Direct – Maternal Genetic Parameters Estimated for Real-Time Ultrasound Scan Measures of Eye Muscle Area, Rib Fat Depth, and their Correlation with Body Weight in Male Philippine Riverine Buffaloes

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Abstract: *Background*: Ultrasound scanning is a non-invasive technique for evaluating animals based on carcass yield and meat quality traits. It has been incorporated into the beef cattle breeding program. However, little has been done in buffaloes. Thus, this study was conducted to estimate the genetic parameters for growth traits- body weights (BW) and a real-time ultrasound scan of eye muscle area (EMA) and rib fat (RF) to determine their suitability as a tool for selection.

Methods: Four hundred thirty-eight (438) male Philippine riverine buffaloes with 1,535 BW records and 417 real-time ultrasound scans of EMA and RF scans at the 12th rib were available for the study. BW was taken and adjusted at birth, 6, 12, 18, 24, 30, and 36 months while RF and EMA scans were taken at 12 & 18 mos. Genetic parameters were estimated with a pedigree-based multi-trait animal model using ASREML software.

Results: The average BW of buffaloes adjusted to 6, 12, 18, 24, 30, and 36 months of age were 135kg, 230.8kg, 323.0kg, 382.7, 453.6, and 502.4kg, respectively. The mean EMA and RF at 12 months were 29.7 cm^2 and 3.2mm, respectively. Direct genetic heritabilities were 0.26±0.16, 0.29±0.12, 0.35±0.19 and 0.67±0.32 for birth, BW12mos, EMA12mos and RF12mos, respectively. Maternal genetic heritability for birth weight. was 0.12±0.09. Genetic correlations among traits were positive except between birth and RF.

Conclusions: Results indicate that ultrasound scanning can be used for selection together with BW at 12mos. and suggest that early performance is an excellent predictor of performance at a later age.

Keywords: EMA, heritability, growth traits, genetic correlations, estimated breeding values, linear mixed model, BLUP, ASREML.

INTRODUCTION

Buffalo meat, or "carabeef," contribution to our country's agricultural production is on the rise, with 461.49 thousand heads slaughtered mainly for meat as of 2014 [1]. This is a 0.97 percent increase from the previous year's total slaughtered carabaos. However, the supplied volume of carabeef is still lower at about 46.27 percent than that of cattle beef. The vital role of carabao in the local meat industry is not yet known to many of us due to consumers' preference for cattle beef rather than carabeef. This can be attributed to the practice of Filipino farmers to preserve younger buffaloes for breeding and draft purposes and slaughter the buffaloes at an older age after they have been retired as draft animals making the meat tough and of poor quality. Without proper identification of meat based on the quality and yield, carabeef is processed and sold in the market at a lower value than that of cattle beef. With a growing dairy buffalo industry, artificial insemination is being done at an

increasing rate on swamp buffaloes and their crosses using riverine buffalo sires. The male buffalo not used for breeding, be it purebred or crossbred, is fattened and sold for slaughter. However, due to the negative perception that carabao meat is tough, the price per kilogram of live weight is lower than cattle. Increasing the growth rate and carcass yield would add value to the animal.

The Philippine Carabao Center (PCC) has initial efforts on the improvement of carabeef. In a study conducted by Lapitan *et al*. [2], results have shown that at similar younger ages and fed with the same diet, the crossbreed water buffaloes are as comparable with crossbreed cattle in relation to growth, carcass, and meat quality. The same study has revealed that carabeef contains 40% less cholesterol and 55% fewer calories, with 11% more protein and 10% more mineral as compared to cattle meat. These characteristics that buffalo meat possesses give us an advantage and a vision for a promising contribution to the meat industry.

The beef cattle industry has long been evaluating and selecting animals in their breeding program based on carcass yield and meat quality traits for their breeding programs. Real-time ultrasound scanning

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(RTUS) for determining the quality and quantity of meat has been an established non-invasive technique used in beef cattle, which utilizes high-frequency sound waves that are above what is perceived by the human ear [3]. Originally, the evaluation of superior lines for meat quality could only be obtained through progeny testing, which is a slow and expensive process. But with the advent of ultrasound technology, many sires can now be evaluated at a younger age, and progeny testing for carcass traits can be completed in a much shorter period. This study aimed to establish ultrasound information on carcass traits measurement for buffalo meat selection that is relatively inexpensive, convenient, and less time-consuming, and eventually, its incorporation into the PCC breeding program. This research is in line with PCC's goal to promote our water buffalo as a significant source of meat and milk besides hide and draft power. Furthermore, measurements taken from individual animals to establish baseline information on ultrasound information can also be used for genetic evaluation so that genetically superior individuals can be identified and used for breeding hence, the objective of this sub-study.

MATERIALS AND METHODS

Four hundred thirty-eight (438) apparently healthy, intact male riverine Murrah buffaloes born from 2014 – 2020 in the Philippine Carabao Center (PCC) National Gene Pool herd were the data source. Individual performance records are routinely taken at the farm as a regular activity following PCC-established protocol. Birth weight and subsequent body weights (BW) were taken from individual animals and adjusted to standard weights of 6, 12, 18, 24, 30, and 36 months of age. Real-time ultrasound scan measures of eye muscle area (EMA) and rib fat (RF) depth were taken at 12 and 18 mos., together with their corresponding body weights at that time. Measurements were taken such that the animals belonging to the same contemporary groups in the herd were weighed on the same day. Thus, adjustment to a standard weight was made given the formula: $AdjWt_i$ = (actual weight, kg – birth wt)/(date of weighing – date of birth) $*30.5_i$ + birth wt, where "*i*" are the different age categories (6, 12, 18, 24 30 and 36 mos.). After applying edits, 1,535 body weight records and 417 EMA scans were available for analysis. The animals belong to a contemporary group, exposed to the same feeding and environmental conditions. Animals were placed in the squeeze chute for safety and ease of handling during measurements. Animals were handled per the routine procedure

established by PCC following the animal welfare act (AWA) certification guidelines. Live animal measurements of the rump (P8) fat depth, 12/13th rib fat depth, and eye muscle area (EMA) were done by real-time scanning using an ultrasound machine (Honda Ultrasound Diagnostic Equipment, Honda®HS-2100V, Honda Electronics Co., Ltd., Oyamazuka Japan) equipped with 180mm 3.0 MHz linear-array transducer. Fixed machine settings were maintained for all animals. The 12/13th rib fat depth (RF) was measured between the 12th and 13th ribs near the backbone, ¾ the length ventrally over the longissimus muscle. Based on International Committee on Animal Recording (ICAR) guidelines, measurement was reported at the nearest millimeter. Cross-sectional scanning is necessary to obtain the eye muscle (*Longissimus dorsi* muscle) area measurement (EMA). The transducer with an offset pad was placed parallel between the 12th and 13th ribs. The boundary of the eye muscle was outlined/traced for area measurement (Figure **1**). Values were automatically calculated by the ultrasound machine. Three images were taken per animal, and the mean values of 12/13th rib fat depth and EMA were calculated.

Figure 1: Site of measurement for rib fat depth and eye muscle area (EMA).

Estimation of Genetic Parameters

Genetic parameter estimation and individual animal estimated breeding values (EBVs) were obtained using a multi-trait full animal model in a Best Linear Unbiased Prediction (BLUP) method for body weight at birth, 6, 12, 18, and 24 months of age as well as EMA measurement at 12, 18, 24 and months. The pedigree-based multi-trait full animal model used for analysis (Model 1) is given as $y_i = X_ib_i + Z_ia_i + e_i$ where the vector y_1 represents the n_1 observations for trait 1 and

y_2 represents n_2 observations for trait two, and so on, and there are p_i fixed effects associated with trait i so that X_i is a n_i x p_i matrix and b_i is a p_i x 1-dimensional column, vector a_i is the vector with random direct genetic effects. X_i and Z_i are incidence matrices for fixed and e_i random effects for trait i, respectively. Analysis for two-, three- and four- and five-trait models were done wherein only additive direct effects for growth traits were fitted (multiple trait BLUP animal model). Fixed effects in the genetic models included the age of the dam at calving and weighing date (as a contemporary group) and the age of the animal at weighing.

This was compared with another model that has both direct genetic effect for all traits and maternal genetic effect for birth weight only (Model 2) given as $y_i = X_i b_i + Z_1 i a_i + Z_2 m + e_i$. where y is the vector of the observations, b is a vector of fixed effects, a is a vector of additive direct genetic effects, m is a vector of maternal genetic effects, and e is a vector of residual effects. X is the incidence matrix for the fixed effects, and Z_1 and Z_2 are incidence matrices relating observations to random effects of animal (additive genetic) and dam (maternal genetic), respectively [4]. Birth weight is the only trait fitted with maternal genetic effects as calves were immediately separated at birth and pail/bottle fed milk until 3 – 4 months of age. Calves are put in group pens upon weaning. The average information residual maximum likelihood, ASREML 4.0 [5] software, was used to form the A-inverse as well as variance component estimation. Estimates of heritability for additive direct, phenotypic, and genetic correlations and their corresponding standard errors were obtained. The variance components for direct genetic effects ($\sigma^2 a$) and residuals ($\sigma^2 e$) were used to calculate the phenotypic

variance for Model 1: $\sigma^2 y_i = \sigma^2 a_i + \sigma^2 e_i$. For Model 2, the phenotypic variance includes random maternal effects term for birth weight: $\sigma^2 y_i = \sigma^2 a_i + \sigma^2 m + \sigma^2 e_i$. Using the VPREDICT function of ASREML 4.0 [5], the heritability estimate for direct genetic, $\sigma^2 a / \sigma^2 y$, and corresponding standard error is reported. Genetic correlation between traits is given as: $r = \sigma a_{12} / \sqrt{\sigma^2 a_1 * \sigma^2 a_2}$ where σa_{12} is the covariance between Trait **1** and Trait **2**.

RESULTS AND DISCUSSION

Table **1** presents the average adjusted body weight and scan measurement at different age categories of the male buffaloes used in the study. Body weight and EMA are all increasing in a linear trend, with the rate of increase gradually slowing down or tapering off with increasing age (Figure **2**), especially at 18 mos. until 30 mos. The trend is more noticeable for EMA compared with body weight. However, the market weight for finished bovine is around 450 kg; hence, the best time to start fattening would be at 18 mos. and finish at around 30 months.

The reported measurements of EMA and RF in these animals were considerably lower than the values obtained in the study conducted by Jorge *et al*. [6] in Mediterranean bulls. Those variations can be explained by several factors, such as the difference in the environmental condition, the type of diet, breed differences, and the genetic merit between the Mediterranean bulls and the Murrah bulls examined in the present study.

Using ultrasound technology to evaluate carcass traits and predict lean meat yield has long been a practice in the cattle industry. Several studies have been conducted using ultrasonography in predicting

Table 1: Summary Statistics for Body Weight and Live Animal Ultrasound Scan Measurement of Eye Muscle Area (EMA) and Rib-Fat (RF) Depth in Male Riverine Buffaloes

| Age Category | Body weight, kg | | | LIVE ANIMAL ULTRASOUND SCAN | | | | | Body height, cm | | |
| | | | | | EMA, cm^2 | | Rib Fat, mm | | | | |
	n	Mean	SD	n	Mean	SD	Mean	SD	n	Mean	SD
Birth	438	33.7	5.4								
6-months	285	135.0	23.1						165	102.2	5.9
12-months	374	230.0	34.5	168	29.7	5.8	3.2	0.9	171	116.3	8.3
18-months	295	323.2	49.1	198	35.2	6.6	3.8	1.1	172	123.7	6.2
24-months	106	382.7	60.4	55	40.2	10.2	4.3	2.1	105	128.9	5.4
30-months	66	453.6	73.1	37	43.3	6.9	4.1	1.9	109	135.1	5.2
36-months	37	502.4	73.7	16	44.2	8.9	4.9	3.6	89	133.4	5.3
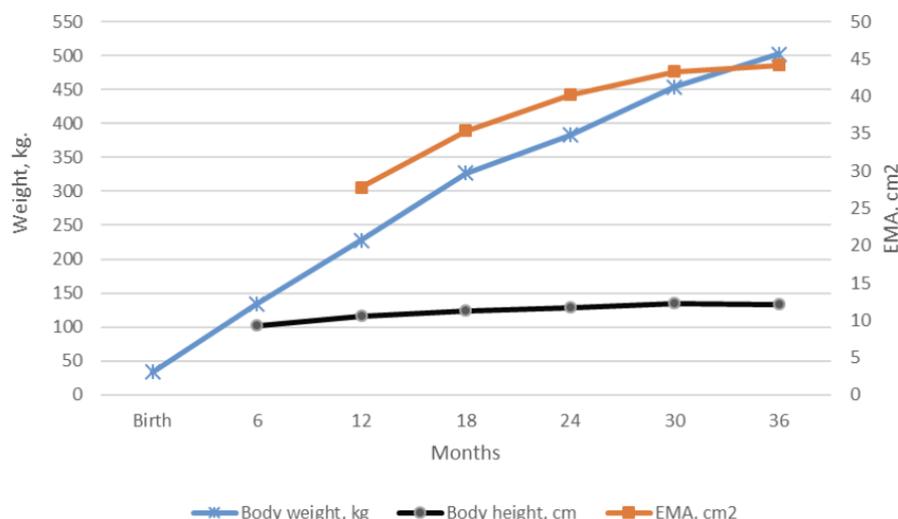
Figure 2: Average body weight and eye muscle area (EMA) measure, body weight and height of male riverine buffaloes at different age categories.

carcass traits in bulls. Live animal measurements are taken from the rib eye muscle area (*longissimus m.*) between the 12th and 13th ribs. The backfat thickness on the same site and on the rump or P8 site [7]. Parameters such as live weight, ultrasound measurements of eye muscle area, and backfat thickness and their corresponding carcass measurements were used as predictors of carcass composition in cattle. In 1990, Australian beef seed stock breeders already had estimated breeding values (EBV) evaluated for their cattle for scanned traits, including eye muscle area (EMA) and backfat thickness at the 12th and 13th rib and rump site for selection criteria [8].

On the other hand, Korea started the genetic improvement of their Hanwoo cattle in 1979, with the National Agricultural Cooperative Federation, the National Institute of Animal Science, and some Hanwoo breeding farms. Initially, superior sires for carcass meat could only be identified through progeny

testing, which is a slow, complicated, and expensive process. The discovery and development of what is considered a non-invasive technique to evaluate carcass quality and composition has stirred interest in researchers and breeders as well. Ultrasound uses high-frequency sound waves that are above what is perceived by the human ear. The tissue appears dark (anechoic), gray (hypoechoic), or white (hyperechoic) depending on its density and the velocity of sound penetrating the tissue. This forms the basis of identifying organs and organ structures and detection of abnormalities present [3].

For this study, Pearson Product-moment correlation for each pair of variables (body weights and ultrasound scans) was done initially to have some idea of the variations and strength of the linear relationship between variables. This is shown in Table **2**, and we observed that there are strong and positive correlations among body weight, rib fat depth, and EMA at 400D and 600D age categories. Rib fat depth generally has a

Table 2: Correlation Coefficients between Body Weight and Ultrasound Parameters at Different Age Categories in Male Riverine Buffaloes

Trait[1]	RF 400D	EMA 400D	Wt. 400D	RF 600D	EMA 600D	Wt. 600D
RF 400D[2]	1.0000					
EMA 400D[2]	0.4520	1.0000				
Wt. 400D[2]	0.4484	0.7156	1.0000			
RF 600D[3]	0.4909	0.3302	0.4368	1.0000		
EMA 600D[3]	0.4691	0.6656	0.6600	0.5158	1.0000	
Wt. 600D[3]	0.3340	0.5582	0.8497	0.2727	0.5820	1.0000

[1]D = age in days; Wt. = body weight, kg.; RF=ultrasound rib fat depth, mm; EMA= ultrasound eye muscle area measurement, cm^2. [2] N=168 RF, EMA &Wt records, [3] N = 198 RF, EMA & Wt records.

moderate correlation within and across traits. We see the highest correlation between body weight at 400D and 600D, followed by EMA in the same age category. The correlation between body weight and EMA at 400D age is moderately high at 0.71, but the figure drops to 0.58 at 600D. Nevertheless, all correlations across and within traits are positive and moderate to high. This is fortunate as it will be difficult to increase EMA without compromising the growth rate if the genetic correlation between the two traits is negative.

Genetic Parameters

Pedigree-based multi-trait full animal model analysis of body weight records had 926 identities in the pedigree extending seven (7) generations. There were 438 animals with birth weight records. However, some animals had missing records hence. Table **1** summarizes the number of records used per age category. The estimated genetic parameters for body weight at different age categories are shown in Table **3A**. The heritability estimate for birth weight is moderately high at 0.57 and slightly higher than reported in cattle [9]. The heritability estimates become lower as the age category increases, and the trend is consistent with some reported studies in cattle [9] but slightly lower than those reported by Malhado *et al*. [10] in buffaloes. These two observations could be due to

decreasing number of records with increasing age categories. Most bulls are removed from the herd at about 16 – 18 mos. Hence they are no longer available for measurements. The standard error of heritability for 24-mos is the same as the heritability estimates at 0.19 ±0.19, suggesting that the true heritability may lie within a range that includes zero.

Furthermore, the genetic correlation with 12-mos is high at 0.80, suggesting that a lot of variation accounted for at 12-mos is also explained at 24 months. Hence, there might be no need to add 24-mos. in the multi-trait animal model. The genetic correlation between 6-month and 18-month body weight was very low, which was unexpected as numerous reports indicate strong positive correlations among growth traits; this may need further inspection.

The results above were compared to another model that includes maternal genetic effects. However, the maternal genetic effect was only considered for birth weight as the calves were weaned immediately after birth and bottle/pail-fed milk until 3 – 4 months of age. In a study on the growth traits of buffaloes in Brazil by Malhado *et al*. [10], they reported very low maternal heritability for birth and 205D weight at 0.03 ±0.02 and 0.09 ±0.03, respectively. The result of this study indicates otherwise (Table **3B**). With partitioning the

Table 3: **Heritability, Genetic & Phenotypic Correlation between Body Weight at Different Age Categories in Male Riverine Buffaloes using a Model with Additive Direct Genetic and Maternal Genetic Effects**

A. Model 1 – additive direct genetic effects only					
Age Category	**Birth**	**6-months**	**12-months**	**18-months**	**24-months**
Birth	0.57 ±0.16	0.19	0.09	0.12	0.19
6-months	0.48	0.27 ±0.18	0.53	0.39	0.55
12-months	0.29	0.85	0.28 ±0.16	0.67	0.70
18-months	0.52	0.0063	0.31	0.14 ±0.12	0.75
24-months	0.41	0.69	0.80	0.36	0.19 ±0.19

B. Model 2 – additive direct genetic and maternal genetic effects						
Age Category	**Direct Genetic**					**Maternal Genetic**
	Birth	**6-mos.**	**12-mos.**	**18-mos**	**24-mos**	**Birth**
Birth	0.18 ±0.14	0.12	0.10	0.13	0.17	0.11 ±0.08
6-mos.	-0.19	0.11 ±0.14	0.42	0.30	0.55	
12-mos.	0.29	0.83	0.10 ±0.12	0.62	0.68	
18-mos.	0.36	0.64	0.94	0.22 ±0.15	0.74	
24-mos.	0.44	0.75	0.97	0.90	0.02 ±0.17	

Note: Diagonal – heritability ±SE, Upper diagonal phenotypic correlation, Lower diagonal – genetic correlations.

birth weight genetic variance into direct genetic and maternal genetic for Model 2 full animal model, the estimates of direct heritability and maternal heritability for birth weight were 0.18±0.14 and 0.11±0.08, respectively. The direct heritability for 24-mos body weight is 0.02 ±0.17, and while this is low compared to the estimated using Model 1 (Table **3A**), the high standard errors for both models indicate the true value of heritability may be close to zero. Furthermore, the high genetic correlation with 12-month and 6-mos body weight suggests the same variation is also accounted for by these traits. Thus, 24-mos may be dropped from the model.

Table **4** shows the estimates obtained when 24-mos. body weight was dropped from the model. Direct genetic heritability for 6-mos and 18-mos body weight is low, while their genetic correlation with 12-mos is moderately high. The standard error of heritability for 6-mos and 18-mos suggests that the range of where the true heritability lies may include zero (0) or no better than zero (0). The 12-mos parameter estimates suggest this trait might be able to account for the genetic variation in growth traits.

Growth traits, mainly adjusted body weight, standardized at the specified age of an animal, or average daily gain, are well-known traits and have been used to select faster-growing animals. However, growth rate is not the only determinant of meat production potential. American and Australian beef seed stock producers are routinely getting scan measurements for evaluating carcass traits and lean meat yield. EBVs are routinely reported and used for selection. Similarly, this study is reporting preliminary estimates of genetic parameters for eye muscle area (Table **5A**) and Ribfat depth (Table **5B**) as a tool for selecting individual animals with genetically better meat yield potential. Table **5A** shows the heritability estimate for 12- and 18-mos EMA at 0.46±0.19 and 0.59±0.19, respectively. The EMA estimate of heritability is higher than the 0.32 reported on yearling Hanwoo cattle [11].

Hanwoo is of different species and breeds and has been selected for beef production for many years; hence, it is possible to have a different estimate from riverine buffaloes. The moderately high estimates of heritability for EMA suggest there is good potential for increasing EMA through selection.

Similarly, for rib fat depth (RF), direct heritability is high to moderate for 12-mos and 18-mos measure at 0.94 ±0.26 and 0.43 ±0.17. For both EMA and RF, there is a high genetic correlation between 12-mos and 18-mos body weight and ultrasound scan measures. This suggests animals with good EMA and RF measures at 12 months are likely to have the same performance at 18 mos. The male buffaloes in this study are generally lean and fat deposition apparently is more visible when vertical growth starts to taper off at about 18 months (Figure **2**). In selecting replacement breeding animals, it is better to have a performance evaluation at an earlier age. Thus, decisions can be made at 12 mos, even without the 18-mos measures.

Table **6** presents the heritability estimates and genetic correlations for the final model, including birthweight, 12-mos BW, EMA, and RF. The direct genetic heritabilities were slightly lower than the previous model, which included the 18-mos measures, as shown in Table **5**. The heritability estimate for birth weight and 12-month body weight of Anatolian buffaloes [12] were higher than what was obtained in this study. However, their model did not include maternal effects, unlike the report of Joshi *et al*. [13] on Murrah buffaloes, wherein their reported heritability estimates for birthweight was out of a model that included partitioning the genetic variance into direct and maternal effects. There was still a difference in estimates between the study of Joshi *et al*. and this study, perhaps because their analysis was univariate or single-trait while the estimated in this study was out of multivariate or multi-trait analyses. Furthermore, previous studies did not include real-time scan measures for EMA and RF. It is expected that with

Table 4: Heritability, Genetic & Phenotypic Correlation between Body Weight at Different Age Categories Up to 18 Months of Age in Male Riverine Buffaloes

Growth Traits	Direct Genetic				Maternal Genetic
	Birth wt.	6-mos. wt	12-mos. wt	18-mos. wt	Birth wt.
Birth wt.	0.10±0.12	0.16	0.06	0.11	0.18±0.09
6-mos. wt	0.66	0.08±0.0.12	0.50	0.39	
12-mos. wt	0.28	0.82	0.24±0.16	0.68	
18-mos. wt	0.24	0.64	0.91	0.04±0.07	

Note: Diagonal – heritability ±SE, Upper diagonal phenotypic correlation, Lower diagonal – genetic correlations.

Table 5: Heritability and Correlation Estimates for Birth Weight, Body Weight, Eye Muscle Area (EMA) and Rib Fat (RF)

A. EMA & Body wt.	Direct Genetic					Maternal Genetic
	Birth wt.	12-mos. wt	12-mos.EMA	18-mos wt	18-mos EMA	Birth wt.
Birth wt.	0.12±0.10	0.09	-0.08	0.12	0.00	0.15 ±0.08
12-mos. wt	0.38	0.04±0.07	0.58	0.60	0.46	
12-mos.EMA	0.33	0.89	0.46±0.19	0.49	0.74	
18-mos wt	0.62	0.82	0.58	0.31±0.15	0.66	
18-mos EMA	0.68	0.91	0.86	0.87	0.59±0.19	

B. RF & Body wt.	Direct Genetic					Maternal Genetic
	Birth wt.	12-mos. wt	12-mos.RF	18-mos wt	18-mos. RF	Birth wt.
Birth wt.	0.22±0.15	0.07	-0.01	0.12	-0.05	0.08±0.08
12-mos. wt	0.23	0.24±0.15	0.51	0.66	0.37	
12-mos.RF	-0.26	0.83	0.94±0.26	0.46	0.59	
18-mos wt	0.24	0.98	0.77	0.36±0.19	0.37	
18-mos. RF	-0.09	0.94	0.96	0.92	0.43±0.17	

Note: Diagonal – heritability ±SE, Upper diagonal phenotypic correlation, Lower diagonal – genetic correlations. EMA – real-time ultrasound scan of eye muscle area measure. RF – real-time ultrasound scan rib fat depth measure.

Table 6: Heritability, Genetic & Phenotypic Correlation between Body Weight, Eye Muscle Area (EMA), and Rib Fat Depth (RF) at 12 Months of Age and Birth Weight in Male Riverine Buffaloes

Trait	Direct Genetic				Maternal Genetic Birth wt.
	Birth wt.	Wt. 12-mos.	EMA 12-mos.	RF 12-mos.	
Birth wt.	0.26±0.16	0.14	-0.09	0.00	0.12±0.09
Wt. 12-mos.	0.42	0.29±0.12	0.59	0.44	
EMA 12-mos.	0.17	0.72	0.35±0.19	0.48	
RF 12-mos.	-0.39	0.58	0.73	0.67±0.32	

Note: Diagonal – heritability ±SE, Upper diagonal phenotypic correlation, Lower diagonal – genetic correlations.

future studies involving larger data sets, genetic parameters, and correlation estimates may change slightly, but the standard error of heritability will be smaller.

There is a moderately high genetic correlation among body weight, EMA, and RF at 12 months. Selection for one trait can have a positively correlated response to the other two traits making genetic progress easier. The addition of birth weight to the model is necessary due to its moderate genetic correlation to body weight and EMA. Selecting faster-growing animals with bigger EMA might inadvertently result in bigger calves being born in the future and cause dystocia. In beef cattle, birth weight is positively correlated with weaning and yearling weight while negatively correlated with calving ease (https://www.beefmagazine.com/mag/beef_birth_weight_versus_calving_ease). The negative genetic correlation of birth weight with RF can balance the correlated response together with the selection of cows with smaller birth weights due to a moderately low maternal genetic heritability. The BLUP multi-trait genetic evaluation model can generate estimated breeding values (EBVs) for individual animals that can be used to rank and identify future breeding animals with confidence, even at an early age. A selection index that will balance response to selection for growth and EMA but at the same time smaller birth weight will be the focus of future studies.

CONCLUSIONS

This research indicates that the use of ultrasound scanning is an effective method for measuring live animal carcass traits even at earlier stages of an animal's life. This method is important for the identification and selection, and genetic evaluation of buffaloes with superior characteristics for meat. Many potential sires can be evaluated at a high degree of

accuracy without sacrificing the animal. Considering that ultrasound offers a relatively inexpensive and less time-consuming alternative progeny test of sires for carcass merits and that the more health and diet-conscious consumers these days are demanding lean and high-quality meat that is convenient and reasonably priced, the potential for improving carcass traits and meat quality of our carabeef by selection can be done without sacrificing response to selection for growth rate due to positive genetic correlations among traits. The estimated genetic parameters revealed enough variation in the male buffalo population under study to generate breeding values for individual animals. Thus, in order to facilitate the development of buffalo meat breeds in the Philippines, estimated breeding values for body weight, EMA, and RF can be used to select for breeding bulls in the genetic improvement program of PCC for meat quality traits in riverine and swamp buffaloes. Further research is warranted with a larger data set for estimating the quality and quantity of buffalo meat production or lean meat yield and for future genetic evaluation of carcass merit.

CONFLICT OF INTEREST

There is no conflict of interest with any financial organization regarding the materials discussed in the manuscript.

AUTHOR STATEMENT

The senior author, EB Flores, was responsible for Conceptualization, Methodology, Investigation, Data analysis, and Manuscript writing, whereas E Bacual was mainly involved in Investigation, Data collection, and Methodology.

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