Evaluation of variation attributable to lab and technician for measurements of beef carcass traits made using ultrasound

Schmidt, B., M.D. MacNeil, and M.G. Gonda

Objective
To partition phenotypic variance into components which are attributable to additive genetic effects, technician, contemporary groups within technician, and residual.

Study Description
Ultrasound data gathered from 2015 to 2017 was provided by the American Angus Association (AAA; n=281,982 animals), American Hereford Association (AHA; n=49,602), and American Simmental Association (ASA; n=59,576) for a total of 391,160 animals. Ultrasound animal ID, contemporary group, scan age, technician, imaging laboratory, ribeye area (REA), backfat (BF), and percent intramuscular fat (IMF) were included in the data for each animal. Imaging laboratory was separated into the three Ultrasound Guidelines Council accredited labs as Lab 1, Lab 2, and Lab 3. A three-generation pedigree was formulated for each animal. Multiple trait derivative free restricted maximum likelihood (MTDFREML) procedures by Boldman et al. (1995) were utilized for analysis of variance components and genetic correlations.

Take home points
Technician explained 12-27%, 4-23%, and 4-27% of variance for IMF, BF, and REA respectively across all three breeds. On average, the variance contributed by technician was greater than the variance contributed by additive genetics but less than that explained by contemporary group. Genetic correlations between labs across breeds ranged from 0.79 to 0.95 for IMF, 0.64 to 0.94 for BF and 0.78 to 0.98 for REA. Technician contributed to variance in ultrasound measurements, but high genetic correlations between labs suggest lab plays a lesser role in contribution of variance to ultrasound measurements. Overall technician contributes to the variance of ribeye area and intramuscular fat ultrasound measurements more than to backfat ultrasound measurements. Still, technician is a contributing factor to variance in each ultrasound carcass measurement. Inclusion of technician variance may increase the accuracy of genetic predictions where ultrasound data is utilized. Imaging laboratories were highly correlated which suggests they play a lesser role in the contribution of variance to carcass ultrasound measurements. The continuation of improvement of ultrasound methods and technology is encouraged the lower contribution of variance by technician for Lab 2 may be due to more advanced technology.

Keywords: beef, carcass merit, ultrasound, imaging laboratory

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Abstract

National cattle genetic evaluations assume technician and imaging lab do not contribute to phenotypic variation when measuring carcass traits by ultrasound. The objective of this study was to estimate variance components of ultrasound carcass measurements, specifically variance contributed by ultrasound technician and imaging laboratory. Accounting for technician and imaging lab variation may increase accuracy of genetic predictions for carcass traits. Ultrasound carcass predictions for ribeye area (REA), percent intramuscular fat (IMF), and backfat (BF) were provided by the American Angus Association (AAA; n=281,982 animals), American Hereford Association (AHA; n=49,602), and American Simmental Association (ASA; n=59,576) for a total of 391,160 animals. Data provided by each association included ultrasound carcass measurements, contemporary group, technician ID, imaging lab, and a three-generation pedigree for each animal with ultrasound measurements. Variance contributed by additive genetics, technician, and contemporary group on ultrasound carcass measurements were estimated for each breed separately. Because technician and lab were confounded, the contribution of lab to ultrasound carcass variation could not be separated from technician. Therefore, we assessed whether lab contributed to ultrasound carcass variation by estimating genetic correlations between laboratories for ribeye area, percent intramuscular fat, and backfat. This analysis separated carcass traits by laboratory and treated measurements interpreted by each lab as a separate trait. Technician explained 12-27%, 4-23%, and 4-27% of variance for IMF, BF, and REA respectively across all three breeds. On average, the variance contributed by technician was greater than the variance contributed by additive genetics but less than that explained by contemporary group. Genetic correlations between labs across breeds ranged from 0.79 to 0.95 for IMF, 0.64 to 0.94 for BF and 0.78 to 0.98 for REA. Technician contributed to variance in ultrasound measurements, but high genetic correlations between labs suggest lab plays a lesser role in contribution of variance to ultrasound measurements.

Introduction

The use of ultrasound to estimate beef carcass traits has been around since the 1950's (Stouffer and Westervelt, 1977). Ultrasound technician and imaging laboratory are critical parts to the evaluation of ultrasound carcass measurements and yet we know very little about their contribution to phenotypic variation. Currently, technician and imaging laboratory are included as part of the contemporary group effect in the National Cattle Evaluation (NCE). Also, differences in additive genetic variance between imaging laboratory would indicate that EPDs produced would have different ranges depending on which laboratory interpreted the images. Ultrasound technicians and imaging laboratories go through accreditation processes designed by the Ultrasound Guidelines Council to reduce variation among them. However, the degree to which this certification process is successful is mostly unknown.

This study aims to partition and quantify variance components of beef carcass ultrasound measurements, which are attributable to additive genetic effects, technician, contemporary groups, and residual. If variance for technician and imaging labs exists, accounting for this variation may improve accuracy of genetic predictions for carcass traits.

Experimental Procedures

Ultrasound data gathered from 2015 to 2017 was provided by the American Angus Association (AAA; n=281,982 animals), American Hereford Association (AHA; n=49,602), and American Simmental Association (ASA; n=59,576) for a total of 391,160 animals. Animal ID, contemporary group, scan age, ultrasound technician, imaging laboratory, ribeye area (REA), backfat (BF), and percent intramuscular fat (IMF) were included for each animal. Imaging laboratory was separated into the three Ultrasound Guidelines Council accredited labs as Lab 1, Lab 2, and Lab 3. A three-generation pedigree was formulated for each animal from parentage records.

Multiple trait derivative free restricted maximum likelihood (MTDFREML) procedures by Boldman et al. (1995) were utilized for analysis of variance components and genetic correlations. For the AHA and ASA data, pedigrees were formulated with animal, sire, dam, grandsires and granddams. Because of size limitations within the MTDFREML software, the AAA pedigree could not be formulated the same as the other breeds due to having over four times the number of animals. Instead, the AAA pedigree was formulated with animal, sire and maternal grandsire. This method allowed the largest number of AAA animals to be included while still having a precise pedigree. Variance components for additive genetic effects, technician, and imaging lab were estimated. The relative contribution of each effect to the total phenotypic variance was estimated by dividing variance of each effect by total phenotypic variance. Because technician and lab were confounded, the contribution of lab to ultrasound carcass variation could not be separated from technician. Therefore, we assessed whether lab contributed to ultrasound carcass variation by estimating genetic correlations between laboratories for ribeye area, percent intramuscular fat, and backfat. This analysis separated carcass traits by laboratory and treated measurements interpreted by each lab as a separate trait.

Results and Discussion

Estimated variance components were separated into variance contributed by additive genetics, technician, contemporary groups within technician and residual. Additive genetics explained 8 to 24% of phenotypic variation for all carcass traits measured in the Hereford breed. Ribeye area had the lowest proportion of variance by additive genetics among carcass traits for all three labs in the Hereford breed (Table 1). Technician explained 4 to 22% of phenotypic variation in Herefords. Backfat had the lowest proportion of variance for all three labs for this trait. Variance contributed by technician from Lab 2 was consistently the lowest among labs for all three carcass traits. Contemporary group within technician explained 36 to 73% of phenotypic variance, which was the highest contributor to phenotypic variance for all traits and labs with the exception of Lab 3 for backfat. Results for the Simmental and Angus data were similar with those of the Hereford data with a few exceptions and are available by request. The genetic correlations between imaging labs for each trait in each breed were consistently high.

The lowest correlation of 0.64 was between Lab 2 and Lab 3 for backfat in the AHA data (Table 2).

Contemporary group explained the majority of variation among carcass traits. Technician was clearly different from zero and did indeed contribute to the variance of beef ultrasound carcass measurements. This variance should be accounted for when making genetic predictions where ultrasound data is used. Lab 2 utilizes a different technology than Lab 1 and Lab 3 to interpret ultrasound images, which may be contributing to the lower proportion of phenotypic variance explained by technician from this imaging lab. Previous studies have shown a higher accuracy of ultrasound estimates for backfat versus ribeye area (Greiner et al., 2003). The higher accuracy may be due to the measurement itself because backfat is easier to measure than ribeye area. As shown by Greiner et al. (2003), the definition of the outline of the longissimus muscle that makes up the ribeye area can be affected by the amount of fat present. The ventral edge of the ribeye area is less easily defined as backfat depth increases. Also, the ribeye area is an odd shaped oval that can range from 70 to 116 cm^2 whereas backfat depth has a more defined shape that ranges from one to three centimeters. Considering these factors may help interpret the lower overall proportion of phenotypic variance by technician for backfat versus ribeye area. The overall high genetic correlations between laboratories among carcass traits suggests laboratory plays a lesser role in the contribution of variance to ultrasound carcass measurements.

Implications

Overall technician contributes to the variance of ribeye area and intramuscular fat ultrasound measurements more than to backfat ultrasound measurements. Still, technician is a contributing factor to variance in each ultrasound carcass measurement. Inclusion of technician variance may increase the accuracy of genetic predictions where ultrasound data is utilized. Imaging laboratories were highly correlated which suggests they play a lesser role in the contribution of variance to carcass ultrasound measurements. The continuation of improvement of ultrasound methods and technology is encouraged the lower contribution of variance by technician for Lab 2 may be due to more advanced technology.

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Table 1. Estimate of percent additive genetic, technician, contemporary group, and residual variance for Hereford ultrasound carcass data among laboratories

Trait [a]	Lab	% Additive Genetics ± SE [b]	% Technician ± SE [b]	% Contemporary Group ± SE [b]	% Residual ± SE [b]
IMF	Lab 1	0.15±0.02	0.21±0.04	0.37±0.02	0.27±0.02
	Lab 2	0.24±0.03	0.13±0.05	0.41±0.03	0.22±0.02
	Lab 3	0.19±0.01	0.21±0.03	0.37±0.02	0.23±0.01
BF	Lab 1	0.17±0.02	0.08±0.02	0.49±0.02	0.26±0.00
	Lab 2	0.14±0.02	0.04±0.02	0.51±0.02	0.31±0.02
	Lab 3	0.20±0.03	0.07±0.02	0.22±0.01	0.51±0.03
REA	Lab 1	0.09±0.01	0.21±0.04	0.56±0.03	0.14±0.01
	Lab 2	0.08±0.01	0.04±0.02	0.73±0.02	0.15±0.01
	Lab 3	0.09±0.01	0.15±0.03	0.62±0.02	0.14±0.01

[a] IMF = % intramuscular fat, BF = backfat, and REA = ribeye area
[b] Percent variation explained by each variable ± standard error

Table 2. Genetic correlations between laboratories among Hereford ultrasound carcass traits [a]

		REA			IMF			BF		
		Lab 1	Lab 2	Lab 3	Lab 1	Lab 2	Lab 3	Lab 1	Lab 2	Lab 3
	Lab 1	--								
REA	Lab 2	0.87	--							
	Lab 3	0.94	0.86	--						
	Lab 1				--					
IMF	Lab 2				0.86	--				
	Lab 3				0.95	0.89	--			
	Lab 1							--		
BF	Lab 2							0.81	--	
	Lab 3							0.87	0.64	--

[a] IMF = % intramuscular fat, BF = backfat, and REA = ribeye area