

Genetic co-variance components within and among muscular, skeletal and functional traits differ among contrasting beef breeds

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Summary

Linear type traits describe the skeletal, muscular and functional characteristics of an animal and are routinely scored globally in both dairy and beef cattle. The objective of the present study was to determine if genetic co-variance components for linear type traits differed among five contrasting cattle breeds. A total of 18 linear type traits scored on 3,356 Angus (AA), 31,049 Charolais (CH), 3,004 Hereford (HE), 35,159 Limousin (LM), and 8,632 Simmental (SI) were used. Data were analyzed using animal linear mixed models which included the fixed effects of sex of the animal, the age at scoring, the parity of the dam, and the contemporary group of herd-date of scoring. Differences ($p < 0.05$) in heritability estimates between at least two breeds existed for 13 out of 18 linear type traits. Irrespective of the breed, genetic correlations were strongest among the muscular traits (0.58 to 0.99) and among the skeletal traits (0.33 to 0.98) and weakest among the functional traits (0.01 to 0.87). However, the continental breeds (i.e. CH, LM, SI) tended to have similar heritability estimates to each other as well as similar genetic correlations among the same pairwise traits, as did the British breeds (i.e. AA, HE). Results for the present study may be used to inform genetic evaluations of the increased accuracy in considering, at least, the British breeds and continental breeds separately during analysis.

Keywords: genetics, linear type traits, beef cattle, breed differences

Introduction

Linear type traits describing skeletal, muscular and functional characteristics of the animal are routinely scored worldwide in both dairy (Veerkamp and Brotherstone, 1997) and beef cattle (Mc Hugh et al., 2012). While genetic parameters of type traits have been extensively researched in Holstein-Friesian dairy cattle (Veerkamp and Brotherstone, 1997), fewer studies have been undertaken in beef cattle. Nonetheless, type traits are often included in multi-trait genetic evaluations as predictors of performance in both dairy (Berry et al., 2004) and beef cattle (Mc Hugh et al., 2012).

Differences in genetic parameters among breeds has been previously demonstrated for carcass traits in beef cattle (Utrera and Van Vleck, 2004). Consequently, genetic parameters of linear type traits may also differ by breed. Knowledge of these possible differences in genetic parameters in linear type traits among breeds is of increasing importance as some populations move towards using a multi-breed, multi-trait statistical model in the pursuit of greater precision of genetic evaluations. The objective, therefore, of the present study was to determine if genetic co-variance components for linear type traits differed among five

contrasting cattle breeds.

Materials and Methods

A total of 18 linear type traits, representing muscular (n=6), skeletal (n=6) and functional (n=4) characteristics of the animal, as well as docility and body condition score, were analysed. Each trait was separately standardised to a common variance within classifier-by-year. Data were available on 81,200 animals in 1,811 herds all scored by 20 classifiers; 3,356 Angus (AA), 31,049 Charolais (CH), 3,004 Hereford (HE), 35,159 Limousin (LM), and 8,632 Simmental (SI). All animals were scored between the years 2000 and 2016, were aged between 6 and 16 months and were from a sire with at least five progeny in the data set.

Co-variance components for each trait in each breed were estimated using a linear animal mixed model where the fixed effects included sex of the animal, age at scoring, parity of the dam, and the contemporary group of herd-date of scoring. Eigenstructures were calculated to determine if the co-variance structures among traits differed by breed. Eigenvectors and eigenvalues were calculated using the co-variance matrices in the individual breeds for the muscular traits, the skeletal traits, and the functional traits separately. Differences in the co-variance structures were then evaluated:

(1)

where E is a matrix consisting of the eigenvectors in CH, CO_i is the estimated co-variance matrix among traits in breed_{*i*} and E_i is the resulting matrix rescaled to have diagonal elements of 1. Evidence of non-zero off-diagonals in the E_i matrix was investigated when the CO_i was used; the closer to zero the off-diagonal elements are, the more similar the co-variance matrices are.

Selection index theory was used to compare the efficiency of selection for a goal trait when using the genetic and phenotypic co-variance matrices among traits from different breeds in relative to a true scenario; in the present study the goal trait was assumed to be height of withers in CH. The index consisted of up to five linear type traits, namely width of chest, hind-leg rear view, body condition score, development of loin and development of inner thigh; these traits were chosen because their genetic correlation with height of withers were most variable among the breeds.

Results and Discussion

The within-breed heritability estimates for the linear type traits ranged from 0.00 (three of the four functional traits in HE) to 0.43 (height in CH) (Table 1 & 2). Heritability estimates for the functional traits were generally the lowest of all the traits and were all ≤ 0.13 . Heritability for the muscular traits varied from 0.10 for development of loin in HE to 0.30 for development of hind quarter in CH. Heritability for the skeletal traits ranged from 0.00 for both width of chest and width at hips in HE to 0.43 for height of withers in the CH. For 13 of the 18 linear type traits, heritability estimates differed ($P < 0.05$) between at least two breeds. Heritability estimates for width of withers, width behind withers, depth of chest, length of pelvis, and hind-leg side view did not differ between breeds. In general, the heritability estimates among the muscular linear type traits and among the skeletal muscular type traits in the continental breeds (CH, LM, and SI) were more similar to each other than to the British breeds (AA, HE).

While the heritability estimates and the genetic standard deviations for the muscular traits were greater in the continental breeds, the coefficients of genetic variation of the muscular traits actually varied little across the five breeds (0.04 to 0.06); this implies that,

once scaled to the breed mean for that trait, the extent of additive genetic variance was similar for all muscle traits. In general, the largest coefficients were for height of withers (0.06 to 0.10) while the lowest coefficients of genetic variation were for the functional traits (0.00 to 0.05). The low coefficients of genetic variation for the functional traits may be explained by the number of environmental effects they may be affected by; i.e. housing type, hoof paring and diet.

Within breed, genetic correlations among the muscular traits were moderate to strong, varying from 0.58 for development of loin and width of withers in HE to 0.99 for development of hind quarter and development of inner thigh in CH (Figure 1a). Moderate to strong genetic correlations also existed between the skeletal traits in all five breeds, ranging from 0.33 for pelvic length and width of chest in SI to 0.98 between height of withers and both length of pelvis and length of back in CH (Figure 1b). The genetic correlations among the functional traits varied considerably among the breeds ranging from -0.08 between foreleg front view and locomotion in SI to 0.87 between the same traits in AA (Figure 1c).

Eigenstructures

Regardless of breed, the first and second eigenvalues from the genetic co-variance matrix of the skeletal linear type traits, combined, accounted for > 90% of the genetic variation. Excluding CH, where the first eigenvalue calculated from the genetic co-variance matrix of the muscular linear type traits accounted for only 51.7% of the genetic variation, the first and second eigenvalues from the genetic co-variance matrix of the muscular linear type traits in the other breeds also accounted for > 90% of the genetic variation. When the eigenvalues were calculated from the genetic co-variance matrix of the functional linear type traits, the first component only accounted for between 44.2% and 65.9% of the genetic variation. For the functional traits, three of the four eigenvalues were required before the genetic variance accounted for was > 90%. The eigenvalues quantify the amount of genetic variation associated with each eigenvector (Kirkpatrick, 2009) and although the eigenvalues may be similar across the breeds, the eigenvectors associated with each eigenvalue differ across the breeds i.e. the axes of the genetic variation differs.

Moderate to strong correlations existed between the i th eigenvector of the skeletal traits in CH and the i th eigenvector of the skeletal traits in LM (0.60 to 0.98). Moderate correlations also existed between the i th eigenvector of the skeletal traits in CH and the i th eigenvector of the skeletal traits in SI (0.15 to 0.99). Weaker correlations existed among the i th eigenvector associated with the skeletal traits in CH and the i th eigenvector in AA (0.04 to 0.92). The correlations among the eigenvectors of the muscular traits across the breeds were weaker than those observed among the skeletal traits, ranging from 0.01 to 0.52 between the i th eigenvectors in CH and LM. Moderate to strong correlations existed between the i th eigenvector of the muscular traits in AA and the i th eigenvector of the muscular traits in HE (0.25 to 0.85). Moderate to strong correlations existed between the i th eigenvector of the functional traits in CH and the i th eigenvector of all other breeds (LM 0.21 to 0.96; AA 0.18 to 0.94).

The rescaled matrices calculated using the separate co-variance matrices of the skeletal, functional and muscular traits in LM had off-diagonal elements most similar to that expected when using the co-variance matrices of CH; i.e. the off-diagonal elements were close to zero. The greatest differences in were calculated using the separate co-variance matrices of the skeletal, functional and muscular traits from AA. The overall moderate to strong across breed correlations between the eigenvectors associated with CH and those associated with LM and the low off-diagonal elements of suggest that these breeds are most similar to one another. In contrast, the generally weaker correlations between the

eigenvectors associated with CH and the eigenvectors associated with AA and HE, and the non-zero off-diagonal elements of suggest these breeds are somewhat different to one another. The similarities between the continental breeds and the differences between these and the British breeds were expected as the French and Swiss breeds have a common origin and have, over time, been subjected to admixture whereas the British breeds are the most genetically isolated (Kelleher et al., 2016).

Selection Index

When the index weights were calculated using the phenotypic and genetic parameters of SI, the efficiency of the index remained largely unchanged (≥ 0.99). The efficiency of the index remained at 0.99 when the phenotypic variances and heritability estimates from LM were used to derive the index weights. However, the efficiency decreased to 0.88 when the correlation structure from LM was also used in the calculation. The biggest decrease in efficiency came from using the parameters of AA in the calculation of the index weights, where the efficiency decreased to as low as 0.762. The high efficiencies associated with using the parameters of LM or SI in place of CH suggest that these breeds are highly similar and could be evaluated together in genetic evaluations. The large decrease in efficiency associated with using the parameters of AA suggests that AA should not be included in multi-breed genetic evaluations with the continental breeds as this may lead to a marked decrease in accuracy. This is further supported by the results from the eigenanalysis, where the correlations between the eigenvectors in the continental breeds and the eigenvectors in the British breeds were more similar within breed group than across it.

Conclusion

Differences among the breeds in both the heritability estimates and in the genetic correlations among the linear type traits existed. The greatest differences existed between the continental breeds and the British breeds suggesting that the accuracy of genetic evaluations may benefit from considering these breed groups separately in evaluations.

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Table 1. Scale of measurement, the number of records (n), the mean, the genetic standard deviation (SD_g) and the heritability estimates (h^2) of the functional and muscular linear type traits.

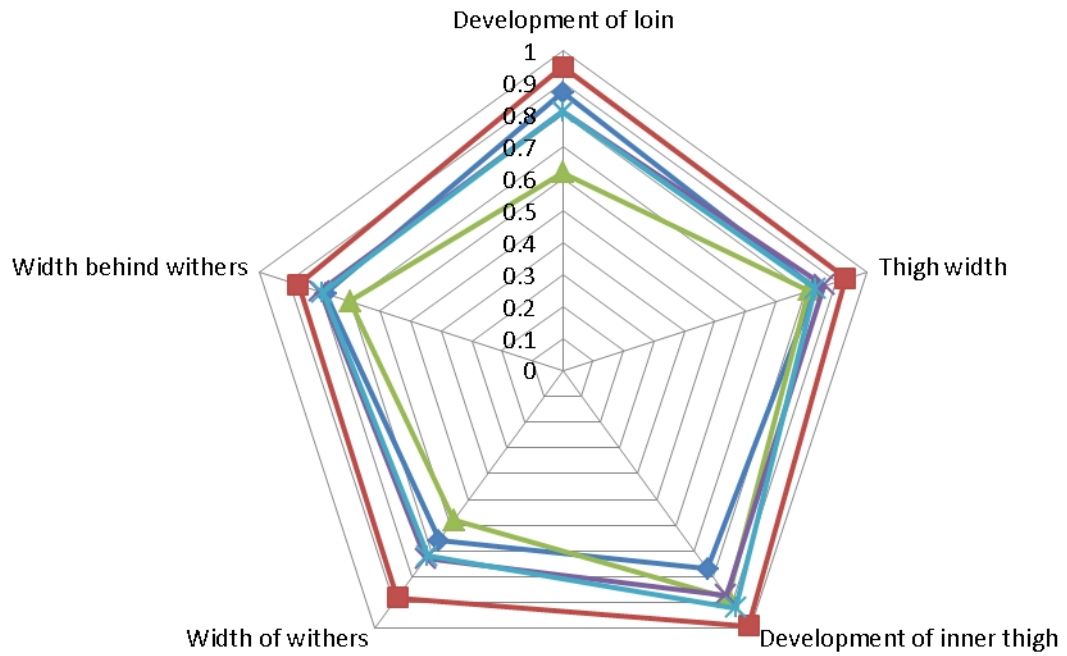
Trait	Scale	Angus ¹			Charolais ¹			Hereford ¹			Limousin ¹			Simmental ¹		
		n = 3,220 - 3,356			n = 23,070 - 31,048			n = 2,390 - 3,004			n = 30,491 - 35,158			n = 6,638 - 8,632		
		μ	SD_g	h^2	μ	SD_g	h^2	μ	SD_g	h^2	μ	SD_g	h^2	μ	SD_g	h^2
<i>Functional</i>		1 - 10														
Locomotion	low - high	7.7	0.28	0.12	7.7	0.32	0.12	7.8	0.00	0.00	8.1	0.17	0.04	8.1	0.18	0.04
Foreleg front view	toes out - toes in	5.3	0.24	0.13	6.2	0.24	0.09	5.5	0.00	0.00	6.2	0.16	0.06	6.7	0.20	0.06
Hind-leg side view	straight - sickled	7.2	0.21	0.08	7.3	0.27	0.09	7.3	0.24	0.11	7.6	0.24	0.08	7.4	0.21	0.06
Hind-leg rear view	toes out - toes in	5.3	0.16	0.04	6.0	0.26	0.06	5.6	0.00	0.00	6.4	0.21	0.04	5.6	0.25	0.06
<i>Muscular</i>		1 - 15														
Development of hind quarter	low - high	8.0	0.43	0.22	9.7	0.60	0.30	8.1	0.35	0.14	11.5	0.52	0.25	10.9	0.51	0.24
Development of loin	low - high	8.2	0.37	0.13	9.4	0.52	0.21	8.7	0.31	0.10	10.6	0.45	0.17	9.9	0.47	0.18
Thigh width	narrow - wide	8.2	0.38	0.14	9.7	0.55	0.22	8.2	0.40	0.16	10.2	0.53	0.23	9.9	0.55	0.24
Development of inner thigh	low - high	8.5	0.37	0.14	10.4	0.62	0.28	8.3	0.43	0.20	11.1	0.54	0.24	10.4	0.51	0.23
Width of withers	narrow - wide	8.9	0.51	0.22	9.4	0.51	0.21	8.9	0.41	0.16	10.3	0.46	0.19	10.2	0.54	0.22
Width behind withers	narrow - wide	7.5	0.39	0.13	8.6	0.46	0.18	7.9	0.40	0.15	9.5	0.43	0.17	9.1	0.48	0.18

¹ Standard error of the heritability estimates in Angus ≤ 0.05 . Standard error of the heritability estimates in Charolais ≤ 0.02 . Standard error of the heritability estimates in Hereford ≤ 0.05 . Standard error of the heritability estimates in Limousin ≤ 0.02 . Standard error of the heritability estimates in Simmental ≤ 0.03 .

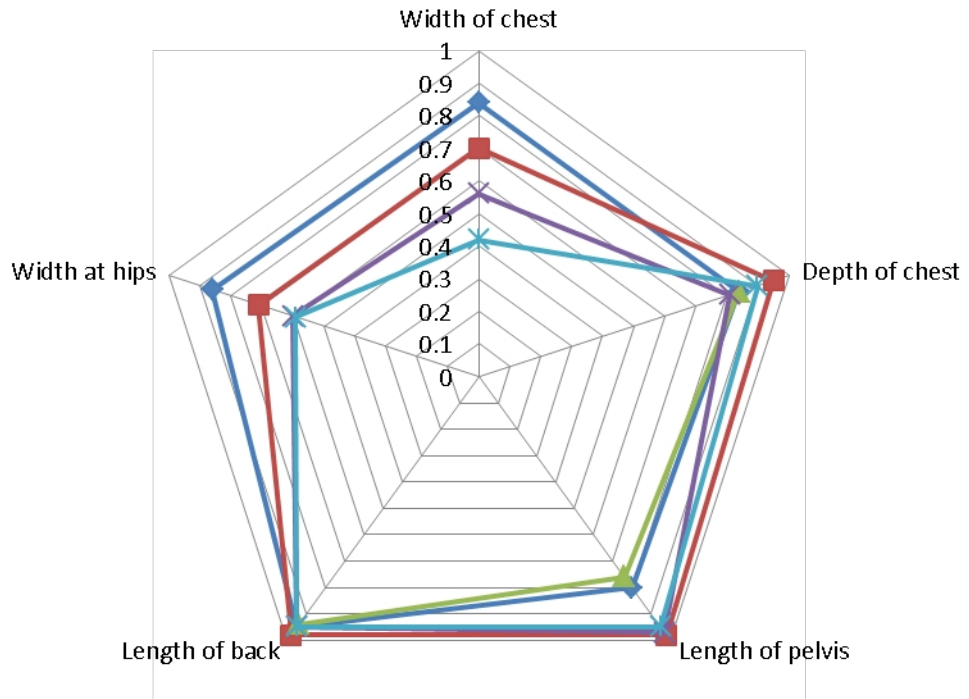
Table 2. Scale of measurement, the number of records (n), the mean, the genetic standard deviation (SD_g) and the heritability estimates (h^2) of the skeletal and other linear type traits.

Trait	Scale	Angus ¹			Charolais ¹			Hereford ¹			Limousin ¹			Simmental ¹		
		n = 3,124 - 3,356			n = 21,341 - 31,044			n = 2,993 - 3,004			n = 30,494 - 35,156			n = 6,637 - 8,631		
		μ	SD_g	h^2	μ	SD_g	h^2	μ	SD_g	h^2	μ	SD_g	h^2	μ	SD_g	h^2
<i>Skeletal</i>	1 - 10															
Width of chest	narrow - wide	6.6	0.20	0.07	6.9	0.24	0.10	6.5	0.00	0.00	6.2	0.24	0.10	6.8	0.30	0.15
Depth of chest	shallow - deep	7.4	0.29	0.15	7.2	0.24	0.13	7.3	0.36	0.25	7.0	0.27	0.15	7.6	0.26	0.14
Height of withers	small- tall	5.8	0.38	0.19	6.8	0.65	0.43	5.7	0.44	0.30	6.6	0.47	0.29	7.2	0.52	0.34
Length of pelvis	short - long	7.1	0.35	0.17	7.4	0.42	0.23	7.0	0.45	0.27	7.8	0.37	0.19	8.0	0.37	0.20
Length of back	short - long	6.8	0.36	0.17	7.7	0.49	0.30	6.8	0.47	0.29	7.7	0.42	0.23	8.0	0.37	0.20
Width at hips	narrow - wide	6.5	0.21	0.06	6.9	0.29	0.13	6.9	0.00	0.00	6.7	0.30	0.14	7.1	0.30	0.14
<i>Other</i>	1 - 10															
Body condition score	lean - fat	7.0	0.18	0.03	5.8	0.35	0.13	7.2	0.00	0.00	6.6	0.31	0.11	7.1	0.23	0.05
Docility	aggressive - docile	8.7	0.36	0.21	8.9	0.34	0.15	9.2	0.26	0.11	9.2	0.37	0.17	9.3	0.30	0.09

¹ Standard error of the heritability estimates in Angus ≤ 0.05 . Standard error of the heritability estimates in Charolais ≤ 0.02 . Standard error of the heritability estimates in Hereford ≤ 0.06 . Standard error of the heritability estimates in Limousin ≤ 0.02 . Standard error of the heritability estimates in Simmental ≤ 0.03 .



1
 2 *Figure 1(a). Genetic correlation of development of hind quarter with other muscular traits*
 3 *within Angus (blue diamond), Charolais (red square), Hereford (green triangle), Limousin*
 4 *(purple X) and Simmental (light blue star).*
 5



6
 7 *Figure 1(b). Genetic correlation of height of withers with other skeletal traits within Angus*
 8 *(blue diamond), Charolais (red square), Hereford (green triangle), Limousin (purple X) and*
 9 *Simmental (light blue star).*

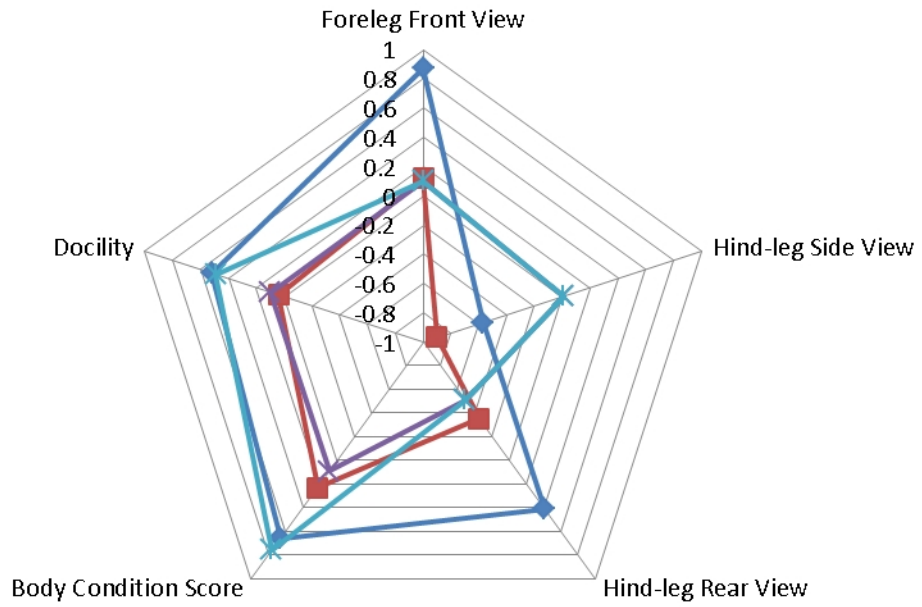


Figure 1(c). Genetic correlation of locomotion with functional traits and other traits within Angus (blue diamond), Charolais (red square), Limousin (green triangle), and Simmental (purple X).