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Predicting Beef Carcass Cutability[1]

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ABSTRACT: Analyses were conducted to develop and test the efficacy of beef carcass cutability prediction equations. Data from 1,602 calf-fed steer carcasses (Germplasm Utilization Project; GPU) were used to develop the equations and an additional 1,160 calf-fed steer carcasses (Germplasm Evaluation Project; GPE) were used to validate the equations. In both experimental groups, USDA yield grade ranged from < 1 to > 5 and the SD of yield grade was > .8 indicating a relatively large amount of variation in carcass cutability. Models were developed to predict boneless, totally trimmed retail product yield (RPYD), fat trim yield (FATYD), and bone yield (BONEYD) using 1) carcass traits, 2) carcass traits and wholesale rib dissection traits, 3) carcass traits and 9-10-11 rib dissection traits, and 4) carcass traits and 9-10-11 rib dissection and chemical traits. For each dependent variable, the best single predictor was a wholesale rib dissection trait, and the best higher order model contained at least one wholesale rib dissection trait. Equations developed explained 87, 88, and 77% of the variation in RPYD, FATYD, and BONEYD, respectively. When validated against GPE carcasses, models developed from GPU carcasses explained 74, 78, and 69% of the phenotypic variation and 96, 94, and 84% of the genetic variation in RPYD, FATYD, and BONEYD, respectively. Prediction of carcass cutability using carcass and wholesale rib dissection traits should allow for rapid, precise, and cost-effective assessment of variation in cutability.

Key Words: Beef, Carcass Yield, Prediction

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Introduction

Collection of complete carcass cutability data is expensive because procedures are labor intensive and result in product devaluation. Numerous equations for estimating carcass yields of boneless, closely trimmed retail cuts have been developed (for review see Kempster et al., 1982). However, to our knowledge, equations to predict boneless, totally trimmed retail cut yields have not been published. Kempster et al. (1982) reported that depending on the sample cut used and the variable being predicted, sample cuts may improve the accuracy of prediction above that which can be achieved from carcass traits. Various rib section cuts have been investigated extensively (Hankins and Howe, 1946; Ledger et al., 1973; Crouse and Dikeman, 1976; Miller et al., 1988). In comprehensive cattle evaluation programs, ribeye steaks are frequently used to evaluate meat palatability (Koch et al., 1976, 1979, 1982b). Thus, an accurate rib-based cutability prediction procedure that does not result in destruction of the ribeye would be most desirable. Therefore, the present analyses were conducted to develop and test the efficacy of rib-based beef carcass cutability prediction equations using diverse biological types of calf-fed steers.

Materials and Methods

Animals. Data from 1,602 calf-fed steer carcasses (Germplasm Utilization Project; **GPU**) were used to develop the equations and an additional 1,160 calf-fed steer carcasses (Germplasm Evaluation Project; **GPE**) were used to validate the equations. Experimental design and carcass handling procedures were reported previously for GPU (Gregory et al., 1994) and GPE (Cundiff et al., 1993). The GPU project consisted of purebred Angus (**A**), Braunvieh (**B**), Charolais (**C**), Gelbvieh (**G**), Hereford (**H**), Limousin (**L**), Pinzgauer (**P**), Red Poll (**RP**), and Simmental (**S**) and three composite populations;

[1]Names are necessary to report factually on available data; however, the USDA neither guarantees nor warrants the standard of the product, and the use of the name by USDA implies no approval of the product to the exclusion of other products that may also be suitable. The authors are grateful to Lei Yen for her assistance with REML analyses.

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MARC I (1/4 C, 1/4 B, 1/4 L, 1/8 H, 1/8 A); MARC II (1/4 S, 1/4 G, 1/4 H, 1/4 A); and MARC III (1/4 RP, 1/4 H, 1/4 P, 1/4 A). The GPE project consisted of F_1 crosses produced by mating H and A dams to H, A, C, G, P, Galloway, Longhorn, Nellore, Piedmontese, Salers, and Shorthorn bulls.

Steers were fed a corn-corn silage diet from weaning to slaughter at 356 to 515 d of age. The length of the feeding period ranged from 228 to 343 d. Steers were slaughtered serially, in four kill groups (balanced across breed groups) spanning 63 d, at a commercial beef processing facility. After chilling, carcasses were ribbed and USDA quality and yield grades were determined (USDA, 1989).

The right side of each carcass was transported to the Roman L. Hruska U.S. Meat Animal Research Center (**MARC**) for fabrication into boneless, totally trimmed retail product according to Koch and Dikeman (1977). Each wholesale cut (round, loin, rib, chuck, flank, and brisket/plate/foreshank) was individually dissected and the following components were weighed: 1) boneless, totally trimmed retail cuts, 2) fat trim, 3) lean trim, and 4) bone. The lean trim was fabricated to contain 20% fat. To insure that the fat content of the lean trim was not biased by the leanness of the carcass, ether-extractable fat content (AOAC, 1980) of the lean trim was determined. Weights of lean and fat trim were adjusted to a constant 20% fat lean trim-basis. Weights of boneless, totally trimmed retail cuts and 20% fat lean trim were summed to give retail product weight.

For GPU carcasses, the 9-10-11 rib section was removed from the wholesale rib and processed following the same procedures as for the wholesale rib. Components of the 9-10-11 rib section were kept separate from the remainder of the rib. Soft tissue from the 9-10-11 rib section was ground and sampled for determination of ether-extractable fat and oven-dry moisture content (AOAC, 1980).

Statistical Analysis. Regression equations were developed to predict retail product yield (**RPYD**), fat trim yield (**FATYD**), and bone yield (**BONEYD**). Yields were expressed as a percentage of the sum of the parts (e.g., RPYD = 100 × retail product weight/[retail product weight + fat trim weight + bone weight]) rather than as a percentage of hot carcass weight (**HCW**) because the length of time that carcass sides were held before fabrication varied from 2 to 20 d and, thus, some sides were subjected to a greater amount of dehydration than others.

Independent variables were grouped as 1) carcass traits, 2) carcass traits and wholesale rib dissection traits, 3) carcass traits and 9-10-11 rib dissection traits, and 4) carcass traits and 9-10-11 rib dissection and chemical traits. Carcass traits included HCW, longissimus muscle area (**LMA**), actual 12th rib fat thickness (**ACTFAT**), adjusted 12th rib fat thickness (**ADJFAT**), estimated kidney, pelvic, and heart fat (**ESTKPH**), USDA yield grade (**YG**), and marbling score (**MARBLE**). Wholesale rib dissection traits included weights of untrimmed wholesale rib (**RIBWHSLWT**), ribeye roll (**RIBRSTWT**), muscle (**RIBMUSWT** = RIBRSTWT + [.8 × weight of rib lean trim]), fat (**RIBFATWT** = weight of rib fat trim + [.2 × weight of rib lean trim]), bone (**RIBBONEWT**), and short ribs (**SHRTRIBWT**), yields (expressed as a percentage of RIBWHSLWT) of ribeye roll (**RIBRSTYD**), muscle (**RIBMUSYD**), fat (**RIBFATYD**), bone (**RIBBONEYD**), and short ribs (**SHRTRIBYD**), muscle:bone ratio (**RIBM:B**), and muscle:fat ratio (**RIBM:F**). Rib section (9-10-11) dissection traits included weights of untrimmed 9-10-11 rib (**911WHSLWT**), muscle (**911MUSWT** = weight of the ribeye roll from the 9-10-11 rib section + [.8 × weight of lean trim from the 9-10-11 rib section]), fat (**911FATWT** = weight of the fat trim from the 9-10-11 rib section + [.2 × weight of lean trim from the 9-10-11 rib section]), and bone (**911BONEWT**), yields (expressed as a percentage of 911WHSLWT) of muscle (**911MUSYD**), fat (**911FATYD**), and bone (**911BONEYD**), muscle:bone ratio (**911M:B**), and muscle:fat ratio (**911M:F**). Rib section (9-10-11) chemical traits included yields of ether-extractable fat (**911EEFATYD**) and oven-dry moisture (**911MOISYD**) and weights of ether-extractable fat (**911EEFATWT**) and oven-dry moisture (**911MOISWT**).

Regression equations were selected using the RSQUARE procedure (SAS, 1988), which selects the single best (highest R^2) equation with a given number of variables. Thus, the RSQUARE technique differs from STEPWISE techniques in that the variables selected for higher order equations do not depend on the variables used in lower order equations. Equations were evaluated with respect to R^2 and residual standard deviation (**RSD**). Contrary to the recommendations of MacNeil (1983), we did not use C_p statistic (Mallows, 1973) as an equation selection criterion because the C_p statistic is not valid for comparing equations derived from different sets of parameters (or experiments). The C_p statistic is weighted for the pure error variance when all parameters are included in the model. Thus, the same equation would have a different C_p statistic if it were derived from carcass and 9-10-11 rib dissection traits than if it were derived from carcass and 9-10-11 rib dissection and chemical traits (e.g., although Equations [331] and [341] are identical, they have different C_p statistics).

The multiple-trait derivative-free REML program of Boldman et al. (1992) was used to determine heritability estimates of actual and predicted variables for the GPE carcasses. The model used included fixed effects of sire line, dam line, year, and slaughter group. Age differences were accounted for by using birth date as a covariate.

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Results

Means, SD, and ranges of the dependent and independent variables for the GPU carcasses are reported in Table 1. The experimental group contained a large amount of variation in carcass cutability measures with RPYD ranging from 51.8 to 80.8% (CV = 7.6%), respectively. All dependent variables had CV in excess of 8%. In both experimental groups (GPU and GPE), YG ranged from < 1 to > 5 and the SD of YG was > .8.

Prediction of Retail Product Yield. Wholesale rib muscle yield, 911MUSYD, RIBFATYD, 911EEFATYD, and 911FATYD explained 83, 81, 79, 77, and 77% of the variation in RPYD, respectively (Table 2). Among carcass traits, ADJFAT was the most accurate predictor of RPYD (r^2 = .58). The most accurate carcass trait-based equation only accounted for 72% of the variation in RPYD (Table 3). The YG equation accounted for 63% of the variation in RPYD (Table 2). For carcass and wholesale rib dissection traits, R^2 and RSD were made optimal by the three-variable equation (Equation [323]), which included RIBMUSYD, SHRTRIBYD and MARBLE, compared with the one-variable equation. None of the equations developed from 9-10-11 rib traits accounted for as much of the variation in RPYD as did Equation [323] (Table 3).

Prediction of Fat Trim Yield. Wholesale rib fat yield, 911FATYD, RIBMUSYD, 911EEFATYD, and RIBM:F explained 88, 85, 83, 81, and 81% of the variation in FATYD, respectively (Table 2). Among carcass traits, ADJFAT was the most accurate predictor of FATYD (r^2 = .64, respectively). Wholesale rib fat yield accounted for so much of the variation in

Table 1. Simple statistics and abbreviations for independent and dependent variables

Variable	Abbreviation[a]	Mean	SD	Minimum	Maximum
Hot carcass wt, kg	HCW	334.7	40.2	218.2	489.4
Longissimus muscle area, cm^2	LMA	78.6	10.4	50.3	117.4
Actual 12th rib fat thickness, cm	ACTFAT	.7	.4	.1	2.5
Adjusted 12th rib fat thickness, cm	ADJFAT	.6	.4	.0	2.5
Estimated kidney, pelvic, and heart fat, %[b]	ESTKPH	2.8	.7	.5	5.0
USDA Yield grade	YG	2.6	.8	.3	5.8
Marbling score[c]	MARBLE	494.7	70.0	290.0	890.0
Wholesale rib wt (untrimmed), kg	RIBWHSLWT	13.9	1.9	8.4	20.2
Wholesale rib muscle wt, kg	RIBMUSWT	7.3	1.0	4.7	10.6
Wholesale rib fat wt, kg	RIBFATWT	3.2	1.0	1.0	7.6
Wholesale rib bone wt, kg	RIBBONEWT	2.1	.3	1.4	3.2
Wholesale rib short rib wt, kg	SHRTRIBWT	1.3	.2	.6	2.1
Wholesale rib muscle yield, %[d]	RIBMUSYD	52.4	4.4	38.1	66.7
Wholesale rib fat yield, %[d]	RIBFATYD	22.5	5.1	8.0	39.6
Wholesale rib bone yield, %[d]	RIBBONEYD	15.2	1.6	9.9	20.6
Wholesale rib short rib yield, %[d]	SHRTRIBYD	9.3	1.1	3.9	15.3
Ribeye roll wt, kg	RIBRSTWT	4.0	.6	2.6	6.1
Ribeye roll yield, %[d]	RIBRSTYD	28.8	2.7	20.8	36.4
Wholesale rib muscle:bone ratio	RIBM:B	3.5	.4	2.3	5.6
Wholesale rib muscle:fat ratio	RIBM:F	2.5	.8	1.0	8.1
9-10-11 Rib section wt (untrimmed), kg	911WHSLWT	5.6	.8	3.3	8.7
9-10-11 Rib section muscle wt, kg	911MUSWT	3.2	.5	1.9	5.0
9-10-11 Rib section fat wt, kg	911FATWT	1.5	.5	.4	3.7
9-10-11 Rib section bone wt, kg	911BONEWT	1.0	.1	.5	1.5
9-10-11 Rib section muscle yield, %[e]	911MUSYD	56.9	5.1	40.2	74.5
9-10-11 Rib section fat yield, %[e]	911FATYD	25.5	5.9	8.7	45.7
9-10-11 Rib section bone yield, %[e]	911BONEYD	17.0	1.9	9.5	26.1
9-10-11 Rib section muscle:bone ratio	911M:B	3.4	.4	1.8	7.0
9-10-11 Rib section muscle:fat ratio	911M:F	2.4	.8	.9	8.3
9-10-11 Rib section ether-extractable fat yield, %	911EEFATYD	33.0	7.6	15.1	63.4
9-10-11 Rib section moisture yield, %	911MOISYD	51.8	5.8	28.5	65.5
9-10-11 Rib section ether-extractable fat wt, kg	911EEFATWT	1.6	.5	.5	4.3
9-10-11 Rib section moisture wt, kg	911MOISWT	2.4	.4	1.3	4.0
Retail product yield, %[f]	RPYD	66.1	5.0	51.8	80.8
Fat trim yield, %[f]	FATYD	18.6	5.8	2.3	35.9
Bone yield, %[f]	BONEYD	15.2	1.4	11.8	22.6

[a]Abbreviations used in Tables 3 through 8.
[b]Expressed as a percentage of hot carcass weight.
[c]200 = Practically devoid^0, 300 = Traces^0, 400 = Slight^0, 500 = Small^0, 600 = Modest^0, 700 = Moderate^0, 800 = Slightly abundant^0, 900 = Moderately abundant^0.
[d]Expressed as a percentage of wholesale rib weight.
[e]Expressed as a percentage of 9-10-11 rib section weight.
[f]Expressed as a percentage of the sum of retail product weight, fat trim weight, and bone weight.

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Table 2. Simple correlation coefficients between independent and dependent variables

Independent variable	Dependent variable: Retail product yield	Fat trim yield	Bone yield
Hot carcass wt	-.17	.20	-.25
Longissimus muscle area	.44	-.39	.06
Actual 12th rib fat thickness	-.73	.77	-.56
Adjusted 12th rib fat thickness	-.76	.80	-.60
Estimated kidney, pelvic, and heart fat	-.33	.36	-.31
USDA Yield grade	-.80	.81	-.51
Marbling score	-.62	.63	-.40
Wholesale rib wt (untrimmed)	-.21	.26	-.33
Wholesale rib muscle wt	.35	-.29	-.02
Wholesale rib fat wt	-.76	.81	-.65
Wholesale rib bone wt	.09	-.15	.30
Wholesale rib short rib wt	-.18	.22	-.29
Wholesale rib muscle yield	.91	-.91	.51
Wholesale rib fat yield	-.89	.94	-.69
Wholesale rib bone yield	.40	-.55	.86
Wholesale rib short rib yield	-.03	.04	-.06
Ribeye roll wt	.31	-.27	-.02
Ribeye roll yield	.76	-.76	.46
Wholesale rib muscle:bone ratio	.36	-.21	-.43
Wholesale rib muscle:fat ratio	.87	-.90	.61
9-10-11 Rib section wt (untrimmed)	-.24	.29	-.34
9-10-11 Rib section muscle wt	.30	-.25	-.04
9-10-11 Rib section fat wt	-.75	.81	-.65
9-10-11 Rib section bone wt	.05	-.11	.27
9-10-11 Rib section muscle yield	.90	-.89	.49
9-10-11 Rib section fat yield	-.88	.92	-.67
9-10-11 Rib section bone yield	.37	-.52	.80
9-10-11 Rib section muscle:bone ratio	.34	-.20	-.36
9-10-11 Rib section muscle:fat ratio	.85	-.88	.59
9-10-11 Rib section ether-extractable fat yield	-.88	.90	-.58
9-10-11 Rib section moisture yield	.87	-.89	.59
9-10-11 Rib section ether-extractable fat wt	-.76	.80	-.62
9-10-11 Rib section moisture wt	.35	-.29	.02
Retail product yield	1.00	-.98	.46
Fat trim yield	-.98	1.00	-.67
Bone yield	.48	-.65	1.00

FATYD (88%) that the addition of other carcass and wholesale rib traits to the prediction model did not significantly reduce the residual variation in FATYD (Table 4). The best equation developed from 9-10-11 rib traits (Equation [442]) accounted for the same amount (88%) variation in FATYD as did RIBFATYD (Equation [421]).

Prediction of Bone Yield. Wholesale rib bone yield, 911BONEYD, RIBFATYD, 911FAYD, and RIBFATWT explained 74, 64, 48, 45, and 42% of the variation in BONEWT, respectively (Table 2). Among carcass traits, ADJFAT accounted for the most variation in BONEYD (35%). Although RIBFATYD accounted for 48% of the total variation in BONEYD, RIBFATYD only accounted for 12% of the residual variation in BONEYD after RIBBONEYD was fit (Table 5). However, the authors believe that because RIBFATYD reduced the residual variation by 15%, Equation [522] was superior to Equation [521]. None of the equations developed from 9-10-11 rib traits accounted for as much of the variation in BONEYD as either Equations [521] or [522].

Validation of Prediction Models. Each of the dependent variables was predicted for the GPE carcasses using the best prediction equation (Equations [323], [421], and [522] for RPYD, FATYD, and BONEYD, respectively) developed from the GPU carcasses. Additional weights of retail product, fat trim, and bone were predicted by multiplying the predicted yields of each component times the hot carcass weight. Means of actual and predicted cutability measures were similar indicating that the equations developed with the GPU carcasses were accurate when applied to the GPE carcasses. For each yield trait, the equations were slightly less precise when applied to the GPE carcasses than GPU (R^2 = .74 vs .87, .78 vs .88, and .69 vs .77 for RPYD, FATYD, and BONEYD, respectively).

Whereas the prediction equations explained from 69 to 78% of the phenotypic variation in cutability, the

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Table 3. Prediction equations for retail product yield (%)

Equation no.	R^2	RSD[a]	b_0	Variable 1 b-value	Variable 1 Trait[b]	Variable 2 b-value	Variable 2 Trait	Variable 3 b-value	Variable 3 Trait	Variable 4 b-value	Variable 4 Trait
Carcass traits											
311	.58	3.3	71.6	-8.4913	ADJFAT	—	—	—	—	—	—
312	.66	2.9	82.2	-6.7120	ADJFAT	-.0237	MARBLE	—	—	—	—
313	.70	2.8	73.7	-6.0628	ADJFAT	-.0227	MARBLE	.0960	REA	—	—
314	.72	2.7	74.9	-5.8402	ADJFAT	-.0205	MARBLE	.1018	REA	-1.0384	ESTKPH
Carcass and wholesale rib dissection traits											
321	.83	2.1	11.7	1.0394	RIBMUSYD	—	—	—	—	—	—
322	.85	1.9	3.1	1.0763	RIBMUSYD	.7098	SHRTRIBYD	—	—	—	—
323	.87	1.8	13.5	.9812	RIBMUSYD	.6840	SHRTRIBYD	-.0104	MARBLE	—	—
Carcass and 9-10-11 rib dissection traits											
331	.81	2.2	16.3	.8762	911MUSYD	—	—	—	—	—	—
332	.83	2.0	29.1	.7739	911MUSYD	-.0140	MARBLE	—	—	—	—
Carcass and 9-10-11 rib dissection and chemical traits											
341	.81	2.2	16.3	.8764	911MUSYD	—	—	—	—	—	—
342	.84	2.0	43.5	.5455	911MUSYD	-.1550	911EEFATYD	—	—	—	—

[a]Residual standard deviation.
[b]Trait abbreviations are defined in Table 1.

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Table 4. Prediction equations for fat trim yield (%)

Equation no.	R^2	RSD[a]	b_0	Variable 1 b-value	Variable 1 Trait[b]	Variable 2 b-value	Variable 2 Trait	Variable 3 b-value	Variable 3 Trait	Variable 4 b-value	Variable 4 Trait
Carcass traits											
411	.64	3.5	11.9	10.3778	ADJFAT	—	—	—	—	—	—
412	.72	3.1	.0	8.3779	ADJFAT	.0266	MARBLE	—	—	—	—
413	.74	3.0	−2.0	8.1545	ADJFAT	.0240	MARBLE	1.2644	ESTKPH	—	—
414	.76	2.9	−5.1	7.5795	ADJFAT	.0230	MARBLE	1.3632	ESTKPH	−.0825	REA
Carcass and wholesale rib dissection traits											
421	.88	2.0	−5.5	1.0721	RIBFATYD	—	—	—	—	—	—
Carcass and 9-10-11 rib dissection traits											
431	.85	2.2	−4.4	.9005	911FATYD	—	—	—	—	—	—
432	.87	2.1	−8.9	.8090	911FATYD	.0140	MARBLE	—	—	—	—
Carcass and 9-10-11 rib dissection and chemical traits											
441	.85	2.2	−4.4	.9007	911FATYD	—	—	—	—	—	—
442	.88	2.0	−5.4	.5986	911FATYD	.2648	911EEFATYD	—	—	—	—

[a]Residual standard deviation.
[b]Trait abbreviations are defined in Table 1.

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Table 5. Prediction equations for bone yield (%)

Equation no.	R^2	RSD[a]	b_0	Variable 1 b-value	Variable 1 Trait[b]	Variable 2 b-value	Variable 2 Trait
Carcass traits							
511	.35	1.1	16.5	-1.8863	ADJFAT	-	-
512	.39	1.1	17.5	-1.7581	ADJFAT	-.3855	ESTKPH
Carcass and wholesale rib dissection traits							
521	.74	.7	3.5	.7713	RIBBONEYD	-	-
522	.77	.7	7.1	.6350	RIBBONEYD	-.0677	RIBFATYD
Carcass and 9-10-11 rib dissection traits							
531	.64	.8	5.1	.5933	911BONEYD	-	-
532	.71	.8	9.3	.4591	911BONEYD	-.0739	911FATYD
Carcass and 9-10-11 rib dissection and chemical traits							
541	.64	.8	5.1	.5933	911BONEYD	-	-
542	.71	.8	9.3	.4591	911BONEYD	-.0739	911FATYD

[a]Residual standard deviation.
[b]Trait abbreviations are defined in Table 1.

prediction equations explained 84 to 96% of the genetic variation in cutability (Table 6). The relatively high genetic correlations (squared correlations are shown in Table 6) between heritability estimates derived from actual cutout data and predicted estimates indicate that selection based on the prediction equations would be very effective in changing actual yields of retail product, fat trim, and bone. Environmental correlations between actual and predicted values were moderate (R^2 = .56 to .79). Actual values were more heritable than predicted values indicating that cutability was more correctly assessed through actual cutout than prediction. Heritability estimates for actual values were similar to estimates reported by Koch et al. (1982a) for previous cycles of GPE.

Discussion

For each dependent variable, the best single predictor was a wholesale rib dissection trait and the best higher order model contained at least one wholesale rib dissection trait. Specifically, RIBMUSYD, RIBFATYD, and RIBBONEYD explained the greatest proportion of the variation in RPYD, FATYD, and BONEYD, respectively (Table 2). Universally, the best predictor of a given dependent variable was the wholesale rib measurement of that same trait (i.e., muscle yield predicted muscle [retail product] yield, fat yield predicted fat yield, bone yield predicted bone yield). It is likely that these wholesale rib variables were better predictors of their respective dependent variables than 9-10-11 rib variables because the wholesale rib represented a higher proportion of the carcass than the 9-10-11 rib. Whereas, in the present study, 911MUSYD explained 81% of the variation in RPYD, others (Lunt et al., 1985; Miller et al., 1988) have reported that composition of the 9-10-11 rib section explained 85% of the variation in carcass composition. In the present experiment, 911EEFATYD

Table 6. Genetic parameters of actual and predicted cutability measures for the Germplasm Evaluation carcasses (n = 1,160)

Variable	Mean Actual	Mean Predicted	Heritability Actual	Heritability Predicted	Coefficient of determination Phenotypic	Coefficient of determination Genetic	Coefficient of determination Environmental
Retail product yield, %	63.6	63.1[a]	.67	.52	.74	.96	.56
Fat trim yield, %	22.7	23.0[a]	.65	.51	.78	.94	.64
Bone yield, %	13.8	14.1[a]	.69	.64	.69	.84	.72
Retail product wt, kg	196.4	192.5[b]	.66	.62	.90	.99	.79
Fat trim wt, kg	71.3	71.4[c]	.65	.62	.88	.97	.76
Bone wt, kg	42.5	43.0[d]	.62	.48	.83	.97	.77

[a]Values were predicted using the best prediction equation for each trait (Equations [323], [421], and [522] for retail product yield, fat trim yield, and bone yield, respectively).
[b]Predicted retail product weight = (predicted retail product yield/100) × hot carcass weight.
[c]Predicted fat trim weight = (predicted fat trim yield/100) × hot carcass weight.
[d]Predicted bone weight = (predicted bone yield/100) × hot carcass weight.

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accounted for 77% of the variation in RPYD, whereas Crouse and Dikeman (1976) reported that 911EEFATYD accounted for 81% of the variation in RPYD. This discrepancy is likely due to the fact that others (Crouse and Dikeman, 1976; Lunt et al., 1985; Miller et al., 1988) removed the 9-10-11 rib section from the carcass according to Hankins and Howe (1946), whereas in the present experiment, the 9-10-11 rib section was simply cut from the wholesale rib. Additionally, differences in the end point of prediction may have caused this difference.

The best equation (Equation [323]) for predicting RPYD explained 87% of the variation in actual RPYD for GPU carcasses and 74% of the variation in actual RPYD for GPE carcasses. By comparison, of the seven equations tested by Cross et al. (1973), the best equation explained 74% of the variation in boneless, closely trimmed (6 mm of fat remaining) retail cut yields. The equations tested by Cross et al. (1973) explained 10 to 26% less variation in their study as the equations had explained in the data sets from which the equations were developed. In the present study, prediction equations developed from GPU carcasses explained 13, 10, and 8% less of the variation in RPYD, FATYD, and BONEYD, respectively, when tested against GPE carcasses. Considering that these equations were developed and tested with two distinct, large (n = 1,602 and 1,160, respectively) groups of genetically diverse, calf-fed steer carcasses, we conclude that these equations would likely provide satisfactory predictive efficiency for comparing genetically diverse populations for differences in carcass composition. Furthermore, the high level of accuracy achieved by rib-based prediction of carcass composition warrants consideration of this methodology in an automated beef carcass assessment system. We believe, however, that further studies should be conducted to determine whether these equations can be applied to heifers and Holstein steers.

Implications

Prediction of carcass cutability using carcass and wholesale rib dissection traits should allow for rapid, precise, cost-effective assessment of variation in cutability. Moreover, these procedures do not result in destruction of the ribeye and, thus, allow for assessment of meat palatability on the longissimus muscle after cutability data collection. This technology could be adapted for automated assessment of beef carcass composition.

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