GENETIC PARAMETERS FOR LINEAR TYPE TRAITS IN HUNGARIAN CHAROLAIS BEEF CATTLE

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SUMMARY

Genetic parameters are reported for 18 linear type traits recorded by the National Association of Charolais Breeders in Hungary: back width (BW), chest width (CW), rump width (RW), shoulder width (SW), back-loin length (BL), rump length (RL), thigh length (TL), canon girth (CG), heart girth (HG), width of hip bones (HW), width of thigh (TW), roundness of thigh (RT), loin thickness (LT), development/frame (DF), top line straightness (TS), muzzle width (MW), fore legs (FL) and hind legs (HL). All traits were scored by Association staff using a linear scale from 1 to 10 based on the system developed by the Institut de L'Elevage in France. Animals averaged 508 days in age when scored. Bivariate models with weight at weaning (WW) were investigated for each trait using BLUPF90, with inclusion of genomic data. There were 2,524 animals with linear trait scores, 42,442 animals with a weight at weaning and 7,660 animals with a genotype. Of animals with trait scores, 88% had a weaning weight and 61% were genotyped. Six generations of pedigree were used, giving a total of 55,928 animals in the analyses. Trait heritability ranged from 0.11 for FL to 0.41 for CG. Genetic correlations with WW ranged from -0.36 for HL to +0.50 for RL. These traits could be incorporated into future genetic analyses of the breed.

INTRODUCTION

The National Association of Hungarian Charolais Cattle Breeders (MCTE) was officially formed in 1992 and currently has 236 members registering around 6,000 calves per year on average. Of calves registered, approximately 61% are recorded for weight at weaning (WW). The MCTE have utilised the BREEDPLAN genetic evaluation service provided by the Agricultural Business Research Institute (ABRI) since 2002, with their most recent evaluation representing 80,954 animals, a multi-trait analysis of gestation length, birth weight, post-birth growth (including WW), scrotal and ultra-sound scan records and a separate analysis of calving ease using birth difficulty scores, birth weights and gestation length records. In late 2019, the MCTE launched its Genome Program to members, with genotypes incorporated in their August 2022 BREEDPLAN evaluation using a Single-Step model (Johnston *et al*. 2008).

In 2016, the MCTE initiated a program of assessing Charolais cattle for 18 structural traits related mainly to the muscularity and skeletal attributes of the animal. ABRI reviewed the data to determine what, if any, level of genetic variation was expressed in the linear type scores. This paper provides preliminary estimates of heritability for the 18 linear traits and their genetic correlation with WW.

MATERIALS AND METHODS

Records for WW were extracted from the August 2022 BREEDPLAN evaluation, these having been pre-adjusted to a constant age at weighing (200 days) and constant age of dam (5 years) as outlined by Graser *et al.* (2005). The contemporary group for WW consisted of herd of origin, sex, year of birth, birth number (single vs twin), birth type (natural vs ET), breeder-defined management group and weigh date. Extracted records were pruned to remove single-animal contemporary groups and those comprising ET calves. The final data set contained 42,442 records for WW (mean 234.3 ± 45.8 kg), with contemporary group size ranging from 2 to 284 (mean of 43).

Linear scores were available on 2,524 animals for 18 type traits: back width (BW), chest width (CW), rump width (RW), shoulder width (SW), back-loin length (BL), rump length (RL), thigh length (TL), canon girth (CG), heart girth (HG), width of hip bones (HW), width of thigh (TW), roundness of thigh (RT), loin thickness (LT), development/frame (DF), top line straightness (TS), muzzle width (MW), fore legs (FL) and hind legs (HL). Age at scoring ranged from 176 to 1,334 days (mean 508.0 days, SD 147.2) and a majority (69%) of the animals scored were female. All scoring was undertaken by a single MCTE-approved technician using a linear scale from 1 (small/weak/thin/worst) to 10 (big/strong/wide/best) according to the guidelines approved by the MCTE (Institut de L'Elevage 2014). Contemporary group was defined as herd of origin, year of birth, breeder-defined management group for WW and date of scoring. After the removal of records for single animal contemporary groups (n=10), group size ranged from 2 to 115 (mean of 19). Sex, birth number and age at scoring to be fitted explicitly in subsequent models.

Genotypes on 8,934 animals were available, coming from a 50K SNP panel (BovineSNP50 BeadChip, Illumina Inc., San Diego, CA.). QC of genomic data was conducted using PLINK software (Chang *et al.* 2015), with SNPs removed at a minor allele frequency of <0.05, a deviation from Hardy–Weinberg equilibrium of $p<1E^{-6}$ and call rates <90%. Only those SNPs located on autosomal chromosomes were used. Individual genotypes were excluded if the call rate for all loci was <85%. Sporadic missing SNPs were imputed using FImpute v3 (Sargolzaei *et al.* 2014) and pedigree information for the genotyped population was included. Genotypes were excluded when a parentage conflict was detected. The final data set comprised 7,660 genotypes and 42,854 SNPs. Most of the genotypes (82%) were from females.

Bivariate models comprising each linear type trait and WW were conducted using the AIREMLF90 program in the BLUPF90 family of software (Misztal *et al.* 2018). The model for type traits included scoring contemporary group, sex and birth number (single or twin) as fixed effects and age at scoring as a linear covariate, with the variance being partitioned into additive genetic and residual components. The model for WW included WW contemporary group only as a fixed effect, with variance being partitioned into additive genetic, maternal genetic (uncorrelated) and residual components. Preliminary analysis of WW fitting an additional random effect for the dam's permanent environment suggested a small variance component (54.8±10.2) that was dropped from subsequent bivariate models. Six generations of pedigree were included, giving 55,928 animals in each analysis. A genotype file and associated map file were included in the analysis, with 20% of genotyped animals having a linear score record and 82% having a WW record. 88% of scored animals were recorded for WW. Default values were used in creating the H matrix (Aguilar *et al.* 2010).

RESULTS AND DISCUSSION

Average scores for type traits ranged from 4.72 for Thigh Length (TL) to 6.09 for Top Line Straightness (TS), with the standard deviation in scores ranging from 0.93 for Heart Girth (HG) to 1.20 for Roundness of Thigh (RT). No scores of 10 were allocated. Score distributions approximated normality within trait, suggesting a linear analysis of scores was appropriate.

The additive genetic variance and heritability for each linear type trait are summarised in Table 1. Most traits related to the muscularity and skeletal attributes were associated with moderate heritability, while functional traits like FL and HL were low. These are comparable to estimates reported by Doyle *et al.* (2018) for a range of subjectively assessed muscularity, skeletal and functional traits in Irish Charolais cattle. The genetic variances reported by Berry *et al.* (2019) were higher for a range of similar traits in a large population comprising 3 European and 2 British breeds, yet the direct heritability estimates were similar to those presented here.

Variance estimates for WW averaged over the 18 bivariate analyses were 581.7, 183.4 and 819.5 kg^2 for the direct genetic, maternal genetic and residual components, respectively. Both the phenotypic variance (1,584.6 kg^2) and the direct heritability (0.37) seem inflated compared to estimates from considerably larger Charolais datasets (Donoghue and Betrand 2004; Phocas and Laloe 2004). In contrast, estimates ranging from 0.30-0.39 were reported for smaller populations of Charolais (El-Saied *et al.* 2006; Herrera-Ojeda *et al.* 2019; Rezende *et al.* 2022) and may partially reflect the heterogeneity of variances reported for WW in the Charolais breed (Quintanilla *et al.* 2002; Donoghue and Bertrand 2004). The maternal genetic heritability (0.12) obtained in this study agrees with estimates reported by others.

The genetic correlations between WW and each linear trait are given in Table 1. Most traits were positively correlated with WW, in the order of 0.30 to 0.50. The correlation for TS, MW and FL was close to zero, while for HL was negative. It is not surprising that positive correlations with body weight are evident in this population, given that most of the linear traits relate to body size and dimensions. Strongly positive genetic correlations between live weight and a range of muscularity and skeletal traits were reported by Berry *et al.* (2019).

Table 1. Estimates of additive variance (V_A) and direct heritability (h^2) for 18 linear type traits and the genetic correlation (r_G) between each trait and weight at weaning

Trait	V_A	h^2	r_G
Back width (BW)	0.269 ± 0.046	0.305 ± 0.049	0.228 ± 0.080
Chest width (CW)	0.181 ± 0.035	0.227 ± 0.042	0.386 ± 0.089
Rump width (RW)	0.278 ± 0.047	0.296 ± 0.046	0.345 ± 0.082
Shoulder width (SW)	0.249 ± 0.045	0.268 ± 0.046	0.343 ± 0.086
Back loin length (BL)	0.236 ± 0.051	0.206 ± 0.043	0.451 ± 0.087
Rump length (RL)	0.196 ± 0.043	0.207 ± 0.043	0.498 ± 0.089
Thigh length (TL)	0.279 ± 0.047	0.295 ± 0.047	0.274 ± 0.083
Canon girth (CG)	0.298 ± 0.040	0.412 ± 0.049	0.395 ± 0.066
Heart girth (HG)	0.144 ± 0.034	0.199 ± 0.045	0.364 ± 0.097
Width of hip bones (HW)	0.260 ± 0.044	0.291 ± 0.046	0.396 ± 0.081
Width of thigh (TW)	0.300 ± 0.053	0.278 ± 0.046	0.381 ± 0.083
Roundness of thigh (RT)	0.306 ± 0.052	0.291 ± 0.046	0.322 ± 0.083
Loin thickness (LT)	0.236 ± 0.046	0.259 ± 0.047	0.345 ± 0.088
Development/frame (DF)	0.207 ± 0.046	0.213 ± 0.046	0.342 ± 0.091
Top line straightness (TS)	0.135 ± 0.044	0.123 ± 0.040	-0.013 ± 0.034
Muzzle width (MW)	0.230 ± 0.046	0.246 ± 0.047	0.152 ± 0.090
Fore legs (FL)	0.094 ± 0.033	0.109 ± 0.039	-0.170 ± 0.144
Hind legs (HL)	0.161 ± 0.047	0.142 ± 0.041	-0.357 ± 0.130

These results indicate that subjectively assessed muscularity and skeletal traits have potential use in Hungarian Charolais breeding programs where the breeding goal includes improvements in the physical appearance of animals. Linear scores for front and hind leg structure show less utility, a similar outcome reported in other EU populations (Doyle *et al.* 2018). While the moderate genetic correlations with live weight suggest that selection for improved growth rate may bring some improvements in animal appearance, there is sufficient scope for gains in muscularity to be achieved without pursuing growth. Berry *et al.* (2019) reported genetic correlations in the order of 0.44 to 0.66 between muscularity traits in registered live animals and carcase conformation in commercial cattle. Positive correlations were also evident between muscularity traits and carcase primal cut yields. Similar results were reported by Bonfatti *et al.* (2013) for Italian Piemontese cattle, with live animal scores for muscularity type traits having a positive genetic correlation with European carcase conformation grades. The genetic correlations reported by Bouquet *et al.* (2010) for Blonde d'Aquitaine and Limousin cattle were considerably stronger (0.54-0.78), suggesting the use of linear muscularity trait scores as indirect criteria for genetic improvements in carcase conformation grade.

CONCLUSION

There is evidence for genetic variation being expressed in the linear type traits recorded in the Hungarian Charolais population - particularly those relating to the muscularity and skeletal attributes – that could facilitate genetic improvements in animal appearance. Although moderately correlated with live weight, these linear type traits may also provide indirect predictors of genetic merit for carcase conformation. This might allow Hungarian breeders to better target the European carcase grading system beyond a weight-based breeding goal.

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