exterior profile of the Slovakian Pied breed, Chrenek (1996) used 16 months old animals and recorded withers height, diagonal length of the trunk, semi-circumference of thighs and chest circumference of 127.5, 149.4, 114.6 and 188.9 cm, respectively. In our experiment the animals were slaughtered at an age of 447 days (15 months) and their body dimensions were measured. Height at withers, diagonal length of the trunk, chest circumference and semi-circumference of thighs reached 126.13, 145.21, 183.48 and 110.74 cm, respectively, thus showing the body dimensions of our animals to be lower than those of the experimental set of Chrenek (1996). This shift could be caused by the average age that differed between the groups. The average values of body dimensions are given in Table 2.

The highest coefficients of linear correlation were observed between weight before slaughter and all parameters of slaughter value. Our results of a very strong, statistically highly significant correlation between ani-

Table 2. Basic statistical-variation values of body dimensions in cm

	$\bar{x}$	S. D
Height at withers	126.13	3.64
Height of the rump	133.49	10.33
Diagonal length of the trunk	145.21	4.60
Length of the chest	79.17	4.21
Width of the chest	42.44	2.31
Width of the chest on the last rib	56.36	3.43
Depth of the chest	64.08	1.91
Front width of the pelvis	42.95	1.95
Central width of the pelvis	45.03	1.43
Length of the pelvis	47.42	1.74
Width of the loins	31.08	2.83
Shoulder width	47.44	3.45
Circumference of the metacarpus	20.71	1.02
Circumference of the cannon bone	22.66	0.94
Circumference of the chest	183.48	6.09
Circumference of the waist	182.96	6.56
Semi-circumference of thighs	110.74	4.77
Circumference of the thigh	188.79	5.84

mal weight before slaughter and the slaughter value indices (r = 0.80–0.94) show that the latter are very well covered by the weight before slaughter. This statement is confirmed by the results of several authors dealing with similar issues (Hamlin *et al.* 1995; Słoniewski *et al.*, 1996). With respect to the sonograpfically measured dimensions maximum correlation coefficients were determined for tissue thickness on the last lumbar vertebra (r = 0.47–0.49), the last thoracic vertebra (r = 0.45–0.49) and on the *ischium* (r = 0.42–0.48). Except for tissue thickness behind the shoulder-blade (r = 0.18–0.28) which was insignificant for the weight of meat in valuable cuts, significant for the warm carcass weight and even highly significant for the weight of meat in the carcass, all sonographically determined dimensions were moderately correlated and statistically highly significant. Sakowski *et al.* (1995) observed maximum correlation with muscle thickness on the *ischium* (r = 0.64–0.70) whereas in our experiment maximum correlation was seen with tissue thickness on the last lumbar vertebra and on the *ischium*. Słoniewski *et al.* (1996) report maximum correlations with muscle thickness behind the shoulder-blade and on the *ischium*. The correlation coefficients between slaughter value indices and the dimensions measured by ultrasound are presented in Table 3.

The correlation coefficients between selected slaughter value indices and body dimensions reveal (with the exception of the height of rump) medium to strong dependence and they are all statistically highly significant. Maximum correlation coefficients were determined for chest circumference (0.69–0.79), central width of pelvis (0.66–0.71), circumference of thigh (0.61– 0.69) and width of chest (0.52–0.56). Our results of correlation analysis only slightly differed from those presented by Sakowski *et al.* (1996). Sakowski *et al.* (1996) employed a combined method to assess the slaughter value of Holstein cattle: sonographic measurement of muscle thickness at different body points coupled with estimate of the body dimensions using computer image analysis. He determined the correlation coefficients between sonographic dimensions and CCW (r = 0.38–0.68), WMVC (r = 0.34–0.66) and weight of meat in the side of beef (r = 0.36–0.70), respectively. The correlation coefficients calculated in our case are somewhat lower (r = 0.18–0.49), however, they reveal a similar tendency. All coefficients of correlation between slaughter value parameters and body dimensions are given in Table 4.

The stepwise procedure was used to include weight before slaughter, tissue thickness on the last thoracic vertebra, circumference of thigh and chest circumference in the model of WCW estimates (model 1). The determination coefficient of the model constructed in this way was $R^2 = 0.92$.

Weight before slaughter, tissue thickness on the last thoracic vertebra, circumference of thigh and chest width were included in the model of MCW assessment (model 2). The determination coefficient reached $R^2 = 0.86$. In the work of Sakowski *et al.* (1996) muscle thickness on the back ahead the projections of the hips, muscle thickness on the shoulder-blade and that on the thighs were included in the linear models of slaughter value paramerers. Of the body dimensions height at withers croup height, circumference of the cannon bone and mean width of the pelvis were included. In our models circumference of the thigh and chest width behind the shoulder-blade had a dominant position. The differences in the use of body dimensions in the models of slaughter value assessment are given by the fact that Sakowski *et al.* (1996) and Słoniewski *et al.* (1996) analyzed a different breed, namely, the holsteinized Polish Black-and-White cattle. From the viewpoint of body dimensions the meat yield of Holstein beef bulls is mainly characterized by height dimensions whereas that of the Slovakian Pied breed by width dimensions and dimensions of the rear body parts.

The linear regression model for WMVC assessment (model 3) was constructed using weight before slaughter, tissue thickness on the last thoracic vertebra, circumference of the thigh, circumference of the chest and chest width. The coefficient of determination in this model was $R^2 = 0.79$. Precision of the models of slaughter value as-

Table 3. Pearson's coefficients of linear correlation between slaughter value parameters, weight before slaughter and the tissue thickness determined by ultrasound

	Warm carcass weight	Weight of meat in carcass	Weight of meat in valuable cuts
Weight before slaughter	**0.94** ++	**0.91** ++	**0.79** ++
Tissue thickness on the shoulder-blade	0.35 ++	0.32 ++	0.30 ++
Tissue thickness behind the shoulder-blade	0.22 +	0.28 ++	0.18
Tissue thickness on the last thoracic vertebra	**0.45** ++	**0.47** ++	**0.49** ++
Tissue thickness on the last lumbar vertebra	0.47 ++	0.49 ++	0.49 ++
Tissue thickness on the *ischium*	0.48 ++	0.47 ++	0.42 ++

Indices given in bold were used in the model equations.
+ $P < 0.05$; ++ $P < 0.01$

Table 4. Pearson's coefficients of linear correlation between slaughter value parameters and body dimensions

	Warm carcass weight	Weight of meat in carcass	Weight of meat in valuable cuts
Height at withers	0. 48 ++	0. 43 ++	0. 43 ++
Height of rump	0. 17	0. 22 +	0. 22 +
Diagonal length of the trunk	0. 63 ++	0. 58 ++	0. 51 ++
Length of the chest	0. 56 ++	0. 50 ++	0. 41 ++
Width of the chest	**0. 52 ++**	**0. 54 ++**	**0. 56 ++**
Width of the chest on the last rib	0. 33 ++	0. 33 ++	0. 29 ++
Depth of the chest	0. 55 ++	0. 49 ++	0. 42 ++
Front width of the pelvis	0. 65 ++	0. 62 ++	0. 62 ++
Central width of the pelvis	**0. 69 ++**	**0. 66 ++**	**0. 72 ++**
Length of the pelvis	0. 55 ++	0. 47 ++	0. 53 ++
Width of the loins	0. 51 ++	0. 49 ++	0. 47 ++
Width of the shoulder	0. 43 ++	0. 39 ++	0. 34 ++
Circumference of the metacarpus	0. 56 ++	0. 56 ++	0. 55 ++
Circumference of the cannon bone	0. 41 ++	0. 41 ++	0. 48 ++
Circumference of the chest	**0. 79 ++**	**0. 74 ++**	**0. 69 ++**
Circumference of the waist	0. 70 ++	0. 63 ++	0. 58 ++
Semi-circumference of thighs	0. 47 ++	0. 47 ++	0. 52 ++
Circumference of the thigh	**0. 64 ++**	**0. 61 ++**	**0. 68 ++**

Indices given in bold were used in the model equations.
+ $P < 0.05$; ++ $P < 0.01$

sessment can be increased by including sonographically determined tissue thickness and body dimensions. The determination coefficients of the models established by instrumentation were $R^2 = 0.91–0.96$ which are values only slightly increased in comparison with those in our estimates. In his work Słoniewski *et al.* (1996) used the sonographically determined muscle thickness in combination with body dimensions. All members of the constructed models are significant at the level of $\alpha = 95$ and outlined in Table 5.

The regression equations for estimating selected slaughter value parameters then assume the following pattern:

– for warm carcass weight (model 1)

$$\text{WCW} = -114.220274 + 0.41595\ \text{WBS} + 0.40292\ \text{LTV} + 0.36510\ \text{CT} + 0.43261\ \text{CC}$$

$$R^2 = 0.916$$

– for meat weight in the carcass (model 2)

$$\text{MCW} = -42.163014 + 0.16301\ \text{WBS} + 0.17158\ \text{LTV} + 0.37240\ \text{CW} + 0.43261\ \text{CC}$$

$$R^2 = 0.858$$

– for meat weight in the valuable cuts (model 3)

$$\text{WMVC} = -61.146895 + 0.04786\ \text{WBS} + 014623\ \text{LTV} + 0.20991\ \text{CT} + 0.56609\ \text{MWP} + 0.31090\ \text{CC}$$

$$R^2 = 0.792$$

WCW – warm carcass weight, MCW – weight of meat in carcass, WMVC – weight of meat in valuable cuts, WBS – weight of bull before slaughter after 24h starvation, LTV – tissue thickness on the last thoracic vertebra, CT – circumference of thigh, CC – circumference of chest, CW – chest width

After substituting the values determined/measured into the equations for slaughter value assessment we obtained results that were compared with those acquired by dis-

Table 5. Comparison of mean values and testing of differences between the selected slaughter value parameters obtained by dissection and assessed by application of regression equations

Index	Obtained at dissection	Assessed by models	Difference
Warm carcass weight	257.65	257.65	0.00 –
Weight of meat in carcass	185.80	184.92	0.88 –
Weight of meat in valuable cuts	100.44	100.42	0.02 –
Dressing percentage	55.24	55.25	0.01 –

– difference statistically insignificant section of the carcass. This "validity test" did not differ statistically from the data recorded in reality and with respect to warm carcass weight the values were even identical. The greatest differences were recorded in meat weight in the carcass (0.88 kg), however, not even did this difference reveal any significance.

CONCLUSION

Ultrasound combined with measurements of body dimensions can be used to assess selected indices of slaughter value in live bulls of the Slovakian Pied breed. The method is advantageous because of its low costs, high precision and reliability of results. The possibility of storing the images and making back-up copies on accessible memory media for later use present a great advantage. Laboriousness and the need for measurement in advance (with view to the guard delay of the tranquilizer employed) can prevent this method from becoming widely introduced as a method of beef bull evaluation in slaughterhouses. In case a single instrument similar to FOM (measuring meat percentage in swine carcasses) could be constructed for measuring muscle tissue thickness, broader dissemination of the method could be expected. Based on the previously said we consider the method to be very suitable for meat yield evaluation in young beef bulls of dual-purpose and meat type cattle in Slovakia. Since there is a lack of systems and capacity for testing of fattening performance and carcass value at stations, it seems to be suitable to use the data obtained by ultrasound in the breeding process of dual purpose and meat breeds.

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Corresponding Author:

Ing. Peter Polák, Výskumný ústav živočíšnej výroby, Hlohovská 2, 949 92 Nitra, Slovak Republic
Tel. +421 87 654 63 28, fax +421 87 654 63 61, e-mail: polak@vuzv.sk

Genetic parameters for the Black Pied Přeštice breed: comparison of different multi-trait animal models

Genetické parametry pro plemeno přeštické černostrakaté: porovnání různých víceznakových animal modelů

J. Wolf, Š. Horáčková, M. Wolfová

Research Institute of Animal Production, Prague-Uhříněves, Czech Republic

ABSTRACT: Genetic parameters were estimated for the Black Pied Přeštice breed using six five-trait animal models. In model variants 1–4, herd and year-season were treated as separate factors which were either fixed or random; model variants 5 and 6 included the combined herd-year-season effect as fixed or random, respectively. The following traits were evaluated: ADGF – average daily gain in the field test (n = 22 407); LMF – lean meat contents in the field test (n = 8 864); NBA, NW – number of piglets born alive and weaned, respectively (n = 8 979); LWW – litter weight at weaning (n = 8 783). Model 6 with herd-year-season random was found to show the lowest residual variances for all traits. The estimates of heritabilities and genetic correlations for model 6 were: ADGF 0.26, LMF 0.54, NBA 0.08, NW 0.08, LWW 0.07, ADGF-LMF –0.30, ADGF-NBA –0.10, ADGF-NW –0.13, ADGF-LWW 0.04, LMF-NBA 0.11, LMF-NW 0.10, LMF-LWW –0.09, NBA-NW 0.87, NBA-LWW 0.34, NW-LWW 0.52. These parameters were recommended for use in the routine genetic evaluation of the breed.

Keywords: pig; genetic parameters; multitrait animal model; Black Pied Přeštice pig; genetic resources

ABSTRAKT: Byly odhadnuty genetické parametry pro plemeno přeštické černostrakaté šesti pětiznakovými animal modely. V modelech 1 až 4 byly stádo a rok-období považovány za samostatné faktory, které byly buď pevné nebo náhodné; modely 5 a 6 zahrnovaly kombinovaný efekt stádo-rok-období jako pevný nebo náhodný. Byly hodnoceny tyto znaky: ADGF – průměrný denní přírůstek v polním testu (n = 22 407); LMF – podíl libového masa v polním testu (n = 8 864); NBA, NW – počet živě narozených a dochovaných selat (n = 8 979); LWW – hmotnost vrhu při odstavu (n = 8 783). Model 6 s náhodným efektem stádo-rok-období měl pro všechny znaky nejnižší reziduální varianci. Koeficienty heritability a genetické korelace odhadnuté modelem 6 byly tyto: ADGF 0,26, LMF 0,54, NBA 0,08, NW 0,08, LWW 0,07, ADGF-LMF –0,30, ADGF-NBA –0,10, ADGF-NW –0,13, ADGF-LWW 0,04, LMF-NBA 0,11, LMF-NW 0,10, LMF-LWW –0,09, NBA-NW 0,87, NBA-LWW 0,34, NW-LWW 0,52. Bylo doporučeno použít tyto parametry pro rutinní genetické hodnocení plemene.

Klíčová slova: prasata; genetické parametry; víceznakový animal model; přeštické černostrakaté; genetické zdroje

INTRODUCTION

Recently, genetic parameters have been estimated for the Czech Landrace and Large White breed and jointly for six sire breeds used in the Czech Republic (Groeneveld *et al.*, 1998; Peškovičová *et al.*, 1999; Wolf *et al.*, 2000) by multitrait animal models. No estimates of genetic parameters calculated by modern methods are available for the Black Pied Přeštice breed.

The Black Pied Přeštice breed is a small Czech pig breed which was originally bred for good fitness and reproduction. During recent years the numbers of animals have steadily decreased. Since 1992 the breed has had the status of a genetic resource. For developing a mating system for this breed and for monitoring the genetic development of the breed it will be useful to know the genetic parameters of traits of interest and the breeding value of all animals of the population. Therefore, the

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first aim of the present paper was to develop a multitrait animal model for the joint genetic evaluation of production and reproduction traits.

A second question of more general interest was the impact of different ways of modelling the herd-year-season complex of environmental factors on the estimates of genetic parameters.

MATERIAL AND METHODS

Animals

The original data set contained 24 261 records for production traits from performance test on farm and 14 037 records for reproduction traits. The data were collected between 1989 and 1998. The following five traits were included in the analyses:

ADGF – Average daily gain in the field test (in g/day) calculated as weight at the end of test divided by age at the end of test. The weight at the end of test ranged from 70 to 110 kg for sows and from 80 to 120 kg for boars. No precorrection for weight was carried out.

LMF – Lean meat contents estimated in the field test (in %) using PIGLOG (ultrasonic measurements - for details see Groeneveld *et al.*, 1998) without any liveweight adjustment.

NBA – Number of piglets born alive.

NW – Number of piglets weaned (at the age of 21 days).

LWW – Litter weight at weaning (at the age of 21 days).

The limitations given in Table 1 were applied to the original data set for generating a subset of data which served as the basis for the estimation of genetic parameters. The basic statistics for this subset of data is given in Table 2. The number of observations for LMF is considerably lower than for ADGF, as LMF has been measured since mid 1995 only.

Statistical methods

A survey of statistical models used in the calculations is given in Table 3. In all calculations, two production traits and three reproduction traits were evaluated jointly in a five-trait animal model with different model equations for different traits. For reproduction traits a formal variable "parity class" was formed which took value 1 for first litter and value 2 for second and later litters. Reproduction traits from first litter were then regressed on age at farrowing (covariable for parity class 1) and age at farrowing squared, reproduction traits for second and later litters were regressed on farrowing interval (covariable for parity class 2) and farrowing interval squared. Two types of feeding were differentiated (*ad libitum* and restricted) for production traits. The litter effect was included for both production traits.

Altogether, six model variants were calculated differing in modelling the herd-year-season complex of factors. In variants 1 to 4, herd and year-season were treated as separate factors, whereas a joint herd-year-season effect was incorporated in variants 5 and 6. Further differentiation

Table 1. Limitations for data

Trait, characteristics	Lower bound	Upper bound
Number of piglets born	6	15
Number of piglets born alive	5	15
Number of piglets weaned	4	14
Number of still born piglets	0	4
Losses during weaning	0	4
Litter weight at weaning (kg)	15	80
Farrowing interval (days)	130	210
Age at 1st farrowing (days)	330	450
Age at 2nd farrowing (days)	480	650
Age at 3rd farrowing (days)	630	850
Age at 4th farrowing (days)	780	1 050
Age at 5th farrowing (days)	930	1 250
Age at 6th farrowing (days)	1 080	1 450
Length of pregnancy (days)	110	120
Parity	1	6
Average daily gain (g/day)	350	850
Lean meat content (%)	44	65
Number of observations in herd, year-season or herd-year-season class for production traits	5	–
Number of observations in herd, year-season or herd-year-season class for reproduction traits	5	–

Table 2. Basic statistics of the data set for the estimation of genetic parameters

Trait	Number of records	Minimum	Maximum	Mean	Standard deviation
ADGF	22 407	350	829	514	61.5
LMF	8 864	44.1	64.4	56.6	3.1
WF	22 407	70	135	88.5	11.5
NB	8 979	6	15	11.0	2.0
NBA	8 979	5	15	10.3	1.9
NW	8 979	4	14	9.6	1.8
LWW	8 783	15.1	79.9	54.4	10.7

ADGF– average daily gain in the field test (g/day), LMF – lean meat contents estimated in the field test using PIGLOG (%), WF – live weight in the field test (kg), NB – number of piglets born, NBA – number of piglets born alive, NW – number of piglets weaned, LWW – litter weight at weaning (kg, at 21 days of age)

Table 3. Statistical models

Factor	Type	Trait					Variant
		ADGF	LMF	NBA	NW	LWW	
		Factors equal for all variants					
Weight at field test	C	–	x	–	–	–	1–6
Sex	F	x	x	–	–	–	1–6
Type of feeding	F	x	x	–	–	–	1–6
Litter	R	x	x	–	–	–	1–6
Animal	A	x	x	x	x	x	1–6
Covariable within parity class	C	–	–	x	x	x	1–6
Covariable squared within parity class	C	–	–	x	x	x	1–6
Parity	F	–	–	x	x	x	1–6
Mating type	F	–	–	x	x	x	1–6
Permanent effect of sow	R	–	–	x	x	x	1–6
		Factors differing for variants					
Herd for production traits	F R	x	x	–	–	–	1, 3 2, 4
Herd for reproduction traits	F R	–	–	x	x	x	1, 3 2, 4
Year-season for production traits	F R	x	x	–	–	–	1, 2 3, 4
Year-season for reproduction traits	F R	–	–	x	x	x	1, 2 3, 4
Herd-year-season for production traits	F R	x	x	–	–	–	5 6
Herd-year-season for reproduction traits	F R	–	–	x	x	x	5 6

C – covariable, F – fixed factor, R – random factor, A – random factor with relationship matrix
For abbreviations of traits see Table 2

of variants was made by assuming the factors to be fixed or random (Table 3).

No residual covariances were assumed between production and reproduction traits yielding a block-diagonal covariance matrix for the residual effect. The covariance matrix for the animal effect (additive genetic covariance matrix) was a complete 5 × 5 matrix. For all other random variables, the block belonging to the production traits (litter, herd for production traits etc.) or the block belonging to the reproduction traits (permanent effect of sow, herd for reproduction traits etc.) was filled with non-zero elements.

Restricted maximum likelihood (REML) and optimisation by a quasi Newton algorithm with analytical gradients (Neumaier and Groeneveld, 1998) as implemented in VCE 4.0 program (Groeneveld and García Cortés, 1998) were used to estimate the (co)variance structure. The number of (co)variance components was between 33 (variants 1 and 5) and 51 (variant 4). Approximate standard errors of the (co)variance components representing the lower border of the real standard errors were calculated from the Hessian matrix. VCE was run on a PC Pentium II, 333 MHZ under LINUX. The CPU time was between 8:54 and 14:45 hours with 86 to 151 iterations. The number of equations was 215 864 for variants 1–4 and 219 026 for variants 5 and 6. The number of non-zero coefficients was nearly three millions.

RESULTS

The estimates of heritabilities and genetic correlations for all five traits are presented in Table 4. The approximate standard errors of the heritabilities were between 0.005 and 0.024, the appropriate standard errors for the genetic correlations ranged from 0.011 to 0.077. LMF had the highest heritability (around 0.50), the heritability of ADGF was approximately in the range from 0.20 to 0.25 and the heritabilities of all three litter traits were in the range from 0.04 to 0.08. Comparing the six model variants with each other, the highest estimates of heritabilities for all traits except LWW were found in variant 6.

Table 4. Estimates of heritabilities and genetic correlations

Trait or combination of traits	Variant 1	2	3	4	5	6
			Heritabilities			
ADGF	0.26	0.21	0.25	0.20	0.23	0.26
LMF	0.50	0.49	0.52	0.51	0.51	0.54
NBA	0.06	0.06	0.06	0.06	0.05	0.08
NW	0.08	0.07	0.07	0.07	0.06	0.08
LWW	0.08	0.07	0.07	0.07	0.04	0.07
			Genetic correlations			
ADGF-LMF	−0.35	−0.36	−0.31	−0.32	−0.35	−0.30
ADGF-NBA	−0.13	−0.12	−0.16	−0.16	−0.13	−0.10
ADGF-NW	−0.10	−0.10	−0.13	−0.13	−0.16	−0.13
ADGF-LWW	0.10	0.10	0.08	0.07	0.18	0.04
LMF-NBA	0.09	0.10	0.06	0.07	0.16	0.11
LMF-NW	0.06	0.07	0.01	0.02	0.15	0.10
LMF-LWW	−0.01	0.00	−0.07	−0.05	−0.13	−0.09
NBA-NW	0.96	0.96	0.95	0.95	0.98	0.87
NBA-LWW	0.41	0.41	0.40	0.39	0.34	0.34
NW-LWW	0.49	0.48	0.47	0.46	0.50	0.52

For abbreviations of traits see Table 2

Table 5. Estimates of variance ratios for litter, permanent, herd, year-season and herd-year-season effects

Trait	Variant 1	2	3	4	5	6
			Variance ratios for litter effect			
ADGF	0.25	0.20	0.24	0.19	0.17	0.12
LMF	0.10	0.10	0.10	0.09	0.06	0.05
			Variance ratios for permanent effect of sow			
NBA	0.05	0.05	0.05	0.05	0.06	0.05
NW	0.05	0.05	0.05	0.05	0.06	0.05
LWW	0.06	0.06	0.07	0.06	0.08	0.07
			Variance ratios for herd (1st row), year-season (2nd row) and herd-year-season (3rd row) effects for production and reproduction traits			
ADGF	–	0.19	–	0.19	–	–
	–	–	0.04	0.03	–	–
	–	–	–	–	–	0.19
LMF	–	0.03	–	0.02	–	–
	–	–	0.01	0.01	–	–
	–	–	–	–	–	0.06
NBA		0.03	–	0.03	–	–
	–	–	0.01	0.01	–	–
	–	–	–	–	–	0. 03
NW	–	0.03	–	0.03	–	–
	–	–	0.01	0.01	–	–
	–	–	–	–	–	0.03
LWW	–	0.03	–	0.03	–	–
	–	–	0.02	0.02	–	–
	–	–	–	–	–	0.07

For abbreviations of traits see Table 2

In general, the heritability estimates differed only little between the variants.

A clearly negative correlation between ADGF and LMF was found. All correlations between production and reproduction traits were less than 0.20 in their absolute values. They were negative between ADGF and litter size traits (NBA, NW) and between LMF and LWW. A very high correlation was found between NBA and NW, the correlations between LWW and litter size traits were in the range from 0.34 to 0.52, the correlation between LWW and NW always being higher than the correlation between LWW and NBA. No remarkable changes of genetic correlations between model variants were observed.

The estimates of variance ratios for nongenetic random factors except the residual effect are summarized in Table 5. The variance ratio for common litter effect was between 0.19 and 0.25 for ADGF and between 0.09 and 0.10 for LMF in model variants with separate herd and year-season effects (variants 1 to 4). In the two remaining model variants 5 and 6 with joint herd-year-season effects, the variance ratio for litter effect was considerably lower. In model variant 6 with random herd-year-season effect, the variance ratios for ADGF and LMF were 0.12 and 0.05, respectively, which was approximately 50% of the values of model variants 1 to 4. The standard errors of the estimates were in the range from 0.003 to 0.006, taking the lowest values of 0.003 to 0.004 in model variant 6.

The variance ratio for the permanent effect of the sow was between 0.05 and 0.06 for NBA and NW and between 0.06 and 0.08 for LWW. The estimates were very similar among all model variants. The approximate standard error of estimates was in the range from 0.004 to 0.010. The highest standard errors (0.010 for all three reproduction traits) occurred in model 3 with herd fixed and year-season random.

When comparing the variance ratios for herd and for year-season, it was found that the herd effect contributes a greater part to the total variance than the year-season effect. For ADGF, NBA and NB, the variance ratio for the herd-year-season effect was of the same magnitude as the variance ratio for the herd effect. For LMF and LWW, the variance ratio for the herd-year-season effect was about twice the variance ratio for the herd effect. The approximate standard errors of variance ratios were 0.006 to 0.012 for the herd effect of production traits, 0.004 to 0.006 for the herd effect of reproduction traits, 0.001 to 0.004 for the year-season effect and 0.003 to 0.005 for herd-year-season effect, both for all traits.

A criterion for comparing different models is the residual variance (Table 6), which was lowest in model variant 6 for all traits. Model variant 6 was therefore the variant which used most information from the data. The residual variance of model variant 6 was set 100% for further considerations. Between model variants 1 to 4 with separate herd and year-season effects there were hardly any differences in the residual variance in all traits except LMF. The residual variance of LMF was lower in model variants 3 and 4 (with random year-season effect) than in model variants 1 and 2 (with fixed year-season effect). Random herd-year-season effect (variant 6) yielded residual variances about 10% lower than fixed herd-year-season effect (variant 5). In reproduction traits this difference was only 1%.

Table 6. Estimates of variance ratios for residual effects (1st row), estimates of residual variances (2nd row) and relative values of residual variances in per cent of the residual variance for model variant 6 (3rd row)

Trait	Variant					
	1	2	3	4	5	6
ADGF	0.50	0.40	0.48	0.39	0.61	0.43
	1 521.81	1 520.34	1 517.35	1 515.87	1 563.92	1 434.59
	106	106	106	106	109	100
LMF	0.40	0.39	0.37	0.36	0.43	0.35
	2.978	2.972	2.868	2.855	3.014	2.717
	110	109	106	105	111	100
NBA	0.89	0.86	0.88	0.86	0.89	0.85
	3.085	3.085	3.085	3.085	3.040	3.024
	102	102	102	102	101	100
NW	0.88	0.85	0.87	0.85	0.88	0.84
	2.826	2.827	2.825	2.826	2.787	2.770
	102	102	102	102	101	100
LWW	0.86	0.84	0.85	0.83	0.88	0.80
	94.629	94.646	94.525	94.541	91.007	90.378
	105	105	105	105	101	100

For abbreviations of traits see Table 2

Reproduction traits had a considerably higher proportion of the residual variance in the total variance (80 to 90%) than production traits (35 to 60%, Table 6). In all traits except ADGF the proportion of residual variance was lowest in model variant 6.

DISCUSSION

The estimated heritabilities are in agreement with literature data for other dam breeds of pig (Landrace, Large White, Yorkshire). Ducos (1994) reported a mean value of 0.43 for the heritability of LMF and a value of 0.27 for the heritability of ADGF. These values were averaged from 6 and 35 literature sources, respectively. Hermesch (1996) gave a mean value of 0.35 for the heritability of ADGF when analysing 18 sources. In more recent papers, values in the range from 0.10 to 0.49 were estimated for the heritability of ADGF (Adamec and Johnson, 1997; Crump *et al.*, 1997; Sévon-Aimonen *et al.*, 1997; Groeneveld *et al.*, 1998; Maignel *et al.*, 1998; Willms *et al.*, 1998; López-Serrano *et al.*, 2000). The low value of 0.11 estimated for the Black Pied Přeštice pig in a former study (Groeneveld *et al.*, 1998) and similar low values estimated for other Czech pig populations might be due to problems with the accuracy of data recording. Meanwhile, multi-trait animal models have been introduced for all large pig breeds in the Czech Republic which have had a positive feed back on the quality of the data. This can explain that the heritability estimates for production traits in the recent study are higher than in Groeneveld *et al.* (1998).

Based on literature values published until 1996, Rothschild (1996) reported mean values of 0.07 and 0.06 for the heritabilities of NBA and NW, respectively. In a more recent paper, Rydhmer (2000) gave 0.1 as median estimate from literature values for the heritability of NBA. For LWW, Hermesch (1996) calculated a mean heritability of 0.11 from 9 literature sources, the interval for field data being 0.06 to 0.17. Adamec and Johnson (1997) calculated a value of 0.09 on a Czech data set.

It was shown in several papers that the litter size in the first parity has a genetic correlation lower than 1 with the litter size of the following parities (Tholen *et al.*, 1996; Bösch *et al.*, 1999; Hanenberg *et al.*, 1999; Wolf *et al.*, 1999; Hermesch *et al.*, 2000; Täubert and Brandt, 2000). The litter size at first parity should preferably be treated as a separate trait therefore. But on the other hand, the genetic correlation between the first parity and the following parities is high enough for justifying the repeatability model at least in certain cases. According to our opinion, the first and the following parities should be treated as two traits in larger breeds with high herd sizes. In small breeds, as in Black Pied Přeštice, the number of observations per herd-year-season class would become too small for a qualified estimation of the environmental effects when treating the first parity separately. Therefore it was decided to use a repeatability model. But a differentiation was made between the first and the following parities by using different covariables through the introduction of the factor "parity class".

Correlations between production traits and litter traits reported in the literature (Rydhmer *et al.*, 1995; Ducos and Bidanel, 1996; Tholen *et al.*, 1996; Crump *et al.*, 1997; Maignel *et al.*, 1998) confirm mostly the low values presented in the present study. But an average correlation of zero does not mean that there are no relations between production and reproduction traits in a particular breeding programme. It can be expected that there is a causal relationship between growth and reproduction, but the measured traits are not chosen for taking maximal advantage from this relation. The relation between production and reproduction traits is probably non-linear yielding different correlation coefficients for different genotypes. Furthermore, genetic correlations may depend on environmental factors like the feeding regime (Rydhmer, 2000).

Schaeffer (1993) concluded that multiple trait models help to improve the accuracy of genetic evaluation. The amount of improvement depends on the heritabilities of the traits included, the genetic correlations between the traits and the amount of information available for traits. As the heritabilities for reproduction traits are very low, any additional information on the reproduction performance will be useful. Therefore, production and reproduction traits should be evaluated simultaneously in a multiple-trait evaluation, as stated by Rydhmer (2000).

In the present study, the residual variance was used as a criterion for comparing models. Frey *et al.* (1997) randomly omitted observations from herd-time effect classes and predicted the excluded observations by different models. They found that models with a random herd-time effect predicted excluded observations from herd-time classes with 10 or less observations more accurately than models with a fixed herd-time effect. There were hardly any differences between fixed and random models to predict observations from larger herd-time classes. This finding supports the above result that models with herd-year-season as random factor should be preferred to models with herd-year-season as fixed factor.

CONCLUSIONS

The comparison of different kinds of modeling the herd-year-season complex of environmental factors implies that the use of a model with a combined random herd-year-season effect ensures the lowest residual variance (uses most information from data) and should therefore be preferred to models with separate herd and year-season effects and models with a fixed herd-year-season effect. In litter traits, different regressions should be used for first parity and for later parities, if the first parity is not treated as a separate trait. Though the genetic correlations between production and reproduction traits are generally low, they may be different from zero in particular breeding populations and may therefore increase the effectiveness of selection for reproduction traits. The estimated genetic parameters should be used for the routine genetic evaluation of the Black Pied Přeštice breed.

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Corresponding Author:

Dr. Jochen Wolf, Výzkumný ústav živočišné výroby, P.O.Box 1, 104 00 Praha-Uhříněves, Česká republika
Tel. +420 2 67 71 07 78, fax +420 2 67 71 07 79, e-mail: wolf@vuzv.cz

Effects of a fattening system on meat performance of crossbred bulls and steers sired by Gascon and Charolais bulls

Vliv různého způsobu výkrmu na masnou užitkovost býků a volů – kříženců po otcích plemen gasconne a charolais

L. BARTOŇ, V. TESLÍK, H. HERRMANN, R. ZAHRÁDKOVÁ, D. BUREŠ

Research Institute of Animal Production, Prague-Uhříněves, Czech Republic

ABSTRACT: Fattening performance, carcass composition and meat quality were investigated in 44 crosses sired by Gascon (GS) and Charolais (CH) bulls. The animals were allocated to three groups. Indoor bulls (IB) and indoor steers (IS) were finished indoors on a diet consisting of maize silage and grass haylage, fodder straw and concentrates and slaughtered at 530 and 500 kg respectively. After 78 days of winter housing on a low energy diet extensive steers (ES) were turned out to pasture for 181 days. It was followed by a finishing period (70 days) in which the animals were offered a high energy diet. Throughout the whole experimental period, the weight gains of IB bulls amounted to 1.101 kg/day while those of IS and ES steers were 0.819 and 0.632 kg/day respectively ($P < 0.001$). The IB bulls had the highest dressing percentage (60.12 vs. 59.37 and 58.35% resp.; $P < 0.05$) and the most favourable carcass conformation (2.14, vs. 2.64 and 2.41; $P < 0.05$). Internal fat production, fatness score, separable fat proportion, fat thickness and lipid content in lean tissue were highest in the IS group. Total meat proportion was highest ($P < 0.05$) in the IB group (80.81 vs. 79.44 and 79.62% resp.) while grade I meat proportions were higher in both the IS and ES steers ($P < 0.01$). The lowest ($P < 0.001$) protein content in lean tissue and the highest ($P < 0.001$) pH measured 24 hours after slaughter were found in the ES group. Breed differences were displayed particularly in lower daily gains, higher production of internal fat and less favourable fatness score of the GS crosses.

Keywords: beef cattle; bulls; steers; fattening system; performance; carcass composition; meat quality

ABSTRAKT: Ukazatele výkrmnosti, složení jatečného těla a kvality masa byly sledovány u 44 kříženců po otcích plemen gasconne (GS) a charolais (CH) rovnoměrně rozdělených do tří skupin podle způsobu použitého výkrmu. První skupinou (IB) byli býci vykrmovaní ve stáji krmnou dávkou podávanou *ad libitum* a sestávající z kukuřičné siláže, travní senáže, krmné slámy a jadrné směsi. Druhou skupinou (IS) byli voli vykrmovaní stejným způsobem jako skupina IB. Zvířata skupin IB a IS byla poražena po dosažení hmotnosti 530, resp. 500 kg. Třetí skupinu (ES) tvořili voli, kterým byla nejdříve po dobu 78 dnů podávána KD s nižším podílem jadrné směsi než u skupin IB a IS, poté následovalo pastevní období v délce 181 dnů zakončené 70 dny intenzivního dokrmu. Za celé období výkrmu byly dosaženy průměrné hodnoty denního přírůstku: 1,101 kg/den pro IB, 0,819 kg/den pro IS a 0,632 kg/den pro ES ($P < 0.001$). Stejná tendence byla zjištěna i u netto přírůstku (0,607; 0,520 a 0,444 kg/den). U skupiny IB byla zjištěna nejvyšší jatečná výtěžnost (60,12 %) a nejpříznivější subjektivní hodnocení zmasilosti jatečného těla. Produkce vnitřního loje, subjektivní hodnocení protučnělosti, podíl tuku oddělitelného z jatečného těla, vrstva tuku na roštěnci i podíl tuku ve vzorcích svaloviny byly nejvyšší u skupiny IS. Nejvyšší podíl masa ($P < 0,05$) v jatečném těle byl u skupiny IB (80,81 vs. 79,44 a 79,62 %), zatímco vyšší podíl masa I. jakosti a větší plocha LLT/100 kg porážkové hmotnosti byly zjištěny u obou skupin volů. Obsah bílkovin ve vzorcích svaloviny byl nejnižší u skupiny ES (208,7 g/kg), u které bylo 24 hodin po porážce naměřeno také nejvyšší pH (5,86). Nejnižší hodnota cholesterolu byla zjištěna u skupiny IB (0,44 g/kg). Plemenné rozdíly se projevily především v nižším denním přírůstku, ve vyšší produkci vnitřního loje a v méně příznivém hodnocení protučnělosti jatečných těl kříženců GS. Lze konstatovat, že byla potvrzena vyšší růstová schopnost býků a zároveň jejich vyšší celková produkce masa v porovnání s voly, u kterých byl naopak zjištěn vyšší podíl cennějších jatečných

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partií. Začlenění pastevní fáze do výkrmu snížilo průměrně dosahovaný přírůstek za celý výkrm, ale zároveň snížilo protučnělost jatečných těl i obsah tuku ve svalovině.

Klíčová slova: **masný skot; býci; voli; způsob výkrmu; výkrmnost; složení jatečného těla; kvalita masa**

INTRODUCTION

The traditional system of beef production in the Czech Republic is to finish young animals indoors. The diets are usually based on *ad libitum* roughage supplemented with concentrates throughout the whole fattening period. Mostly entire males are used for fattening, the importance of steers and heifers is rather low. However, in the Czech Republic as well as in the EU countries, some agricultural sectors are encouraged to look for less intensive production systems. At the same time the significance of permanent grasslands increases, especially in mountain and submountain regions. Thus the introduction of summer grazing into the cattle fattening system has been suggested when looking for production alternatives complying with the above mentioned current trends.

Beef production systems using forage may range from finishing cattle on grass, grazing cattle on grass, then finishing them intensively for a relatively short period of time, or feeding a high-roughage diet in drylot (Schaake *et al.*, 1993). Restricted feed intake and reduced energy content in pasture diet result in extended growing period and delaying fat deposition in carcasses so that especially small-framed cattle can reach higher and therefore more acceptable slaughter weights at a specified fat thickness (Owens *et al.*, 1993).

The advantage of grain feeding appears to be the ability to attain higher growth rates, which means that cattle can reach optimum slaughter weights at a younger age. Thus grain feeding might affect those meat quality parameters which are affected by age, e.g. tenderness and meat colour. Provided cattle are fed on pasture to achieve high growth rates, so that they achieve acceptable slaughter weights and degree of finish at a similar "early" age to that possible in grain-fed cattle, it is likely that beef produced on pasture can be of comparable eating quality to that produced off a grain diet (Muir *et al.*, 1998a).

Drouillard and Kuhl (1999) reviewed the nutrition and management factors employed during the grazing period such as effects of grazing pressure, duration of the grazing season, supplementation on pasture or implanting pasture cattle, which influence subsequent finishing performance of animals.

Beef producers are often interested in using pasture because of the high costs associated with feedlot finishing (McCaughey and Cliplef, 1996). Economic results favourable for fattening systems with a grazing period in spite of slightly poorer animal performance are also reported by Dufrasne *et al.* (1995), and Keane and Allen (1998).

The differences between bulls and steers in growth characteristics and carcass quality were reviewed by many authors. Generally bulls gain more rapidly and more efficiently and produce leaner carcasses with higher proportion of muscle than steers. However, beef from young bulls can often be characterised by lower palatability and tenderness (Seideman *et al.*, 1982).

MATERIAL AND METHODS

A total of 48 animals was used in the experiment, 24 sired by Gascon (GS, 4 sires) and 24 sired by Charolais (CH, 4 sires) bulls. The breed of the dams was equally represented by Czech Pied and Black and White breeds. The spring-born calves were reared outdoors with their dams. After weaning, they were housed in an experimental facility of the Research Institute of Animal Production in Prague-Uhříněves. After a transition period, the animals were allocated to two groups with equal average weight and proportion of Gascon and Charolais breeds. The bulls of one group were castrated with emasculator and again allocated to two equal groups. The resulted groups were Indoor bulls (IB, $n = 24$), Indoor steers (IS, $n = 12$) and Extensive steers (ES, $n = 12$). Four animals were removed from the experiment due to health problems so that the number of animals was reduced to 21, 11 and 12 in IB, IS and ES respectively.

The IB and IS animals were loose-housed indoors throughout the whole fattening period (12 animals per box). A mixed diet was offered *ad libitum* and consisted of maize silage and grass haylage, wheat straw and concentrates. The concentrates (33% on a dry matter basis) consisted of wheat and soybean meal.

The ES steers were housed in the same place as the other animals during winter and fed a mixed diet with 27% of concentrates. After 78 days of winter housing, they were turned out to pasture. The grazing period continued for 181 days. At the end of the grazing period (the last 60 days), the steers were supplemented with grass haylage due to worsened grazing conditions as a result of dry summer. The finishing period of 70 days followed. During the first 30 days the animals were given a diet *ad libitum* consisting of maize silage and grass haylage. The last 30 days they were offered a high energy diet with 54% of concentrates on a dry matter basis. The diets were calculated using the software "Operative Management of Cattle Nutrition v 5.5" on the basis of regular monthly weighing of animals and repeated chemical analyses of diet ingredients.

The target slaughter weights were 530 and 500 kg for the groups IB and IS respectively. The ES steers were slaughtered after 70 days of finishing period. All the animals were slaughtered in the experimental abattoir of the Research Institute of Animal Production. After slaughter, warm carcass weight and internal fat weight (kidney, rumen and intestinal fats) were recorded. Carcass gain was calculated as a ratio of carcass weight and days to slaughter. The carcasses were classified for conformation and fat cover (scale from 1 to 5) according to the method described by Burda *et al.* (1988).

After chilling (24 hours after slaughter), the cold carcass weight was recorded and the right sides were dissected into prime cuts. Yields of saleable meat, separable fat and bones plus tendons in different cuts were determined. The total meat yield was calculated as the total meat from individual cuts plus lean trimmings. The grade I meat yield was determined as the total weight of meat from rump, shoulder, fillet and sirloin and the grade II meat yield as the meat from the other cuts plus lean trimmings. Backfat thickness and *m. longissimus lumborum et thoracis* (LLT) area were measured at the section between 8th and 9th thoracic vertebrae.

Samples of LLT (9–11th thoracic vertebrae) were obtained for determination of meat quality characteristics. Meat colour (% remission at 685 nm) and pH of meat 24 hours after slaughter (pH meter Orion 250 A) were measured. Chemical analysis involved determination of dry matter (drying at 105°C), protein (Kjeltec AUTO 1030 Analyzer), lipid (Soxtec 1047) and cholesterol contents.

Data were analysed using the GLM procedure of the Statistical Analysis Systems Institute (SAS Institute Inc., 1998). The model included the fixed effects of fattening system ($i = 1, 2, 3$) and sire's breed ($i = 1, 2$). According to the results of preliminary analysis, the interactions between the two effects were not statistically significant and therefore the interaction was excluded from the final model. The significance of differences between the fattening systems was determined by Tukey's method.

RESULTS AND DISCUSSION

Fattening performance

Fattening characteristics are shown in Table 1. The differences in live weight and age at the start of the experiment between the groups are small and not significant. Live weight gain in different experimental periods was calculated only for ES steers. During the stable, pasture and finishing periods, the steers gained 0.633, 0.518 and 0.912 kg/day respectively. The feed restriction before the grazing period may allow high gains on pasture if quality and highly digestible grass is available (Therkildsen *et al.*, 1998). In our case the grazing conditions were rather poor and it resulted in even lower growth rate during the pasture period than in winter indoor period with restricted feeding. Average daily gains on grass reported by other authors are usually higher. Keane and Allen (1998) reported daily gains from 0.88 to 0.97 kg/day in Charolais × Friesian steers, the results of Dufrasne *et al.* (1995) with Belgian Blue bulls ranged from 1.00 to 1.15 kg/day. During the following finishing period, growth rate increased considerably as a result of a high concentrate diet and compensatory growth, which is in agreement with Berge *et al.* (1991).

The IB, IS and ES animals reached their slaughter weights (531.3; 501.2 and 478.8 kg resp.; $P < 0.001$) at the age of 531.5; 577.0 and 630.3 days respectively ($P < 0.001$). For the whole experimental period, the IB bulls gained 1.101 kg/day while the IS and ES steers gained 0.819 and 0.632 kg/day respectively ($P < 0.001$). The difference between bulls and steers under a similar management system (groups IB, IS) in growth rate was about 26%.

Table 1. Fattening characteristics

	Fattening system (FS)			Breed (B)		S.E	Significance	
	IB ($n = 21$)	IS ($n = 11$)	ES ($n = 12$)	GS ($n = 22$)	CH ($n = 22$)		FS	B
Age at start (days)	295.2	310.5	308.8	308.6	301.0	7.79		
Live weight at start (kg)	275.1	283.8	275.8	277.9	278.6	5.97		
Liveweight gain – indoor period (kg/day)			0.633	0.585	0.681	0.058		
Liveweight gain – pasture period (kg/day)			0.518	0.439	0.597	0.037		
Liveweight gain – finishing period (kg/day)			0.912	0.878	0.945	0.049		
Liveweight gain throughout the experiment (kg/day)	1.101^{a}	0.819^{b}	0.632^{c}	0.779	0.922	0.021	***	***
Age at slaughter (days)	531.5^{a}	577.0^{ab}	630.3^{b}	590.4	568.7	8.76	***	
Weight at slaughter (kg)	531.3^{a}	501.2^{b}	478.8^{b}	491.8	515.7	4.88	***	*

*$P < 0.05$ **$P < 0.01$ ***$P < 0.001$

Values with different superscripts (^{a}, ^{b}, ^{c}) differ significantly ($P < 0.05$).

This difference is larger than that found by Andersen and Ingvartsen (1984) – 15% and by Steen (1995) – 16%. The live weight gain of ES steers was considerably lower in comparison with IB (43%) and IS (23%) as a result of the above mentioned restricted winter feeding and poor grazing conditions in summer. Higher daily gains of cattle intensively fattened indoors in comparison with cattle fattened on pasture with a subsequent finishing period are reported also by Berge *et al.* (1991), Dufrasne *et al.* (1995) and Myers *et al.* (1999).

Irrespective of the fattening system, live weight gains of Charolais crosses over the whole experimental period were significantly higher ($P < 0.001$; CH 0.853 vs. GS 0.779 kg/day). Outstanding results of Charolais crosses in terms of live weight gain compared with other beef crosses are reported also by Hearnshaw *et al.* (1995) and Frelich and Voříšková (1997).

Slaughter characteristics

Slaughter characteristics are given in Table 2. Mean carcass weight was significantly higher ($P < 0.001$) for the IB group than for the IS and ES groups (319.4 vs. 297.3 and 279.3 kg resp.). The same tendency was also found in dressing percentage (60.12 vs. 59.37 and 58.35% resp.; $P < 0.05$) and carcass gain (0.607 vs. 0.520 and 0.444 kg/day resp.; $P < 0.001$). The highest dressing percentage of the IB group is connected particularly with the increased slaughter weight of the animals which is in agreement with findings of Andersen and Ingvartsen (1984) reporting that dressing percentage was unaffected by castration in animals of the same live weight and plane of nutrition. Dufrasne *et al.* (1995) concluded that dressing percentage was higher in the bulls which had been grazed previously in comparison with those fattened indoors as a result of a larger body frame developed in grazing bulls. However, this is in contrast to our study, again mainly due to the lower slaughter weight of the ES steers. Carcass gain higher for bulls than for steers when they were offered either *ad libitum* or restricted diet was reported by Steen (1995), which is in line with our results.

Proportions of internal fat (kidney, rumen and intestinal) were significantly higher ($P < 0.001$) in the IS group while in the IB and ES groups they were similar. The values of total internal fat proportions for the groups IB, IS and ES were 2.64, 4.38 and 2.65% respectively. The difference between the IB and IS animals is associated with greater potential of steers for fat deposition and higher average slaughter age of the IS animals. The similar difference between the IS and ES steers is a result of different fattening conditions and diet formulation. In agreement with this suggestion, Therkildsen et *al.* (1998) found that kidney fat weight was depending on slaughter weight from 4.52 to 7.81 kg for bulls fattened indoors and only from 1.45 to 3.29 kg for bulls initially grazed and then shortly finished on concentrates.

Conformation score was significantly better ($P < 0.05$) for the IB group than for the IS group. The highest fatness score ($P < 0.001$) was found in the IS group. Similar results of classification of bulls and steers under the same fattening system were reported by Steen (1995). There were no significant differences in conformation and fatness score between the IB bulls and ES steers. When compared to the IS steers, inclusion of the grazing period resulted in similar conformation score and more favourable fatness score in the ES steers in spite of higher slaughter age and lower slaughter weight of the animals. These findings are in agreement with Therkildsen *et al.* (1998).

Table 2. Slaughter characteristics

	Fattening system (FS)			Breed (B)		S.E.	Significance	
	IB ($n = 21$)	IS ($n = 11$)	ES ($n = 12$)	GS ($n = 22$)	CH ($n = 22$)		FS	B
Carcass weight (kg)	319.4^{a}	297.3^{b}	279.3^{b}	295.1	302.2	3.25	***	
Dressing percentage (%)	60.12^{a}	59.37^{ab}	58.35^{b}	59.94	58.61	0.288	*	*
Carcass gain (kg/day)	0.607^{a}	0.520^{b}	0.444^{c}	0.5111	0.537	0.009	***	
Kidney fat (% slaughter weight)	1.38^{a}	2.15^{b}	1.43^{a}	1.81	1.49	0.068	***	*
Rumen fat (% slaughter weight)	0.85^{a}	1.53^{b}	0.78^{a}	1.18	0.92	0.061	***	*
Intestinal fat (% slaughter weight)	0.42^{a}	0.71^{b}	0.44^{a}	0.58	0.46	0.026	***	*
Total internal fat (% slaughter weight)	2.64^{a}	4.38^{b}	2.65^{a}	3.57	2.88	0.133	***	*
Conformation[1]	2.14^{a}	2.64^{b}	2.41^{ab}	2.53	2.28	0.076	*	
Fatness[2]	2.18^{a}	2.83^{b}	2.08^{a}	2.56	2.17	0.071	***	**

*$P < 0.05$ **$P < 0.01$ ***$P < 0.001$

[1] Scale 1 (best) to 5 (poorest)

[2] Scale 1 (leanest) to 5 (fattest)

Values with different superscripts (^{a}, ^{b}, ^{c}) differ significantly ($P < 0.05$).

Breed differences were displayed especially in dressing percentage, internal fat proportion and fatness score. The GS animals had higher dressing percentage (59.94 vs. 58.61%; $P < 0.05$), higher total internal fat proportion (3.57 vs. 2.88%; $P < 0.05$) and less favourable fatness score (2.56 vs. 2.17; $P < 0.01$). Higher dressing percentage and internal fat production of GS crossbred bulls in comparison with commercial crosses with Blond d'Aquitaine were also reported by Bartoň *et al.* (1999).

Carcass composition

Fattening system and sex considerably affected carcass composition of the animals (Table 3). Total meat proportion was highest ($P < 0.05$) in the IB group in comparison with the IS and ES animals (80.81 vs. 79.44 and 79.62% resp.). The proportion of total meat in this group was higher mainly due to the larger proportion of grade II meat (40.69 vs. 38.58 and 38.22 resp.; $P < 0.001$). Conversely, the proportion of grade I meat was lower in the IB group (40.12 vs. 40.86 and 41.40% resp.; $P < 0.05$). These differences are well expressed by the ratio of grade I meat to grade II meat, which is higher ($P < 0.001$) and thus more favourable in both groups of steers. Similarly the steers had a larger ($P < 0.01$) area of the LLT relative to slaughter weight (18.08 vs. 19.71 and 20.90 cm^2/100 kg slaughter weight for IB vs. IS and ES resp.). The IS group had a higher proportion of separable fat ($P < 0.001$) and fat thickness ($P < 0.05$), which is consistent with the results of internal fat production. Bone plus tendons proportion was found higher ($P < 0.001$) in the carcasses of the ES group (18.74%) in comparison with IB (16.94%) and IS (17.11%). Consequently meat : bone ratio was significantly lower ($P < 0.001$) for the ES steers.

The higher meat and lower fat content in the carcasses of bulls than in those of steers fattened under a similar management system were reported by Steen and Kilpatrick (1995). In agreement with our findings they also found a significantly lower proportion of grade I meat in bulls than in steers. The fact that entire bulls from our experiment had a higher content of grade II meat can be explained as a result of greater development of forequarter muscles in bulls, which is agreement with Shahin *et al.* (1993). The higher bone production of steers fed only grass than of steers fed concentrates in their diet was reported by Schaake *et al.* (1993). The results of carcass composition are in general agreement with the findings of Keane and Allen (1998) who compared three production systems of different intensity.

The effect of sire's breed on carcass composition was small. The only significant differences were the higher area of LLT/100 kg slaughter weight in the GS animals ($P < 0.05$) and the greater thickness of backfat ($P < 0.05$) in the same group which is in consistency with internal fat production and carcass fatness score in this group.

Meat quality

The results of meat quality are shown in Table 4. Chemical analysis of the lean tissue from the LLT samples indicated a higher content of dry matter and lipids ($P < 0.001$) in the IS group (262.4 and 36.2 g/kg resp.) in comparison with IB (247.4 and 19.6 g/kg resp.) and ES (245.2 and 24.0 g/kg resp.). The higher lipid content in the lean tissue of the IS group corresponded with the greater production of internal fat and separable fat found in this group. Lipid content differences between bulls and steers fattened under similar conditions are reported by a number of authors (Seideman *et al.*, 1982; Dikeman *et al.*, 1986; Knight *et al.*, 1999). However, there were no significant differences in our experiment between the IB and ES animals in the muscle lipid concentration probably

Table 3. Carcass composition

	Fattening system (FS)			Breed (B)		S.E	Significance	
	IB ($n = 21$)	IS ($n = 11$)	ES ($n = 12$)	GS	CH		FS	B
Total meat (% right side)	80.81^{a}	79.44^{b}	79.62^{b}	79.86	80.06	0.203	*	
Grade I meat (% right side)	40.12^{a}	40.86^{ab}	41.40^{b}	40.71	40.87	0.196	*	
Grade II meat (% right side)	40.69^{a}	38.58^{b}	38.22^{b}	39.14	39.18	0.186	***	
Separable fat (% right side)	1.86^{a}	3.10^{b}	1.99^{a}	2.35	2.28	0.101	***	
Bones + tendons (% right side)	16.94^{a}	17.11^{a}	18.74^{b}	17.62	17.58	0.158	***	
Meat : bone	4.792^{a}	4.652^{a}	4.262^{b}	4.557	4.581	0.0494	***	
Meat I : meat II	0.987^{a}	1.062^{b}	1.085^{b}	1.044	1.045	0.0086	***	
LLT area/100 kg slaughter weight (cm^2)	18.08^{a}	19.71^{b}	20.90^{b}	20.42	18.71	0.368	**	*
Fat thickness (mm)	6.3^{a}	8.3^{b}	6.0^{a}	7.5	6.2	0.30	*	*

*$P < 0.05$ **$P < 0.01$ ***$P < 0.001$

Values with different superscripts (^{a}, ^{b}, ^{c}) differ significantly ($P < 0.05$).

Table 4. Meat quality traits

	Fattening system (FS)			Breed (B)		S.E.	Significance	
	IB (*n* = 21)	IS (*n* = 11)	ES (*n* = 12)	GS	CH		FS	B
Dry matter (g/kg)	247.4^{a}	262.4^{b}	245.2^{a}	251.1	252.3	1.32	***	
Protein (g/kg)	215.1^{a}	213.7^{a}	208.7^{b}	214.4	210.6	0.66	***	**
Fat (g/kg)	19.6^{a}	36.2^{b}	24.0^{a}	24.0	29.2	1.31	***	*
Cholesterol (g/kg)	0.44^{a}	0.54^{b}	0.52^{b}	0.49	0.51	0.012	**	
pH24	5.56^{a}	5.61^{a}	5.86^{b}	5.68	5.67	0.019	***	
Meat colour (% remission at 685 nm)	29.7	30.4	28.8	27.7	31.5	0.76		*

*$P < 0.05$ **$P < 0.01$ ***$P < 0.001$

Values with different superscripts (^{a}, ^{b}, ^{c}) differ significantly ($P < 0.05$).

due to different energy content in the diets which is in agreement with Keane and Allen (1998). Also Schaake *et al.* (1993) found that pasture steers had a lower percentage of ether extract in the lean tissue than drylot steers. Most authors report that there are no significant differences in percentage of protein due to the type of diet (Leander *et al.*, 1978; Schaake *et al.*, 1993; French *et al.*, 2000). In our experiment, however, the content of protein in the ES group was lower ($P < 0.001$) than in the other groups.

Cholesterol in the lean tissue was lower ($P < 0.01$) in the IB bulls (0.44 g/kg) than in the IS and ES steers (0.54 and 0.52 g/kg resp.). These values correspond with the values of cholesterol found in meat of steers differing in sire growth potential, time on feed and growing-finishing strategy (Rule *et al.*, 1997). Lower values (35–45 g/kg) are reported by Aharoni *et al.* (1995) for Friesian bulls fed different diets.

As reviewed by Muir *et al.* (1988a), lean colour is affected by a number of factors, e.g. increased marbling score or muscle myoglobin concentrations which are higher in grazing animals. However, there were no significant differences in lean colour between the groups differing in the fattening system in the present experiment. The ES steers had higher ($P < 0.001$) pH measured 24 hours after slaughter than the IB (5.56) and IS (5.61) animals. The same tendency was found by Muir *et al.* (1998b), who explained it as a result of lower susceptibility of grain-fed animals to higher pH because they become more accustomed to people and housing in boxes. However, in our experiment there was no pH value exceeding 6.2 which would mean the incidence of DFD meat (Šubrt and Schmidt, 1994).

Breed differences were expressed in higher contents of protein ($P < 0.01$) and lower contents of lipids ($P < 0.05$) in the GS group. The lower lipid concentrations in lean meat of the GS animals did not correspond with the production of internal fat and separable fat which was higher for this group. Bartoň *et al.* (1999) found no differences in lipid content between meat samples from Gascon and Blond d'Aquitaine crosses.

CONCLUSIONS

The results of the present experiment showed the superiority of bulls over steers in growth capacity under the same feeding conditions. Bulls also produced more total meat while steers had a higher proportion of grade I meat in carcass. Inclusion of a grazing period resulted in considerably lower live weight gain, lower overall fatness and lower content of lipids in lean meat. To improve the growth characteristics, it is necessary to provide animals with a high-quality forage. A product of acceptable quality can be expected when using an extensive fattening system with a grazing period.

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Corresponding Author:

Ing. Luděk Bartoň, Výzkumný ústav živočišné výroby, Přátelství 815, 104 01 Praha 10- Uhříněves, Česká republika
Tel. +420 2 67 71 17 47, fax +420 2 67 71 07 79, e-mail: barton@vuzv.cz

Effect of *Saccharomyces cerevisiae* and syringaldehyde on the fermentation parameters of meadow hay *in vitro*

Vplyv *Saccharomyces cerevisiae* a syringaldehydu na fermentačné parametre lúčneho sena *in vitro*

Z. VÁRADYOVÁ, I. ZELEŇÁK, P. SIROKA

Institute of Animal Physiology, Slovak Academy of Sciences, Košice, Slovak Republic

ABSTRACT: The influence of the phenolic compound syringaldehyde (SA) and the yeast culture of *Saccharomyces cerevisiae* (YS) upon the end products of rumen fermentation *in vitro* has been investigated. Two rumen fistulated sheep were used as a source of inoculum. Meadow hay (MH) as a substrate with the following combination of additives was used: (1) MH without additive; (2) MH with YS; (3) MH with 1 mmol/l SA; (4) MH with 5 mmol/l SA; (5) MH with 10 mmol/l SA; (6) MH plus YS with 1 mmol/l SA; (7) MH plus YS with 5 mmol/l SA (8) MH plus YS with 10 mmol/l SA. Fermentation was carried out in 120 ml serum bottles and measurements were made by means of the pressure transducer technique. Syringaldehyde decreased ($P < 0.001$) the hay dry matter degradability in all combinations. Total gas and methane production were lower ($P < 0.001$) in combinations with 10 mmol/l of syringaldehyde. Total volatile fatty acids (VFA) production was positively affected in the combinations MH plus YS with 1 mmol/l and 5 mmol/l of SA. Application of 10 mmol/l syringaldehyde had a negative effect. It was impossible to subdue this negative effect by combination with *Saccharomyces cerevisiae*.

Keywords: fermentation; *in vitro;* meadow hay; phenolic compound; *Saccharomyces cerevisiae*

ABSTRACT: Bol sledovaný vplyv fenolickej látky syringaldehydu (SA) a kvasinkovej kultúry *Saccharomyces cerevisiae* (YS) na konečné produkty bachorovej fermentácie *in vitro*. Ako zdroj inokula boli použité dve ovce s bachorovými fistulami. Substrátom bolo seno (MH) a nasledovné kombinácie prídavkov: (1) MH bez prídavkov; (2) MH s prídavkom YS; (3) MH s 1 mmol/l SA; (4) MH s 5 mmol/l SA; (5) MH s 10 mmol/l SA; (6) MH plus YS s 1 mmol/l SA; (7) MH plus YS s 5 mmol/l SA; (8) MH plus YS s 10 mmol/l SA. Fermentácia prebiehala v 120 ml fľašiach na sérum a merania sa uskutočnili metódou techniky tlakového transducera. Syringaldehyd znížil ($P < 0.001$) stráviteľnosť sušiny sena vo všetkých kombináciách. Celková plynová produkcia a metán boli nižšie ($P < 0.001$) v kombináciách s 10 mmol/l syringaldehydu. Celková produkcia únikavých mastných kyselín bola pozitívne ovplyvnená v kombinácii sena s kvasinkami a s 1 mmol/l a 5 mmol/l syringaldehydu. Aplikácia 10 mmol/l syringaldehydu mala negatívny účinok. Tento negatívny účinok nebolo možné zmierniť ani kombináciou s kvasinkami *Saccharomyces cerevisiae*.

Kľúčové slová: fermentácia; *in vitro*; seno lúčne; fenolická látka; *Saccharomyces cerevisiae*

INTRODUCTION

Dietary supplements of yeast culture, based on dried *Saccharomyces cerevisiae*, have been reported to improve livestock productivity by an increased viable count of rumen bacteria and consequently to improve protein flow to the small intestine (Newbold, 1995). Several studies have described their ability to stabilize the rumen pH when the animals are fed diets rich in highly fermentable carbohydrates and subsequently to stimulate the activity of cellulolytic microorganisms (Dawson 1992; Michalet-Doreau and Morand, 1996). Treatment with some yeast cultures increased the number of total and cellulolytic bacteria in the rumen and increased cellulose degradation

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(Newbold *et al.*,1995). Delignification of feeds leads to accumulation of non-tannin phenols such as low-molecular weight phenolic compounds (Reid, 1991; Wood and Plumb, 1995). Syringaldehyde is a phenolic compound of low molecular weight arising in the rumen by the degradation of lignin. The objective of the present study was to find out whether the positive effect of *Saccharomyces cerevisiae* on fermentation could be subdued by the negative effect of syringaldehyde upon the end products of *in vitro* rumen fermentation of meadow hay.

MATERIAL AND METHODS

The rumen fluid inoculum used in the present experiment was obtained from two rumen fistulated Merino sheep fed meadow hay *ad libitum* and ground barley at a ratio of 80 : 20. Samples of rumen fluid were taken three hours after the morning feeding, transferred to the laboratory, squeezed trough four layers of gauze and purged with CO_2. The rumen fluid inoculum was mixed with McDougall's buffer (McDougall, 1948) at a ratio of 1 : 1 and pumped by an automatic pump into each of the preheated fermentation bottles containing 0.25 g of meadow hay as a substrate. Throughout the incubation the temperature in the incubator was maintained at 39 ± 0.5°C. Meadow hay was milled through an 0.15–0.4 mm screen, bulked and stored in sealed plastic containers until required. The experiment comprised 8 treatment groups of 35 ml inoculum/120 ml serum bottle in triplicate repeated on 3 separate occasions. The following combinations of additives were used: (1) Meadow hay (MH) without additives; (2) MH with *Saccharomyces cerevisiae* (YS); (3) MH with 1 mmol/l syringaldehyde (SA); (4) MH with 5 mmol/l SA; (5) MH with 10 mmol/l SA; (6) MH plus YS with 1 mmol/l SA; (7) MH plus YS with 5 mmol/l SA; (8) MH plus YS with 10 mmol/l SA. A commercial yeast culture Levucel (Lallemand, Canada) containing 5 x 10^8 of *Saccharomyces cerevisiae* yeast cells per 1 g was used at the amount of 0.5 g/l (i.e. 17.5 mg per bottle). Syringaldehyde was obtained from a commercial source (Sigma). Each of the fermentation series contained control bottles (rumen inocula plus buffer) without any substrate.

The volume of released accumulated gas was measured after 24, 48, 72 and 96 h by the pressure transducer technique (Váradyová *et al.*, 1998). This involved anaerobic fermentation of the substrates in a buffered medium kept in sealed serum bottles using an inoculum prepared from fresh rumen fluid. The metering system consisted of a three-way valve, mechanical pressure manometer, gas-tight syringe and needle. The three-way valve was connected with the pressure-manometer (to measure the pressure in the serum bottles) and gas-tight syringe (to measure the volume of gas production). The third port was connected with a needle by a hose. The needle was used to punch the rubber stopper on the serum bottle.

The concentration of VFA in the medium was determined after 96h by gas chromatography (Cottyn and Boucque, 1968) using crotonic acid as the internal standard and the Perkin-Elmer 8500 gas chromatograph.

Dry matter degradability was estimated from the difference in substrate weight before and after 96 h incubation. The contents of the fermentation bottles were transferred into a tube and centrifuged at 3 500 g for 10 min. The residues were washed twice with distilled water, centrifuged and dried to constant weight at 105°C (Mellenberger *et al.*, 1970).

The means of the individual parameters were compared using the parametric Student's *t*-test (Snedecor and Cochran, 1971). Hydrogen recovery was calculated according to Demeyer and Van Nevel (1975).

RESULTS

As compared to MH significantly lower values ($P < 0.05$; $P < 0.001$) of dry matter degradability (DMD) were obtained in combinations of MH with 1, 5 and 10 mmol/l SA and in combinations of MH with YS and 1, 5 and 10 mmol/l of SA (Figure 1a). As compared to the values for MH, total gas (Figure 1b) was significantly lower for MH with 10 mmol/l SA ($P < 0.05$) and for MH plus YS with 10 mmol/l SA ($P < 0.01$). Methane production was significantly suppressed ($P < 0.001$) by the addition of 1 and 10 mmol/l of SA (Figure 2a) and also in the combination of MH plus YS with 10 mmol/l of SA. On the other hand, it was increased ($P < 0.001$) by the addition of 5 mmol/l SA and in the combination of MH plus YS with 5 mmol/l of SA. Methane production was slightly enhanced ($P < 0.05$) by MH plus YS containing 1 mmol/l SA. Total VFA production of MH was increased by the addition of 5 mmol/l SA and 1 and 5 mmol/l SA to MH containing YS (Figure 2b). The combination of 10 mmol/l SA with YS decreased ($P < 0.01$) total VFA production. Acetate and butyrate productions were increased in all combinations of SA (Table 1). Propionate and iso-valerate were reduced in all combinations of SA (except MH +YS + 10 mmol/l SA for propionate). Iso-butyrate was decreased in combinations of MH with 10 mmol/l SA and MH plus YS with 10 mmol/l SA. The addition of YS to MH increased valerate production. On the other hand, valerate was decreased in combinations of MH +5 mmol/l SA, MH +10 mmol/l SA and MH +YS + 10 mmol/l SA. Acetate propionate ratio was increased by combinations of MH + 5 mmol/l SA, MH +10 mmol/ SA , MH + YS +1 mmol/l SA and MH +YS +5 mmol/l SA. It follows from Table 1 that hydrogen recovery revealed a decrease in the combinations MH with 1 mmol/l and 10 mmol/l SA and MH plus YS with 1 mmol/l SA and 10 mmol/l SA.

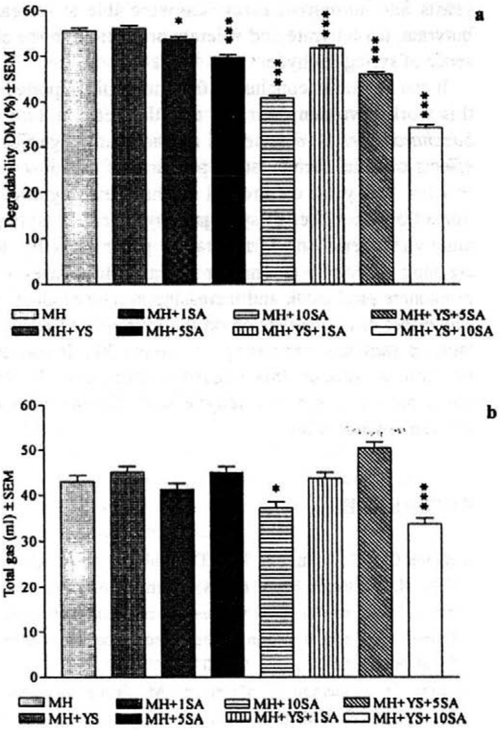

Figure 1. Effect of *Saccharomyces cerevisiae* (YS) and syringaldehyde (SA) on dry matter degradability and total gas production of meadow hay (MH) *in vitro*. Values are means ± SEM. 1, 5, 10 SA = mmol/l of syringaldehyde. Differences between means were considered significant at $P < 0.05$ (*), $P < 0.01$ (**) and $P < 0.001$(***)

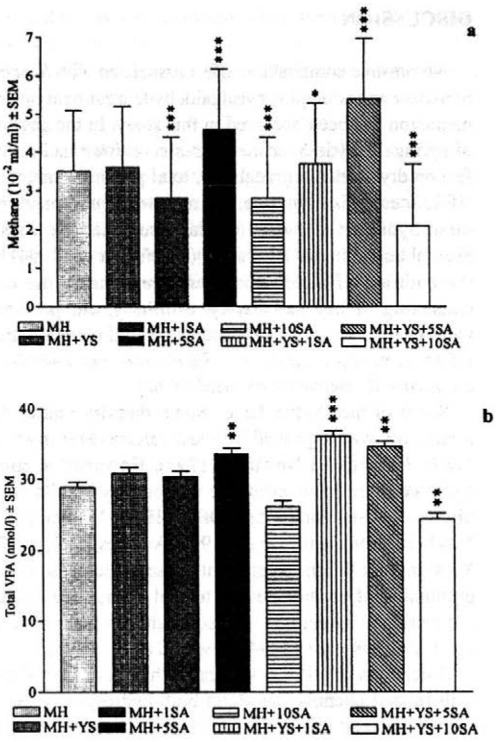

Figure 2. Effect of *Saccharomyces cerevisiae* (YS) and syringaldehyde (SA) on methane production and total VFA of meadow hay (MH) *in vitro*. Values are means ± SEM. 1, 5, 10 SA = mmol/l of syringaldehyde. Differences between means were considered significant at $P < 0.05$ (*), $P < 0.01$ (**) and $P < 0.001$ (***)

Table 1. Effect of the yeast *Saccharomyces cerevisiae* and syringaldehyde on individual volatile fatty acids and hydrogen recovery after 96 h of incubation

	MH	MH+YS	MH+1SA	MH+5SA	MH+10SA	MH+YS+1SA	MH+YS+5SA	MH+YS+10SA	SEM
Acetate (mol%)	64.0	64.4	65.6^{a}	67.5^{c}	67.7^{c}	65.8^{a}	66.9^{c}	65.9^{a}	0.4
Propionate (mol%)	23.4	22.2^{a}	22.4^{a}	20.2^{c}	22.0^{a}	21.6^{b}	19.8^{c}	24.3^{a}	0.3
Iso-butyrate (mol%)	1.4	1.7	1.2	1.1	0.5^{c}	1.4	1.2	0.8^{c}	0.1
Butyrate (mol%)	6.9	7.4^{a}	7.4^{a}	8.8^{c}	8.2^{c}	7.5^{b}	9.1^{c}	7.0	0.1
Iso-valerate (mol%)	2.4	2.7^{a}	2.1^{b}	1.4^{c}	0.6^{c}	2.2^{a}	1.7^{c}	0.8^{c}	0.1
Valerate (mol%)	1.3	1.5^{c}	1.2	1.0^{c}	0.9^{c}	1.4	1.3	1.1^{c}	0.03
A : P ratio	2.8	2.9	2.9	3.3^{c}	3.1^{b}	3.1^{b}	3.4^{c}	2.8	0.04
2H-Recovery (%)	62.0	60.6	54.6^{c}	60.4	54.7^{c}	56.1^{b}	64.7	54.0^{c}	1.2

MH = meadow hay, YS = yeast *Saccharomyces cerevisiae*, 1SA = 1 mmol/l of syringaldehyde, 5SA = 5 mmol/l of syringaldehyde, 10SA = 10 mmol/l of syringaldehyde, 2H-Recovery = hydrogen recovery, A : P ratio = acetate/propionate ratio

$^{a}P < 0.05$, $^{b}P < 0.01$, $^{c}P < 0.001$ different from meadow hay

DISCUSSION

No positive combination effect associated with *Saccharomyces cerevisiae* plus syringaldehyde treatment on fermentation has been observed in this study. In the absence of syringaldehyde *Saccharomyces cerevisiae* had no effect on dry matter degradability, total gas, methane, total VFA, acetate, iso-butyrate, the acetate to propionate ratio or hydrogen recovery. Similar results had previously been obtained in our laboratory (Zeleňák *et al.*, 1994) by the addition of *Saccharomyces cerevisiae* to the diet consisting of hay and barley. Similarly, our previous work (Zeleňák *et al.*, 1997) showed a slight combination effect of phenolic acids and *Saccharomyces cerevisiae* on *in vitro* fermentation of meadow hay.

Some of the studies have shown that dry matter degradability was improved by yeast culture (Martin *et al.*, 1989; Wallace and Newbold, 1993). However, in some cases no significant influence or contrary results were observed (Chademana and Offer, 1990; Williams and Newbold, 1990; Smith *et al.*, 1993; Angeles *et al.*, 1998). Yeast culture in our experiment caused a decrease in the production of propionate and tended to increase acetate production in agreement with some studies (Kumar *et al.* 1994; Zeleňák *et al.*, 1994; Newbold *et al.*, 1998).

Asiegbu *et al.* (1995) suggested that a number of cell wall-related phenols can affect both hydrolysis of polysaccharides and microbial activity in a simulated rumen. There is some evidence that phenolic compounds inhibit cellulose degradation (Jung and Fahey, 1983; Fukusima *et al.*, 1991) and methane production (Martin, 1988). In our study dry matter degradability of meadow hay was significantly decreased by syringaldehyde in all combinations after 96 h of incubation. With regard to gas production only the addition of 10 mmol/l syringaldehyde decreased both total gas and methane production. It seems that this could possibly be related to the fact that gas production is a more sensitive parameter of fermentation than dry matter degradability (France *et al.*, 1993; Getachew *et al.*, 1998). Supplementation of fermentations with phenolic compounds reduced the values for acetate and propionate production according to Asiegbu *et al.* (1995); our results revealed a decrease in propionate production only. It was also observed that both yeast culture and syringaldehyde influenced the total volatile fatty acid production. The changes in the mol% of the individual VFA were inconsistent in agreement with studies (Offer, 1990; Angeles *et al.*, 1998). The acetate/propionate ratio (2.7– 3.3) was comparable with our previous *in vitro* studies (Zeleňák *et al.*, 1997; Váradyová *et al.*, 2000). In these studies the fermentation process induced in meadow hay with the same inoculum resulted in an acetate/propionate ratio ranging from 1.6 to 3.4 and more. The results revealed that the yeasts *Saccharomyces cerevisiae* were able to increase butyrate, iso-butyrate and valerate production in the absence of syringaldehyde.

It can be said in conclusion that the results reported in this work have demonstrated that the yeast culture of *Saccharomyces cerevisiae* did not have any significant effects on final fermentation products of meadow hay *in vitro*. The yeast culture did not have any significant impact on the effect of syringaldehyde, either. Syringaldehyde altered the fermentation parameters by decreasing especially dry matter degradability, gases and propionate production and increasing acetate production. The effect of syrinaldehyde on the investigated fermentation parameters was strongly unfavourable. It was impossible to subdue this negative effect even by the combination of syringaldehyde with *Saccharomyces cerevisiae* yeast culture.

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Corresponding Author:

MVDr. Zora Váradyová, Ústav fyziológie hodspodárskych zvierat SAV, Šoltésovej 4–6, 040 01 Košice, Slovenská republika
Tel. +421 95 76 31 21, +421 95 63 362 68, fax +421 95 76 21 62, e-mail: varadyz @saske.sk

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Czech J. Anim. Sci., 46, 2001 (4): 185–187 Short Communication

Genetic variability in the *ESR* locus in pigs of the Landrace and Large White breeds kept in the Czech Republic

Genetická variabilita v lokusu *ESR* u prasat plemene landrase a bílé ušlechtilé v ČR

I. Vrtková, J. Dvořák

Mendel University of Agriculture and Forestry, Brno, Czech Republic

ABSTRACT: The estrogen receptor (*ESR*) gene is a genetic marker for reproductive traits in sows. In LW breed, *ESR-PvuII* polymorphism is associated with litter size. *ESR-PvuII* variability in Landrace (L) breed has not yet been described in literature and in the Czech Republic there are no available data on Large White (LW) breed. In this study, *ESR-D* allele frequency *ESR-D* = 0.10 was found in sows of the L breed (284 animals) and the variability on four breeding farms ranged from 0.02 to 0.13. In sows of the LW breed (539 animals) the *ESR-D* frequency was *ESR-D* = 0.35. Variability in representation of *D* allele in the framework of nine observed breeding farms ranged from 0.18 to 0.50.

Keywords: pig; *ESR*; Landrace; Large White

ABSTRAKT: Genetickým markerem pro plodnost u prasnic je gen estrogenového receptoru (*ESR*). Polymorfismus *ESR* je asociován u plemene LW s počtem narozených selat. Variabilita *ESR-PvuII* u plemene landrace (L) není v literatuře popsána a v České republice nejsou k dispozici ani informace o plemeni bílé ušlechtilé. V této práci byla u prasnic plemene L (284 ks) zjištěna frekvence alely *ESR-D* = 0,10 (variabilita ve čtyřech šlechtitelských chovech byla 0,02 až 0,13). U prasnic plemene BU (539 ks) byla frekvence *ESR-D* = 0,35. U devíti sledovaných šlechtitelských chovů byla frekvence alely *D* v rozmezí od 0,18 do 0,50. Průměrné zastoupení alely *D* ze šlechtitelských chovů BU v ČR je poloviční oproti čtyřem superplodným liniím LW v chovatelsky vyspělých zemích.

Klíčová slova: prase; *ESR*; landrase, bílé ušlechtilé

In porcine estrogen receptor (*ESR*) gene, three polymorphic loci have been described. In each of them, the occurrence of two codominant alleles has been identified by PCR-RFLP methods. DNA primers for detection of two polymorphisms with the use of restriction enzymes – *AvaI* and *MspA1I* – were described by Drögenmüller *et al.* (1997). PCR conditions, primer sequences, and *PvuII* restriction enzyme for detection of the third polymorphism in *ESR* were discussed by Short *et al.* (1997).

In sows, the *ESR* locus has been identified as candidate gene for litter size. Differences in litter size in sows with different *ESR* genotypes – *ESR-AvaI* and *ESR MspA1I* – in Large White (LW) breed were described by Dvořák *et al.* (1998). Because of a low number of animals the obtained results could be evaluated only as preliminary ones.

Significant differences between *ESR-PvuII* genotypes in litter size in sows of LW lines were described by Short *et al.* (1997). A total of 9 015 litter records from 4 262 sows were analyzed to determine whether *ESR* influenced total number born (TNB) and number born alive (NBA). The TNB and NBA were increased per *D* allele of *ESR* ($P < 0.01$) with additive effects of 0.42 (0.31) and 0.39 (0.31) pigs/litter in the first parity (later parities), respectively. Dominance effects were near zero in parity one, but they were 0.16 and 0.14 pigs for TNB and NBA, respectively, in later parities.

The attention of breeders of dam breeds and lines of pigs was therefore focused on *ESR-PvuII* polymorphism. Data that have been published about the representation of genotypes and alleles concerned only Large White

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breed. Information about the Landrace breed has not been published yet.

Although the *D* allele is associated with a larger litter size, no differences in number of corpora lutea or number and percentage of vital Day 35/36 embryos were found by Rens *et al.* (2000). This indicates that the difference in litter size is not due to differences in oocyte maturation, fertilization, implantation or embryonic survival, but is likely caused by a difference in fetal survival. However, a difference in placental size was found. Embryos of *DD* gilts had significantly longer placentae than embryos of *CC* gilts. These results suggest a higher chance for placental insufficiency in *CC* gilts, leading to the expected higher fetal mortality compared with the *DD* gilts.

The objective of this study was to detect variability in genotypes and allele frequencies in the polymorphic locus *ESR-PvuII* in breeding sows reared on breeding farms of Landrace (L) and Large White (LW) breeds in the Czech Republic.

In LW and L breeds, total numbers of 539 and 284 sows on nine and four breeding farms, respectively, were investigated.

For *ESR-PvuII* polymorphism detection, primers and PCR-RFLP method as described by Short *et al.* (1997) were used. In accordance with the data of the authors of this method, two alleles and three different genotypes were identified. The alleles were marked with the symbols *C* and *D*. The results of the PCR-RFLP analysis are presented in Figure 1.

The results and analyses of L breeding sows are given in Table 1. A low frequency of the *D* allele (0.05), positively associated with litter size, was found out also in sires of the L breed. Among the total number of 30 breeding sires, there were 28 animals with *CC* genotype, 1 animal with *CD*, and 1 animal with *DD* genotype.

Frequencies of *ESR* genotypes and alleles in LW breed are documented in Table 2. In the whole group of 539 sows investigated, the frequency of *D* allele was *D* = 0.35. The frequency of *D* allele in boars of LW breed was *D* = 0.33. In the total number of 94 observed breeding boars, there were 14 animals with *CD* genotype, and 14 animals with *DD* genotype.

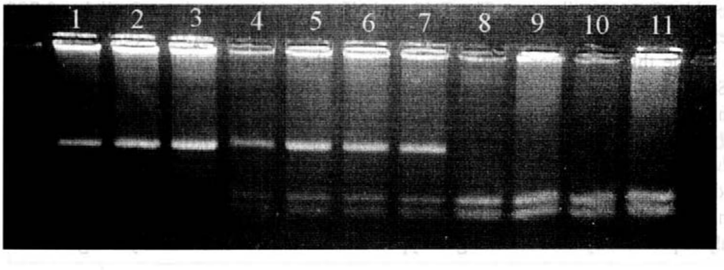
Results obtained with LW animals could be compared with data published by Short *et al.* (1997), who in three LW lines found the frequency of *D* allele ranging from 0.64 to 0.74. In the synthetic line, LW females with boars from Duroc and backcrossing the F_1 to the Duroc line, the frequency *D* = 0.17 is given by the authors.

Table 1. Frequency of *ESR-PvuII* genotypes and alleles in sows from four breeding farms of the Landrace breed

Farm	Number of sows	*ESR* genotypes (%)			Frequency of *D* allele
		CC	*CD*	*DD*	
I	139	75.5	23.0	1.5	0.13
II	56	80.4	19.6	0	0.10
III	45	93.3	4.4	2.3	0.04
IV	44	95.5	4.5	0	0.02
Total	284	82.4	16.5	1.1	0.09

Table 2. Frequency of *ESR-PvuII* genotypes and alleles in sows from nine breeding farms of the Large White breed

Farm	Number of sows	*ESR* genotypes (%)			Frequency of *D* allele
		CC	*CD*	*DD*	
I	121	41.3	49.6	9.1	0.34
II	72	27.8	44.4	27.8	0.50
III	71	35.2	53.6	11.2	0.38
IV	70	50.0	38.6	11.4	0.31
V	67	46.3	41.8	11.9	0.33
VI	58	58.1	36.2	5.7	0.23
VII	39	38.5	56.4	5.1	0.46
VIII	22	68.2	27.2	4.6	0.18
IX	19	48.1	41.1	10.8	0.47
Total	539	43.2	44.2	12.6	0.35



1 – amplified fragment of *ESR – PvuII* gene (120 bp)
2, 3 – homozygotes *CC* – 120 bp
4, 5, 6, 7 – heterozygotes *CD* – 120 bp; 65 bp; 55bp
8, 9, 10, 11 – homozygotes *DD* – 65bp; 55bp

Figure 1. Results of PCR-RFLP analysis by agarose gel electrophoresis

In nine breeding herds of LW breed, the frequency of *D* allele (0.35) detected in the Czech Republic was equal to approximately 50% those found in lines investigated by Short *et al.* (1997).

In the L breed, the detected frequency of *D* allele was $D = 0.10$. This result, obtained on four breeding farms in the Czech Republic, can be compared only with frequencies observed in the L breed in Poland (Dvořák *et al.*, 1999 – unpublished data). The frequency of *D* allele determined there in more than 350 animals – both dams and sires – originating from a number of breeding herds, was $D = 0.05$.

In further studies it will be necessary to verify if there is a positive effect of the *ESR-PvuII* – *D* allele on litter size in the L breed, and especially in sows of LW × L hybrid combination because these animals are used for production of slaughter animals within the framework of hybridization programs.

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Corresponding Author:

Prof. Ing. Josef Dvořák, CSc., Mendelova zemědělská a lesnická univerzita, Zemědělská 1, 613 00 Brno, Česká republika
Tel. +420 5 45 13 31 75, e-mail: dvorakJ@mendelu.cz

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Czech J. Anim. Sci., 46, 2001 (4): 189–192 *Short Communication*

Effect of semen extender components on rabbit sperm motility

Vliv přídavku dvou různých kryokonzervačních přípravků na motilitu králičích spermií

W. H. KISHK

Suez Canal University, Faculty of Agriculture, Ismailia, Egypt

ABSTRACT: Three different rabbit semen extenders based on Tris-egg yolk extender were used in this experiment to examination of 1% glycerol or 6% dimethyl sulfoxide (DMSO) addition effect and control (free of glycerol and DMSO) on rabbit semen motility and acrosomal changes over a period of three days of storage at 5°C. Semen samples of White New Zealand (WNZ) bucks were evaluated for initial concentration, pH value and volume in relation to sperm motility and acrosome loss. The obtained results showed that there were significant differences ($P < 0.05$) according to extender type used. Sperm motility % were 38.0 ± 4.5, 47.3 ± 1.3 and 37.9 ± 4.1 for control, 1% glycerol and 6% DMSO extender, respectively. The correlated studied characters of % acrosomal loss for the same extenders differed significantly ($P < 0.05$) and were 8.5 ± 0.67, 4.5 ± 0.33 and 7.0 ± 66%, respectively.

Keywords: rabbit; buck; extender; semen; cryoprotectants; glycerol; dimethyl sulfoxide

ABSTRAKT: V tomto pokusu jsme použili tři různá ředidla králičího spermatu na bázi ředidla Tris-vaječný žloutek ke sledování vlivu doplňku 1% glycerolu nebo 6% dimetylsulfoxidu (DMSO) a kontroly (bez použití glycerolu a DMSO) na motilitu králičího spermatu a na procentuální podíl akrozomálních změn během tří dnů skladování při teplotě 5 °C. Vzorky spermatu bílých novozélandských králíků byly hodnoceny z hlediska jejich počáteční koncentrace, hodnoty pH a objemu ve vztahu k motilitě spermií a procentuální ztrátě akrozomů. Výsledky naznačily významné rozdíly ($P < 0,05$) podle typu použitého ředidla. Motilita spermií v procentech činila u kontroly, u ředidla s doplňkem 1% glycerolu a s doplňkem 6% DMSO 38,0 ± 4,5, 47,3 ± 1,3 a 37,9 ± 4,1. Sledované znaky procentuální ztráty akrozomů se pro stejná ředidla významně lišily ($P < 0,05$) a dosahovaly hodnot 8,5 ± 0,67, 4,5 ± 0,33 a 7,6 ± 0,66 %.

Klíčová slova: králík; samec; ředidlo; sperma; kryoprotektiva; glycerol; dimetylsulfoxid

INTRODUCTION

Many research works were conducted to study the effects of glycerol addition to rabbit semen extenders on both sperm motility and acrosome integrity (Weitze, 1977; Weitze *et al.*, 1982). The most popular theory for the beneficial effect of glycerol addition to semen extenders is a protection impact of glycerol through salt-buffering mechanism (Lovelock, 1953; Polge and Soltys, 1959). Others reported that glycerol can penetrate through the sperm cell membrane and concentrate in the posterior part of the sperm head (Pickett and Merilan, 1957). Mechanisms of respective effects of cryoprotectants have been intensively studied especially for glycerol. Hammerstedt and Graham (1992) stated that glycerol could alter sperm membrane fluidity by becoming intercalated into the lipid bilayer, and change the intercellular cytoplasmic viscosity thus affecting all metabolic reactions. Some authers stated that cryprotectants containing amides or methyl groups like DMSO were been recommended and used successfully in rabbit sperm preservation (Arriola, 1982; Chen *et al.*, 1988).

The objectives of this study were to investigate the effects of cryoprotectants like glycerol and DMSO on rabbit sperm motility and acrosome changes in relation to essential semen characteristics on cooled preserved rabbit semen at 5°C.

MATERIAL AND METHODS

Bucks and semen collection and processing

Three New Zealand White (NZW) bucks were used in this experiment with an average body weight 2.5–3.5 kg and 12 months of age. The bucks were housed in wire cages and the doe was transferred to buck's cage for semen collection. Semen samples were collected by using a glass artificial vagina according to Morrell (1995) supported with a graduated collecting tube and the added water was adjusted to 45°C at the time of semen collection.

The collected semen samples were put in a water bath at 38°C. The samples were subjected to the following examinations: general appearance, sample volume, sperm concentration/ml, pH value and initial motility. Sperm motility was estimated by using a light microscope at 100x magnification on a stage warmed at 38°C.

Tris-egg yolk extender was prepared according to Fischer and Odenkirchen (1988). Tris-egg yolk extender contained 360 mM Tris, 33.3 mM glucose and 113.7 mM citric acid for the control treatment. The second treatment contained 1% glycerol in the Tris-egg yolk extender while the third treatment contained 6% (vol./ vol.) dimethyl sulfoxide (DMSO) in Tris-egg yolk extender. For all treatments egg-yolk, penicillin and streptomycin were added to give a final concentration of 5% (vol./vol.), 0.01% (wt/vol.) and 0.05% (wt/vol.) respectively.

As for acrosomal change determination, two smeared slides of diluted semen samples were prepared directly after dilution and daily during the storage period. The dried smeared slides were examined directly without staining for acrosomal changes according to Watson and Martin (1972) by using the oil lens of a light microscope to obtain 1 000x magnification. A total count of one hundred sperm cells was examined for the acrosomal changes % for each slide. The average of two slides was recorded for each determination.

After semen assessment the evaluated semen samples were diluted (1 : 5) with three different treatments as mentioned previously at room temperature. The diluted semen samples were put in a closed test tubes (5 ml) in a refrigerator at 5°C. The storage period of the diluted semen samples was 3 days. To achieve the required cooling temperature the tubes were put in a water bath provided with a thermometer to check the required cooling temperature (5°C) in the water bath every day of the storage period.

Statistical analysis

Analysis of variance (ANOVA) was carried out using starting spss/pc (1993) to study the effects of semen extender ingredients and storage period on both sperm motility % and percentage of acrosomal loss of different semen samples. Correlation was estimated between raw semen characteristics and each of sperm motility % and acrosomal changes % and between sperm motility % and acrosome changes %.

RESULTS AND DISCUSSION

Sperm motility examination

Results presented in Table 1 show that the sperm motility % was superior and differed significantly ($p < 0.05$) as for Tris-egg yolk extender containing 1% glycerol which was 74.4 ± 3.8 % for the entire storage period of three days. Whereas, sperm motility % of control treatment (Tris-egg yolk free of glycerol and DMSO) and Tris-egg yolk extender containding 6% DMSO were 38.0 ± 4.5 and

Table 1. Mean ± SE of sperm motility percent of different semen extenders during a storage period at 5°C

Sample No	Initial motility (%)	Sample volume (ml)	Valume of pH	Sperm conc. x 10^6 before dilution (B.D)	Sperm conc. x 10^6 after dilution (A.D)	Sperm motility (%)											
						control				glycerol				DMSO			
						A.D	1st day	2nd day	3rd day	A.D	1st day	2nd day	3rd day	A.D	1st day	2nd day	3rd day
1	70	0.3	7.79	195	39.0	70	20	10	10	60	50	20	30	65	30	30	30
2	75	0.75	7.07	196.9	39.4	75	50	20	10	70	60	20	20	65	50	30	10
3	75	1.0	7.04	336	67.2	70	70	55	25	70	70	65	45	75	60	40	20
4	70	0.3	7.60	179.7	35.9	65	20	10	10	75	40	35	20	70	40	20	10
5	75	0.5	7.05	257	51.4	75	25	20	10	75	40	35	20	70	40	20	10
6	70	0.6	7.07	387	77.4	70	50	45	40	70	70	70	55	70	60	50	40
7	60	0.8	7.12	328	65.6	60	30	30	20	60	50	35	30	60	30	30	25
Mean	70.7	0.61	7.25	268.5	53.7	69	38^{A}	27^{C}	18^{E}	67	54^{B}	38^{D}	30^{F}	68	41	30^{C}	21^{E}
± SE	2.0	0.1	0.12	31.1	6.2	2.0	7.0	7.0	4.0	2.0	5.0	8.0	6.0	2.0	6.0	5.0	4.0
Overall mean						38.0^{A}				47.3^{B}				37.9^{A}			
± SE						4.5				3.8				4.1			

Means with the same letters showed no significant differences using *t*-test for paired samples

37.9 ± 4.1%, respectively for the same storage period. These significant differences may be due to the effect of glycerol in avoiding or controlling cold shock when sperm cells are preserved at 5°C, when it is obvious that rabbit sperm is sensitive and may be killed by chilling at temperatures above the freezing point as declared by Watson (1979) and for other animal species by Kumar *et al.* (1994), Singh *et al.* (1994), Katila (1997). The beneficial effect of glycerol which was achieved at this added concentration (1%) may be associated with the non-toxicity of glycerol to rabbit sperm especially at this level. The useful effect of glycerol addition was not achieved in the case of DMSO which demonstrates that it is not necessary to add DMSO alone as a cryoprotective agent to rabbit semen extenders for cooling preservation. Whereas, other authors found that cryoprotectants containing amide or methyl groups were recommended and used successfully for frozen semen (Hanada and Nagase, 1980; Arriola, 1982). Sperm motility percent varied significantly ($p < 0.05$) according to the storage period for different treatments (Table 1). The addition of 1% glycerol to Tris-egg yolk extender maintained sperm motility significantly, differing from the control or DMSO treatments (Table 1). It is obvious that both glycerol and DMSO addition maintained sperm motility in relatively good condition compaired to the control treatment during the storage period, especially glycerol treatment during the third day of the storage period (Table 1). Also there was a sharp decrease in sperm motility after the first day of storage period for all treatments (Table 1), especially the control and DMSO treatments. The explanation of this phenomenon may be due to the high sensitivity of rabbit sperm to cooling preservation.

Table 2. Mean ± SE of sperm acrosomal changes percent of different semen extenders during a storage period at 5°C

Sample No.	Sperm acrosomal loss (%)											
	Control				Glycerol				DMSO			
	A.D	1st day	2nd day	3rd day	A.D	1st day	2nd day	3rd day	A.D	1st day	2nd day	3rd day
1	3	8	12	12	2	5	5	7	2	5	8	13
2	4	6	10	10	4	3	5	6	4	4	8	12
3	2	7	9	10	2	3	7	8	3	6	9	14
4	4	8	10	11	3	4	4	5	4	5	7	12
5	5	7	11	13	4	3	4	6	5	5	9	14
6	4	8	12	14	2	4	6	7	4	6	10	12
7	6	9	11	13	4	2	5	7	4	6	10	12
Mean	4	8^{A}	11^{D}	12^{G}	3	3^{B}	5^{E}	7^{H}	4	5^{C}	9^{F}	13^{G}
±SE	49	37	42	59	38	37	4	37	36	29	42	43
Overal mean	8.5^{A}				4.5^{B}				7.6^{A}			
± SE	0.63				0.33				0.68			

Means with the same letters showed no significant differences using Duncan's multiple range test

Acrosomal changes assessment

Studying the acrosomal loss percentage showed that, there were significant differences ($p < 0.05$) between the different treatments. The acrosomal changes % were 8.5, 4.5 and 7.6 for the control, 1% glycerol and 6% DMSO extenders, respectively, for the complete storage period at 5°C (Table 2). The addition of 1% glycerol to Tris-egg yolk extender significantly increased ($p < 0.05$) the preservation of acrosomal integrity across the storage period as compared to the other treatments during three successive days of cooling as shown in Table 2. There were different stages of acrosomal loss. The oil lens of a light microscope was used to examine acrosomal status. The observed acrosomal status was found to be five different stages as shown in Figure 1. To distinguish between the different stages of acrosomal loss, sperm cell of shape No 1 was considered to be an intact acrosome for the typical complete or non-changed acrosome, while shapes from No. 2 to No. 5 were considered to be acrosomal changes (Figure 1). There are many changes which can occur to a sperm cell at acrosomal level during cooling preservation. One of these alterations is the spatial arrangements of the internal structure and outer covering of the cells. A contraction of the protoplasm may occur, at different rates depending on the chemical components of the various structures (Salisbury *et al.*, 1978) including acrosomal structures. The beneficial effect of glycerol at this level in this experiment (1%) may come from the ability of glycerol to reduce mechanical destructiveness to rabbit sperm cells at acrosomal level.

It can be concluded that rabbit sperm is sensitive to a great extent to cooling preservation, and the extenders which are used must contain a cryoprotectant agent like glycerol but at a low concentration to avoid toxicity of rabbit sperm (1% glycerol could be recommended). Also, to obtain a moderate rate of rabbit sperm motility, it is

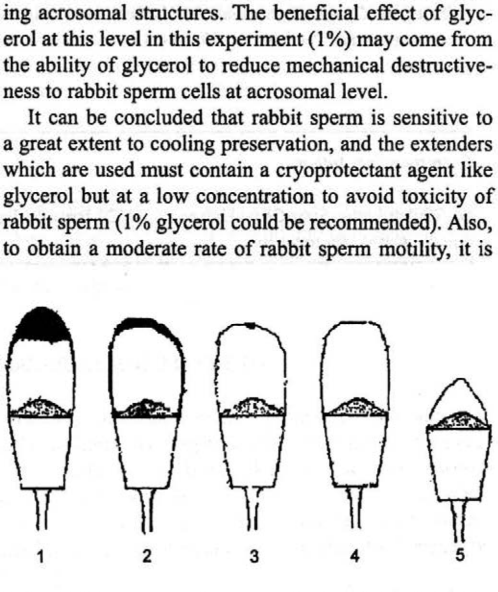

Figure 1. Different stages of acrosomal changes of rabbit sperm during cooling storage. No. 1 considered as normal acrosome while No. 2 to No. 5 are changed acrosomes when examined by using oil lens of loght microscope (1 000x magnification).

useful to store rabbit semen for only one day at 5°C. The technique of acrosomal loss % determination using oil lens of light microscope without any kind of staining is a rapid and simple method for assessing acrosomal changes during storage.

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Corresponding Author:

Dr. Wailed Kishk, Suez Canal University, 41522 Ismailia, Egypt
e-mail: wkishk@hotmail.com

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