

Effects of Logarithmic Transformation on Ultrasound Measurements in Hanwoo (Korean Native Beef Cattle)



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Introduction

- Hanwoo is a popular beef enjoyed in South Korea.
- As a result, Hanwoo has been genetically improved for more than 50 years.
- As the buying power of the consumers increases, more interest has been targeted toward the meat quality.
- Meat quality can only be measured after harvest.
- A non-invasive method is through a ultrasound device.
- Often times, ultrasound measurements present a skewed distribution which is against the assumption of the normal distribution in genetic analysis.
- This study seeks to assess the effect of ultrasound measurements with log transformation on genetic evaluation.

Materials and Methods

Three different analyses were performed to estimate breeding values and heritabilities. Each analysis contains the data of:

- Yearling weight (YW) and carcass traits (CT)
- YW, CT, and ultrasound traits at 12 and 24 months of age
- YW, CT, and logarithmic transformed ultrasound traits at 12 and 24 months of age

- The data were collected from the performance and progeny tests used to select Hanwoo proven bulls.
- Information on the national genetic evaluation system of Hanwoo has been reported by Park et al. (2013).
- YW and ultrasound traits at 12 months of age (UT12) were collected from the performance tests that are tested between 6 months to 12 months of age.
- YW, UT12, ultrasound traits at 24 months of age (UT24), and carcass traits were collected from the progeny tests that are tested between 6 months to 24 months of age.

- The carcass traits included:
 - carcass weight (CWT)
 - loin muscle area (LMA)
 - backfat thickness (BFT)
 - fat content (FC, %)

- The ultrasound traits included:
 - loin muscle area (LMA)
 - backfat thickness (BFT)
 - fat content (FC, %)
 - rump fat thickness (RFT)

which were measured using the Aquila Vet model (Pie Medical®) by experienced technicians.

- For the carcass traits, the data were collected by Korea Institute for Animal Products Quality Evaluation.
- The ultrasound scanning site for LMA was between the 13th thoracic and 1st lumbar vertebrae by keeping the probe parallel along the 13th rib.
- Similarly, BFT and FC was measured between the 13th thoracic and 1st lumbar vertebrae, but measured from a third quadrant distal and parallel to the spine.
- Observations measured from ultrasound device were plotted and the 1.5×IQR rule was applied to the data to identify and eliminate outliers.



Statistical Model

- The model for genetic evaluation of yearling weights is

$$y_{ij} = \mu + cg_i + a_j + e_{ij} \dots\dots\dots (1)$$

where is cg_i is the i^{th} fixed effect of housing–birth–progeny test group, a_j is the additive genetic effect of the j^{th} individual, and e_{ij} is the random error of the observation.

- The statistical model for the genetic evaluation of carcass traits is

$$y_{ij} = \mu + cg_i + \beta Wt + a_j + e_{ij} \dots\dots\dots (2)$$

where is cg_i is the i^{th} fixed effect of progeny testing group–testing station–harvest date, β is a linear covariate of body weight (Wt) at harvest, a_j is the additive genetic effect of the j^{th} individual, and e_{ij} is the random error of the observations.

- The statistical model for the genetic evaluation of ultrasound traits is

$$y_{ij} = \mu + cg_i + \beta Wt + a_j + e_{ij} \dots\dots\dots (3)$$

where is cg_i is the i^{th} fixed effect of testing group – housing – ultrasound measure date – technician – image reader, β is a linear covariate of body weight (Wt) at the ultrasound measure, a_j is the additive genetic effect of the j^{th} individual, and e_{ij} is the random error of the observations.

- Genetic parameters, such as heritability and genetic correlations, were estimated using REMLF90 among the BLUPF90 family of programs, and the convergence criterion was 1×10^{-22} .
- SAS/STAT software 9.2 was used to analyze the rank correlation of breeding values (SAS Institute Inc., 2008).

Table 1. Descriptive statistics for traits used to estimate breeding values in Hanwoo beef cattle

Category	Trait	N	Mean	S.D.	Min.	Max.	
Growth	YW (kg)	15,665	360.76	41.832	245	476	
	Carcass	CW (kg)	6,826	351.14	46.763	220	482
		LMA (cm ²)	6,820	79.382	8.7594	54	105
FC (%)		5,037	3.4719	1.6338	1	9	
Ultrasound at 12 months	LMA (cm ²)	8,614	54.214	7.5178	33.5	75	
	BFT (cm)	8,483	3.5798	0.9152	1.2	6	
	FC (%)	8,245	2.3142	1.0045	0.1	5.3	
	RFT (cm)	8,473	3.4651	1.0588	0.8	6.6	
Ultrasound at 24 months	LMA (cm ²)	3,800	86.564	8.3509	64.1	109.2	

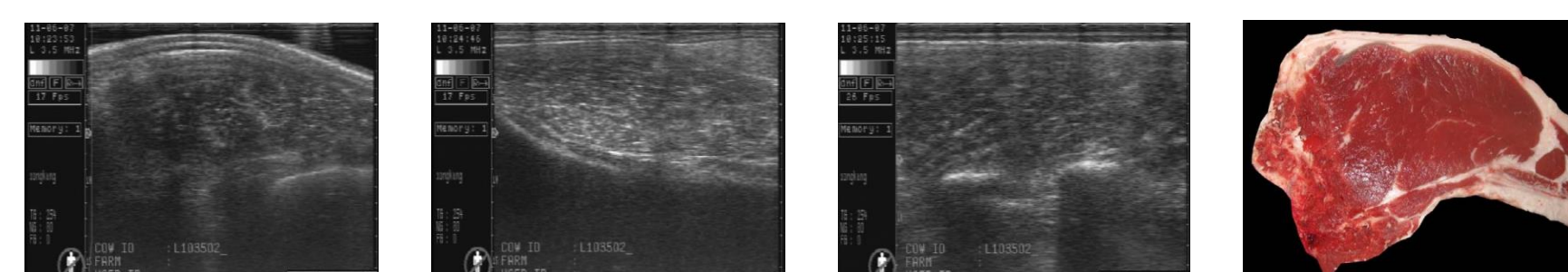


Table 2. Heritability estimates of yearling weight and carcass traits

	A	B	C	B-A	C-A
YW	29.2%	29.3%	29.0%	0.1%	-0.2%
CWT	35.1%	35.7%	35.7%	0.6%	0.6%
LMA	43.8%	43.8%	43.9%	0.0%	0.1%
BFT	46.2%	46.6%	46.8%	0.5%	0.6%

Table 3. Heritability estimates of UT

Trait		B	C	C-B
12 months of age	LMA	35.7%	38.0%	2.3%
	BFT	23.9%	23.2%	-0.7%
	FC	19.9%	23.2%	3.3%
	RFT	27.5%	27.4%	-0.1%
24 months of age	LMA	21.9%	25.6%	3.7%
	BFT	36.3%	40.2%	3.8%
	FC	25.7%	28.3%	2.6%
	RFT	39.9%	40.7%	0.8%

Table 4. Genetic correlations between YW, CT and UT12

	Ultrasound at 12 months of age			
	LMA	BFT	FC	RFT
YW	0.09	-0.07	-0.15	-0.08
CWT	0.08	-0.21	0.05	-0.16
LMA	0.57	-0.20	0.23	-0.27
BFT	-0.09	0.61	0.18	0.52

Table 5. Genetic correlations between YW, CT and log-transformed UT12

	Ultrasound at 12 months of age			
	LMA	BFT	FC	RFT
YW	0.13	-0.08	-0.23	-0.12
CWT	0.11	-0.21	-0.00	-0.18
LMA	0.59	-0.21	0.17	-0.31
BFT	-0.08	0.62	0.18	0.52

Table 6. Genetic correlations between YW, CT and UT24

	Ultrasound at 24 months of age			
	LMA	BFT	FC	RFT
YW	0.14	-0.09	0.15	-0.03
CWT	0.38	0.05	0.35	0.10
LMA	0.81	-0.23	0.36	-0.25
BFT	-0.11	0.89	0.01	0.64

Table 7. Genetic correlations between YW, CT and log-transformed UT24

	Ultrasound at 24 months of age			
	LMA	BFT	FC	RFT
YW	0.14	-0.08	0.13	-0.01
CWT	0.36	0.06	0.32	0.12
LMA	0.75	-0.22	0.30	-0.22
BFT	-0.10	0.87	0.02	0.59

Table 8. Genetic correlations between UT12 and UT24 using method B

B	Ultrasound at 24 months of age				
	LMA	BFT	FC	RFT	
Ultrasound at 12 months of age	LMA	0.62	-0.01	0.02	-0.16
	BFT	0.06	0.70	0.13	0.54
	FC	0.38	0.12	0.71	0.17
	RFT	-0.14	0.50	0.00	0.79

Table 9. Genetic correlations between UT12 and UT24 using method C

C	Ultrasound at 24 months of age				
	LMA	BFT	FC	RFT	
Ultrasound at 12 months of age	LMA	0.56	-0.02	0.02	-0.15
	BFT	0.05	0.64	0.12	0.48
	FC	0.31	0.16	0.61	0.13
	RFT	-0.15	0.48	0.01	0.73

Table 10. Rank correlations of EBV of YW and CT among different methods

	N'	A-B	A-C	B-C
YW	18,475	0.996	0.995	0.999
CWT	18,475	0.989	0.989	0.999
LMA	18,475	0.958	0.955	0.998
BFT	18,475	0.930	0.926	0.996

*Number of individuals with at least one observation of all the traits that were used in the analysis

Table 11. Rank correlations of EBV of YW and CT among different methods

	N'	A-B	A-C	B-C
YW	15,665	0.995	0.994	0.999
CWT	6,526	0.989	0.989	0.999
LMA	6,820	0.984	0.982	0.999
BFT	6,723	0.982	0.982	0.998

*Number of individuals measured in each trait

Table 12. Rank correlations of EBV of UT between methods B and C

Ultrasound traits	N'	B-C	
12 months of age	LMA	18,475	0.996
	BFT	18,475	0.993
	FC	18,475	0.978
	RFT	18,475	0.986
24 months of age	LMA	18,475	0.994
	BFT	18,475	0.989
	FC	18,475	0.991
	RFT	18,475	0.985

*Number of individuals with at least one observation of all the traits that were used in the analysis

Table 13. Rank correlations of EBV of UT between methods B and C

Ultrasound traits	N'	B-C	
12 months of age	LMA	8,614	0.995
	BFT	8,483	0.991
	FC	8,245	0.976
	RFT	8,743	0.985
24 months of age	LMA	3,800	0.989
	BFT	3,786	0.986
	FC	3,824	0.989
	RFT	3,745	0.98

*Number of individuals measured in each trait

Discussion

- Few studies regarding transforming ultrasound measurements
- “log-transforming ultrasonic fat depth caused the heritability to decrease” and “other traits did not show sufficient improvement to justify a transformation” (Heelsum and Lewis, 2001)
- Log transformation does not alter genetic variation, as measured by heritability (DeStefano and Van Vleck, 1991)

Conclusion

- Not much difference in ranks between original and transformed data.
- No major difference in estimations among the three different analyses.
- In LMA and BFT, possible changes in ranks may occur using analyses A and B.
- Transformed data didn't show a big difference from the original data.
- Further study (i.e. simulation study) will be needed to investigate the true effect of transformation.

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