Genetic parameters for live animal ultrasound measures, scrotal circumference, carcass and growth traits in Aberdeen Angus

***Z. Vesela*[1*]*, A. Birovas*[1]*, M. Brzakova*[1]*, A. Novotna*[1]*, L. Vostry*[1]**

[1] *Institute of Animal Science, Pratelstvi 815, 10400 Prague, Czech Republic*

* *vesela.zdenka@vuzv.cz*

Abstract

Genetic parameters were estimated for body weight at scanning (SCW), scrotal circumference (SC), rump fat thickness (P8FT), rib fat thickness (RBFT), eye muscle area (EMA), intramuscular fat content (IMF), carcass weight (CW), carcass conformation (CC), carcass fatness (CF), adjusted weaning weight (AWW) and adjusted yearling weight (AYW) in the Czech Aberdeen Angus. Live ultrasound measures were collected on 1,949 animals and SC on 1,021 bulls aged 250 to 500 days through 2019, 2020, and 2022. Furthermore, there were 7,672 animals with carcass EUROP classification from commercial abattoirs, 36,958 animals with AWW and 15,572 with AYW collected since 2006. The fixed effect of contemporary group, sex*twin, age of the animal (for ultrasound, SC and carcass traits), age of dam (for ultrasound traits, SC, AWW, and AYW), and heterosis (for carcass traits, AWW and AYW) were included in the model equation. Random effects considered were the direct additive genetic effect and the residual effect. Heritability estimates for SCW, SC, P8FT, RBFT, EMA, IMF, CW, CC, CF, AWW and AYW were 0.69, 0.77, 0.49, 0.44, 0.71, 0.25, 0.57, 0.37, 0.33, 0.45 and 0.38 respectively. As expected, strong genetic correlations were estimated between SCW, CW, AWW, and AYW (0.55-0.99). Genetic correlations between ultrasound and carcass traits were moderate to high. The highest genetic correlations were estimated between P8FT (resp. RBFT) and CF (0.99). The genetic correlation between EMA and CC was 0.98, and between IMF and CF 0.60. Genetic correlations between SC and ultrasound traits were low to moderate (0.19-0.60), and between SC and carcass traits were high (0.85-0.97). Genetic correlations between carcass and growth traits were low (0.09-0.27), and between ultrasound and growth traits were low to moderate (-0.51-0.47). The results show a negative genetic correlation between IMF and CW (-0.17) and between IMF and AWW (-0.51), which indicates that selection on high AWW could lead to lower IMF in the Aberdeen Angus. The results support the potential value of live animal ultrasound measurements in the Czech Aberdeen Angus breeding program to generate indicator traits for carcass quality.

Key words: beef cattle, genetic parameters, ultrasound, carcass traits, Aberdeen Angus

Introduction

Meat quality is one of the most crucial performance traits for beef cattle. Although meat quality is still not reflected in the price of meat at commercial abattoirs in the Czech Republic, many beef cattle farmers prefer animals with better meat quality. These are mainly producers who implement a system of selling meat from farms. In this case, customers are more likely to demand high-quality meat. For further selection, it is therefore essential for these breeders to focus not only on the intensity of growth of the animals but also on the correct proportion of the individual parts and their correct fat content, which helps further process the meat and improves its taste characteristics. For this reason, in 2019, based on the interest of the Aberdeen Angus Association in the Czech Republic, regular annual live animal ultrasound measurements of meat quality-related traits were launched.

The aim of this work was to estimate genetic parameters for live animal ultrasound measures and investigate their genetic correlations with carcass and growth traits.

Materials and Methods

Live ultrasound measures were collected on 1,949 animals aged 250 to 500 days through 2019, 2020, and 2022. Unfortunately, it was not possible to take measurements in 2021 due to the coronavirus pandemic. Ultrasound measurement was performed according to the internationally recognized Breedplan methodology (Breedplan, 2022). The advantage of this approach is that we have standardized results that can be used in the future for international genetic evaluation. A sole accredited ultrasound scanning technician recorded all measurements. Four measurements were collected - rump fat thickness (**P8FT**), rib fat thickness (**RBFT**), eye muscle area (**EMA**), and intramuscular fat content (**IMF**). In addition, two other characteristics were recorded during the measurement - the weight at scanning (**SCW**) and the scrotal circumference (**SC**) for bulls.

Furthermore, there were 7,672 animals with carcass EUROP classification from commercial abattoirs (carcass weight – **CW**, carcass conformation – **CC**, carcass fatness – **CF**), 36,958 animals with adjusted weaning weight (**AWW**), and 15,572 with adjusted yearling weight (**AYW**) collected since 2006. For evaluation purpose, CC was transformed into numerical score (E = 5, U = 4, R = 3, O = 2, and P = 1).

Variance components estimation

Standard data editing procedures for variance component estimation were used. Extreme records were excluded. The minimum size of the contemporary group was 5, and the minimum number of offspring of the sire was set to 3. The numbers of records and summary statistics of the dataset after editing are presented in table 1.

Table 1. – Summary statistic of the dataset for variance components estimation

Trait	Unit	N	Mean	SD	Min	Max
SCW	kg	1,452	448.9	91.0	220.0	766.0
SC	cm	659	35.0	3.6	25.0	51.0
P8FT	mm	1,452	5.1	2.3	1.0	13.0
RBFT	mm	1,452	3.9	1.7	1.0	9.0
EMA	cm^2	1,450	73.0	15.6	36.0	126.0
IMF	%	1,452	5.1	1.8	0.4	8.3
CW	kg	3,409	360.2	84.7	105.6	586.3
CC	score	3,409	3.0	0.7	1.0	5.0
CF	score	3,409	2.5	0.7	1.0	5.0
AWW	kg	29,102	278.0	41.4	150.0	427.0
AYW	kg	10,776	409.9	87.8	195.0	726.0

SCW - body weight at scanning, SC - scrotal circumference, P8FT - rump fat thickness, RBFT - rib fat thickness, EMA - eye muscle area, IMF - intramuscular fat content, CW - carcass weight, CC - carcass conformation, CF - carcass fatness, AWW - adjusted weaning weight, AYW - adjusted yearling weight

Estimates of variance components were obtained using average information restricted maximum likelihood (REML) as implemented in AIREMLF90 (Misztal et al., 2002). Multi-trait animal models were used to estimate (co)variances within each group of traits – for live ultrasound traits, carcass traits, and growth traits separately. (Co)variances between traits from different groups were estimated using a pairwise bivariate animal model since the full multi-trait model for all traits didn't converge. The model is represented in matrix notation as

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

where **y** is the vector of the observations for the traits of interest; **b** is the vector representing the fixed effects, including contemporary group, combined sex × twin effect (4 levels), the class effect of age of dam for ultrasound measures, and growth traits (9 levels), quadratic regression on the age of the animal for ultrasound measures and carcass traits and linear regression on heterosis for carcass traits and growth traits; **u** is the vector of random genetic additive effects; **e** is the vector of random residual effects; and **X** and **Z** are incidence matrices related to the fixed and random genetic additive effects, respectively.

The (co)variance matrix of random effect was

$$Var(u) = G \otimes A$$

where **G** is the additive genetic (co)variance matrix between traits and **A** is the numerator relationship matrix, and

$$Var(e)$$

$$= \left[\begin{matrix} R_U \otimes I & 0 & R_{UG} \otimes I \\ R_C \otimes I & & \end{matrix}\right| \quad \left| R_G \otimes I \right| \quad \Big]$$

where $\mathbf{R_U}$ is the residual (co)variance matrix for live ultrasound measures, $\mathbf{R_C}$ is the residual (co)variance matrix for carcass traits, $\mathbf{R_G}$ is the residual (co)variance matrix for growth traits, $\mathbf{R_{UG}}$ is the residual covariance matrix between ultrasound measures and growth traits, and $\mathbf{R_{CG}}$ is the residual covariance matrix between carcass and growth traits. Residual covariances between ultrasound measures and carcass traits were set to zero because only a few (69) animals had both live ultrasound measures and carcass traits records; therefore, residual covariance was not estimable.

Results & Discussion

Heritability

The heritability estimates are shown in table 2 (diagonal elements). Estimates for heritability were moderate for the growth traits: 0.38 for AYW and 0.45 for AWW. Heritabilities for carcass traits were moderate for CC (0.37) and CF (0.33). The most heritable carcass trait was CW, with heritability of 0.57. Heritabilities were higher compared to our previous study concerning carcass traits (Vesela et al., 2011).

The heritability estimates for live ultrasound measurements obtained in our study were moderate to high, except for IMF, with a heritability of 0.25. Heritability for IMF obtained in our study is slightly lower compared to those presented recently by Weik et al. (2022) for New Zealand Beef Cattle (0.52), Su et al. (2017) for Hereford and admixed Simmental beef cattle (0.45), and Seroba et al. (2011) for South African Angus cattle (0.38). Naserkheil et al. (2021), on the other hand, reported lower heritability for IMF 0.19 in Hanwoo cattle. Heritability for P8FT and RPFT in our study was moderate 0.49, resp. 0.44 and was within the range of reported estimates by other studies 0.29 – 0.54 (Naserkheil et al., 2021; Seroba et al., 2011; Su et al., 2017; Wiek et al., 2022). The highest heritability of all live ultrasound traits in our study was for EMA (0.71), which was higher than the values of 0.31 – 0.36 reported by other authors (Naserkheil et al., 2021; Seroba et al., 2011; Su et al., 2017; Wiek et al., 2022).

Heritability for SC, as the trait recorded during ultrasound measurement, was high 0.77. It was higher than the value 0.28 obtained in our previous study by Novotna et al. (2022), which was, however, investigating the heritability of SC for bulls of all beef breeds since the year 1996.

Genetic correlations

The estimated genetic correlations are shown in table 2 (below diagonal) and residual correlations (above diagonal). As expected, the strong genetic correlations were estimated among different weights ranging from 0.55 (AWW and CW) to 0.99 (SCW and AYW, and SCW and CW).

A strong genetic correlation of 0.87 (resp. 0.88) between IMF and P8FT (resp. RBFT) is in agreement with 0.68 (rep. 0.76) reported by Weik et al. (2022) and 0.71 (resp. 0.72) reported by Seroba et al. (2011). The strong and positive genetic correlation between measures of fat is unfavorable, since selection for reduced subcutaneous fat will be associated with a decrease in intramuscular fat (Seroba et al., 2011).

Correlations between live ultrasound traits and corresponding carcass traits were strong positive. A very strong genetic correlation of 0.99 was estimated among CF, P8FT, and RBFT, as well as between EMA and CC. The correlation between IMF and CF was 0.6. Interestingly there was a very strong genetic correlation of 0.99 between SC and CW and 0.97 between SC and CC. However, the number of bulls with SC measurement in our study was limited (659) and therefore the results could be biased.

Moderate positive correlations 0.47 and 0.43 were estimated between EMA and AWW (resp. AYW). On the contrary, the correlation between IMF and AWW was moderate negative, and the correlation between RBFT (resp. P8FT) and AWW was low positive 0.24 (resp. 0.16).

Table 2. Genetic (below diagonal) and residual (above diagonal) correlations, heritabilities (diagonal), and their standard errors in brackets

	Live animal ultrasound measures						Carcass traits			Growth traits	
	SCW	SC	P8FT	RBFT	EMA	IMF	CW	CC	CF	AWW	AYW
SCW	**0.69**	0.35	0.04	0.04	0.01	0.00	0	0	0	0.66	0.90
	(0.05)	(0.11)	(0.02)	(0.04)	(0.01)	(0.03)				(0.04)	(0.01)
SC	0.38	**0.77**	0.15	0.34	0.09	-0.12	0	0	0	0.35	0.33
	(0.09)	**(0.06)**	(0.15)	(0.14)	(0.02)	(0.15)				(0.12)	(0.41)
P8FT	0.54	0.19	**0.49**	0.48	0.09	0.11	0	0	0	0.24	0.34
	(0.08)	(0.16)	**(0.08)**	(0.05)	(0.02)	(0.05)				(0.19)	(0.08)
RPFT	0.61	0.20	0.99	**0.44**	0.07	0.15	0	0	0	0.23	0.29
	(0.07)	(0.15)	(0.01)	**(0.07)**	(0.03)	(0.04)				(0.06)	(0.33)
EMA	0.90	0.42	0.35	0.43	**0.71**	0.08	0	0	0	0.39	0.49
	(0.05)	(0.07)	(0.07)	(0.06)	**(0.01)**	(0.05)				(0.06)	(0.07)
IMF	0.70	0.60	0.87	0.88	0.50	**0.25**	0	0	0	0.26	0.27
	(0.05)	(0.11)	(0.04)	(0.04)	(0.06)	**(0.03)**				(0.06)	(0.04)
CW	0.99	0.99	0.61	0.80	0.99	-0.17	**0.57**	0.49	-0.14	0.38	0.00
	(0.01)	(0.01)	(0.13)	(0.07)	(0.01)	(0.01)	**(0.10)**	(0.14)	(0.19)	(0.06)	(0.00)
CC	0.44	0.97	0.28	0.78	0.98	0.23	0.41	**0.37**	0.11	-0.87	0.00
	(0.19)	(0.01)	(0.27)	(0.12)	(0.01)	(0.02)	(0.15)	**(0.12)**	(0.13)	(0.00)	(0.01)
CF	0.24	0.85	0.99	0.99	0.03	0.60	0.92	0.19	**0.33**	0.52	0.00
	(0.22)	(0.08)	(0.01)	(0.01)	(0.30)	(0.06)	(0.03)	(0.24)	**(0.13)**	(0.05)	(0.01)
AWW	0.94	-0.16	0.16	0.24	0.47	-0.51	0.55	0.20	0.27	**0.45**	0.73
	(0.01)	(0.14)	(0.06)	(0.07)	(0.05)	(0.17)	(0.04)	(0.01)	(0.01)	**(0.01)**	(0.01)
AYW	0.99	0.57	-0.07	0.43	0.43	-0.05	0.70	0.09	0.15	0.89	**0.38**
	(0.01)	(0.22)	(0.11)	(0.08)	(0.08)	(0.05)	(0.06)	(0.01)	(0.01)	(0.01)	**(0.02)**

SCW - body weight at scanning, SC - scrotal circumference, P8FT - rump fat thickness, RBFT - rib fat thickness, EMA - eye muscle area, IMF - intramuscular fat content, CW - carcass weight, CC - carcass conformation, CF - carcass fatness, AWW - adjusted weaning weight, AYW - adjusted yearling weight

Conclusions

The heritability estimates and strong genetic correlations between live animal ultrasound measures and corresponding carcass traits obtained in this study indicate that genetic evaluation for live animal ultrasound measures is feasible and genetic improvement through selection should be effective. Correlations between live animal ultrasound measures and growth traits suggest that selection on the high adjusted weaning weight in Czech Aberdeen Angus could be associated with an increase of red meat yield; however, at the same time could lead to a decrease of intramuscular fat content, which is undesirable for meat quality specific to this beef breed. This genetic antagonism should be considered in breeding programs in the future.

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