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ESTIMATION OF GENETIC PARAMETERS FOR LINEAR TYPE TRAITS AND SELECTION INDEX IN ROMANIAN BLACK AND WHITE DAIRY CATTLE

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Abstract

This paper presents the results of a study on the estimation of genetic parameters for exterior traits in the Romanian Black and White (BNR) cattle breed. Sixteen linear type traits and a composite Exterior Selection Index (ESI) were analysed in a population of n = 2,956 cows, evaluated using the standard linear description methodology on the 1-9 scale applied by the General Association of Cattle Breeders of Romania (A.G.C.T.R.). Descriptive statistics revealed high means for skeletal traits (stature: $\bar{X}$ = 8.888 ± 0.007; CV% = 4.43%) and elevated variability for limb and teat traits (chest width: CV% = 28.72%; hock angle: CV% = 26.53%). Heritability estimates obtained by REML, using a sire model (BLUP), ranged from h^2 = 0.10 (stature) to h^2 = 0.63 (rump width - pin bones), with a general mean of $h^2 \approx 0.18$. ESI recorded a mean of 85.544 ± 0.057 and a heritability of h^2 = 0.17. Results are broadly consistent with estimates reported in the international literature for Holstein-type breeds, with the notable exception of rump width - pin bones, which exceeded reference intervals (h^2 = 0.25-0.38), suggesting superior genetic potential for improving this trait in the analysed BNR population. The study provides baseline data for the development and optimisation of national genetic improvement programmes for BNR breed conformation

Key words*: exterior selection index, genetic parameters, heritability, linear type traits, Romanian Black and White cattle, selection*

INTRODUCTION

The Romanian Black and White breed (BNR) is one of the most important dairy cattle breeds in Romania. The assessment of exterior conformation through the linear description of type traits (Brotherstone, 1994) represents an essential tool in modern genetic improvement programmes for dairy cattle (Misztal et al., 1992). Unlike traditional overall scoring systems, linear description quantifies each anatomical trait independently on a biological scale from 1 to 9, reflecting the actual population variability between biologically defined extremes (Brotherstone & Hill, 1990). This approach enables precise estimation of genetic parameters - heritability and genetic correlations - which constitute the theoretical foundation of effective selection for conformation.

The importance of exterior traits extends beyond aesthetics: udder, limb and rump conformation are genetically correlated with productive longevity, udder health, reproductive efficiency and adaptability to mechanical or robotic milking (Williams et al., 2022; Short & Lawlor, 1992). In the context of increasing milk production intensity and the growing adoption of automated milking technologies in Romanian farms, knowledge of the genetic parameters for conformation traits is becoming a strategic priority for BNR breed improvers.

Nevertheless, the scientific literature on the estimation of genetic parameters (Harris et al., 1992) for conformation traits in the BNR breed remains limited, with most available studies focusing on production traits - milk yield and composition. International studies conducted on Holstein populations in the Czech Republic (Němcová et al., 2011), Brazil (Campos et al., 2015) and the United States (Short & Lawlor, 1992) have provided reference values for heritabilities of linear type traits (Table 1), but extrapolation of these results to the BNR population requires validation through dedicated studies, given the specific genetic and environmental charac-teristics of Romanian herds.

Table 1. Reference heritability values for linear type traits in Holstein cattle reported in the international literature

Trait	h^2 (literature)	Source
Dairy form/Angularity	0.10-0.29	Brotherstone & Hill (1990); Campos et al. (2015); Foster et al. (1989); Kőrösi et al. (2025); Lactanet (2021); Němcová et al. (2011); Short & Lawlor (1992); Sousa Junior et al. (2024); Williams et al. (2022)
Stature/Rump height	0.35-0.46	
Body depth	0.15-0.25	
Chest width	0.09-0.20	
Rump width (pin bones width)	0.25-0.38	
Rump angle	0.15-0.30	
Hock angle	0.09-0.18	
Hock quality/appearance	0.10-0.22	
Heel height	0.09-0.15	
Rear leg set (side view)	0.10-0.20	
Fore udder attachment	0.15-0.28	
Rear udder height	0.15-0.25	
Median suspensory ligament	0.10-0.20	
Udder depth	0.10-0.20	
Teat placement	0.10-0.20	
Teat length	0.25-0.38	

The objective of this study was to estimate descriptive statistics and heritabilities for 16 linear type traits and the Exterior Selection Index (ESI) in the BNR breed, integrating the results comparatively within the international literature, with a view to providing concrete recommendations for national selection programmes

MATERIALS AND METHODS

Biological material and data sources

The study was conducted on a population of n = 2,956 cows of the Romanian Black and White breed, originating from multiple farms located in different counties of Romania. Data were collected over the period 2014-2025. Exterior appraisal data were obtained from the General Association of Cattle Breeders of Romania (A.G.C.T.R.), in accordance with the official linear description methodology applied to the BNR - Holstein Friesian breed.

Conformation assessment methodology

The linear description of exterior traits was performed by A.G.C.T.R.-certified classifiers according to the European standardised linear description system for the Holstein-Friesian breed. Sixteen traits were evaluated, grouped into four sections:

- Dairy type morphoproductive characteristics: dairy form;
- Body conformation: stature, body depth, chest width, rump width (pin bones), rump angle;
- Feet and legs: hock angle, hock quality/ appearance, heel height, rear leg set (side view);
- Mammary system: fore udder attachment, rear udder height, median suspensory ligament, udder depth, teat placement, teat length.

Each trait was scored on a biological scale from 1 to 9, in which the extreme values represent biologically opposite expressions of each trait, and the value 5 represents the midpoint of the scale.

Based on the individual scores assigned to the 16 traits, the Exterior Selection Index (ESI) was calculated, expressed on a continuous scale with values theoretically ranging from 0 to 100, according to the weighting algorithm used by A.G.C.T.R.

Statistical analysis

Descriptive statistics - arithmetic mean ($\bar{X}$), standard error of the mean (SE), standard deviation (S), coefficient of variation (CV %), minimum and maximum values - were calculated for each trait using standard descriptive statistical procedures.

Variance components (sire, phenotypic and residual) and heritabilities (h^2) were estimated by REML (Restricted Maximum Likelihood) applied to a sire model (BLUP - Best Linear Unbiased Prediction). Given the large number of traits (17) and animals (2,956), canonical transformation and simultaneous diagonalisa-tion were applied. The statistical model used was:

$$\mathbf{y = Xb + Za + e}$$

where:

y = vector of observations;

b = vector of fixed effects;

a = vector of random additive genetic effects;

e = vector of residual errors;

X and Z = corresponding incidence matrices.

Fixed effects included in the model were: herd-year-season of evaluation and parity number.

Heritability was calculated according to the classical formula:

$$\mathbf{h^2 = 4V_s / V_p}$$

where V_s is the sire variance and V_p is the total phenotypic variance (Falconer & Mackay, 1996).

RESULTS AND DISCUSSIONS

The results obtained in the study are presented and analysed below, discussed in relation to data available in the international literature

Descriptive statistics of exterior traits

The descriptive statistics estimated for the 16 linear type traits and ESI in the BNR breed are presented in Table 2.

Table 2. Descriptive statistics for exterior traits in the BNR breed (n = 2,956)

Trait	N	Mean ± SE	S	CV%	Min.	Max.
Dairy form	2956	8.140 ± 0.018	0.985	12.10	2	9
Stature		8.888 ± 0.007	0.393	4.43	4	9
Body depth		7.553 ± 0.020	1.090	14.43	2	9
Chest width		5.070 ± 0.027	1.456	28.72	1	9
Rump width (pin bones)		7.459 ± 0.025	1.356	18.18	2	9
Rump angle		7.465 ± 0.022	1.211	16.22	2	9
Hock angle		5.008 ± 0.024	1.329	26.53	1	9
Hock quality		6.584 ± 0.027	1.458	22.14	1	9
Heel height		7.351 ± 0.026	1.409	19.16	2	9
Rear leg set (side view)		7.525 ± 0.023	1.260	16.75	2	9
Fore udder attachment		7.641 ± 0.021	1.166	15.25	2	9
Rear udder height		7.594 ± 0.022	1.195	15.74	2	9
Median suspensory ligament		7.513 ± 0.022	1.209	16.09	2	9
Udder depth		6.798 ± 0.027	1.461	21.49	1	9
Teat placement		5.342 ± 0.025	1.356	25.39	1	9
Teat length		5.165 ± 0.019	1.041	20.16	1	9
ESI		85.544 ± 0.057	3.117	3.64	64.055	91.559

Dairy type morphoproductive characteristics

Dairy form recorded $\bar{X}$ = 8.140 ± 0.018 and CV% = 12.10%, with values predominantly in the upper range of the scale, indicating good expression of dairy morphoproductive characteristics in the analysed population. This result suggests that the genetic component makes a substantial contribution to the phenotypic expression of this trait.

Body conformation

Stature recorded the highest mean among all analysed traits ($\bar{X}$ = 8.888 ± 0.007), with a standard deviation of S = 0.393 and a coefficient

of variation of only CV% = 4.43%, indicating a homogeneous population with values close to the upper extreme of the biological scale. This homogeneity suggests that the BNR population analysed has been subjected to intense prior selection for this trait. Similar results were reported by Němcová et al. (2011) on 78,886 first-parity Holstein cows in the Czech Republic, confirming that stature shows low phenotypic variability in intensively selected Holstein populations. Brotherstone & Hill (1990) demonstrated that the phenotypic homogeneity of body conformation traits is consistently superior to that of limb and udder traits - a trend confirmed in the present study.

Body depth ($\bar{X}$ = 7.553 ± 0.020; CV% = 14.43%) showed moderate variability, with values predominantly distributed in the upper half of the scale, suggesting a well-developed trunk on average, with acceptable individual differences. Chest width recorded the lowest mean within the group ($\bar{X}$ = 5.070 ± 0.027) and the highest variability in the entire study (CV% = 28.72%), with values covering virtually the entire scale (1-9), indicating a heterogeneous population for this trait, strongly influenced by environmental factors.

Rump width (pin bones) ($\bar{X}$ = 7.459 ± 0.025; CV% = 18.18%) and rump angle ($\bar{X}$ = 7.465 ± 0.022; CV% = 16.22%) showed high means and moderate variability.

Feet and legs

Feet and leg traits showed moderate to high phenotypic variability, with CV% ranging from 16.75% (rear leg set, side view) to 26.53% (hock angle). Means varied between $\bar{X}$ = 5.008 ± 0.024 (hock angle) and $\bar{X}$ = 7.525 ± 0.023 (rear leg set, side view).

Mammary system (udder and teats)

Udder traits showed high means and moderate variability: fore udder attachment ($\bar{X}$ = 7.641 ± 0.021; CV% = 15.25%), rear udder height ($\bar{X}$ = 7.594 ± 0.022; CV% = 15.74%) and median suspensory ligament ($\bar{X}$ = 7.513 ± 0.022; CV% = 16.09%) were situated in the upper range of the scale, with low variability.

Udder depth ($\bar{X}$ = 6.798 ± 0.027; CV% = 21.49%) showed a lower mean and higher variability, being a trait of particular importance for productive longevity (Williams et al., 2022). The high means and moderate to low variability for fore udder attachment, rear udder height and median suspensory ligament indicate a good level of morphofunctional development in the analysed population but also limited potential for rapid genetic progress through selection due to the relatively low variability. In contrast, udder depth, characterised by higher variability, offers greater opportunities for genetic improvement and represents an important selection criterion given its impact on productive longevity.

Teat traits showed moderate means and high variability: teat placement ($\bar{X}$ = 5.342 ± 0.025; CV% = 25.39%) and teat length ($\bar{X}$ = 5.165 ± 0.019; CV% = 20.16%) indicate a heterogeneous population with significant practical implications for the efficiency of mechanical and robotic milking.

Variance components and heritability of exterior traits

Heritability estimates ranged from h^2 = 0.10 to 0.63, with a general mean of $h^2 \approx 0.18$. According to the conventional classification in quantitative genetics (Falconer & Mackay, 1996), most exterior traits showed low ($h^2 < 0.20$) or moderate (h^2 = 0.20-0.40) heritability, with the exception of rump width - pin bones (h^2 = 0.63), the only value falling into the high category ($h^2 > 0.40$). These values are broadly consistent with estimates reported in the international literature for Holstein-type breeds, where the interval h^2 = 0.05-0.46 is frequently documented for linear type traits (Sousa Junior et al., 2024; Lactanet, 2021).

The estimated variance components and heritability values for each analysed trait are presented in Table 3.

Table 3. Variance components and heritability of exterior traits in the BNR breed

Trait	n	Sire variance	Phenotypic variance	Residual variance	h^2	SE of h^2
Dairy form	2956	0.047	0.873	0.826	0.22	0.068
Stature		0.003	0.140	0.137	0.10	0.065
Body depth		0.042	1.117	1.075	0.15	0.066
Chest width		0.076	1.689	1.613	0.18	0.067
Rump width (pin bones)		0.257	1.622	1.365	0.63	0.076
Rump angle		0.076	1.288	1.212	0.24	0.068
Hock angle		0.047	1.653	1.606	0.11	0.065
Hock quality		0.102	2.000	1.898	0.20	0.068
Heel height		0.054	1.826	1.772	0.12	0.066
Rear leg set (side view)		0.061	1.389	1.328	0.18	0.067
Fore udder attachment		0.040	1.284	1.243	0.13	0.066
Rear udder height		0.044	1.340	1.296	0.13	0.066
Median suspensory ligament		0.041	1.349	1.308	0.12	0.066
Udder depth		0.070	2.079	2.009	0.14	0.066
Teat placement		0.051	1.811	1.761	0.11	0.065
Teat length		0.030	1.064	1.034	0.11	0.065
ESI		0.377	9.142	8.765	0.17	0.067

Dairy type morphoproductive characteristics

Dairy form recorded a heritability of $h^2 = 0.22$ (SE = 0.068), a moderate value comparable to estimates for angularity (an equivalent concept) reported by Campos et al. (2015) ($h^2 = 0.10$-0.29) and Němcová et al. (2011) ($h^2 = 0.14$-0.25) for Holstein populations in Brazil and the Czech Republic, respectively. The moderate additive genetic variance (sire variance = 0.047) indicates an acceptable potential response to selection for improving the expression of dairy morphoproductive type in the BNR breed.

Body conformation

Stature showed the lowest heritability in the study ($h^2 = 0.10$; SE = 0.065), with an extremely low sire variance (0.003) relative to total phenotypic variance (0.140). This result may appear surprising compared to values reported in the international literature ($h^2 = 0.35$-0.46; Short & Lawlor, 1992; Lactanet, 2021), but must be interpreted in the context of the exceptional phenotypic homogeneity of the analysed population (CV% = 4.43%). As discussed in the descriptive statistics section, the intense prior selection for this trait resulted in very low total phenotypic variance, which tends to underestimate true heritability (Falconer & Mackay, 1996).

Body depth ($h^2 = 0.15$; SE = 0.066) and chest width ($h^2 = 0.18$; SE = 0.067) showed low heritabilities, consistent with estimates of 0.15-0.25 and 0.09-0.20, respectively, reported in the international literature (Němcová et al., 2011; Campos et al., 2015). The low sire variances for these traits suggest that a significant proportion of their high phenotypic variability is attributable to environmental factors - housing system, nutrition level, parity.

Feet and legs

Rump width (pin bones) recorded the highest heritability in the study: $h^2 = 0.63$ (SE = 0.076), with a sire variance of 0.257 against a phenotypic variance of 1.622. This value is clearly superior to the intervals reported in the international literature (h^2 = 0.25-0.38; Němcová et al., 2011; Campos et al., 2015), placing rump width at the top of the analysed traits in terms of the genetic contribution to phenotype. A heritability of 0.63 implies that approximately 63% of the phenotypic variability of rump width is explained by additive genetic variability, conferring an exceptionally high

potential response to selection. Short & Lawlor (1992) reported that rump width shows moderate to high heritability in American Holstein populations, noting that selection for this trait generates rapid and predictable genetic progress. The value of 0.63 may reflect a specific genetic structure of the BNR population or the effect of bulls with contrasting breeding values used in the herds included in the study, an aspect that warrants investigation through genealogical data analysis.

Rump angle showed a heritability of $h^2 = 0.24$ (SE = 0.068), a moderate value consistent with the interval $h^2 = 0.15$-0.30 reported by Short & Lawlor (1992); Němcová et al. (2011), with direct implications for calving ease and reproductive efficiency.

Hock angle ($h^2 = 0.11$; SE = 0.065) and heel height ($h^2 = 0.12$; SE = 0.066) showed low heritabilities, consistent with estimates of 0.09-0.18 reported by Němcová et al. (2011); Brotherstone & Hill (1990). These low heritabilities, combined with high phenotypic variabilities (CV% = 26.53% and 19.16%, respectively), confirm that improvement of these traits in the BNR breed is largely dependent on optimisation of environmental factors - flooring type, hoof management, mineral nutrition - rather than direct genetic selection.

Mammary system (udder and teats)

Udder traits showed low and relatively uniform heritabilities, ranging from $h^2 = 0.12$ (median suspensory ligament) to $h^2 = 0.14$ (udder depth). Although these values suggest a significant environmental influence on udder conformation, the estimated sire variances (0.040-0.070) confirm the existence of a real additive genetic component amenable to long-term improvement through selection.

Fore udder attachment ($h^2 = 0.13$; SE = 0.066) and rear udder height ($h^2 = 0.13$; SE = 0.066) show heritabilities slightly below the interval of 0.15-0.28 reported by Short & Lawlor (1992); Campos et al. (2015). Udder depth ($h^2 = 0.14$; SE = 0.066) is of particular importance for productive longevity. Williams et al. (2022) demonstrated that udder depth, together with rear udder height and teat length, represents an important genetic predictor of survival and productive longevity. The heritability estimated in the present study ($h^2 = 0.14$) is considerably lower than values reported by other authors ($h^2 = 0.41$; Kőrösi et al., 2025).

Median suspensory ligament ($h^2 = 0.12$; SE = 0.066) showed the lowest heritability among udder traits, slightly below the value of 0.22 reported by Kőrösi et al. (2025). Despite its low heritability, this trait has major practical importance due to its favourable phenotypic and genetic correlations with mastitis resistance and milking efficiency, and is therefore included in most functional selection indices used in modern Holstein breeding programmes.

Teat placement ($h^2 = 0.11$; SE = 0.065) and teat length ($h^2 = 0.11$; SE = 0.065) showed the lowest heritabilities in the entire study. The result for teat length is notable in contrast with international literature: Campos et al. (2015) reported one of the highest heritabilities for this trait ($h^2 = 0.38$), a value also supported by other authors ($h^2 = 0.36$ - Williams et al., 2022; $h^2 = 0.25$-0.32 - Short & Lawlor, 1992). The discrepancy may be attributed to: (i) the relatively small effective population size compared to reference studies; (ii) the potential effect of multiple classifiers introducing systematic variability; (iii) the specific genetic structure of the BNR population.

Exterior Selection Index (ESI)

ESI showed a heritability of $h^2 = 0.17$ (SE = 0.067), with the highest sire variance in the study (0.377) and the highest total phenotypic variance (9.142). The attenuation of ESI heritability relative to the individual heritabilities of the best-determined component traits is consistent with selection index theory (Hazel, 1943; Miglior et al., 2005), reflecting the dilution effect generated by aggregating traits with variable heritability. The use of ESI as a practical selection tool remains justified by its ability to integrate genetic information from multiple correlated traits, providing a more stable global assessment than any individual component trait taken separately (Miglior et al., 2005).

Estimation precision and implications for selection

Standard errors of heritability were relatively uniform across traits (SE = 0.065-0.076), reflecting comparable estimation precision

throughout the data set. These values are, however, higher than those reported in studies with much larger populations (SE < 0.04 in Němcová et al., 2011, n = 78,886; SE < 0.03 in Campos et al., 2015, n = 18,831), indicating that the confidence intervals of the present estimates are wider and that reported h^2 values should be interpreted with caution for traits with $SE/h^2 > 0.5$ (e.g., stature: $SE/h^2 = 0.65$).

From the perspective of selection priorities, the present study identifies rump width - pin bones ($h^2 = 0.63$) as the most promising trait for rapid genetic improvement in the BNR breed, followed by rump angle ($h^2 = 0.24$) and dairy form ($h^2 = 0.22$). Traits with low heritability - feet and legs, udder and teats - require long-term improvement strategies based on the use of proven bulls with favourable breeding values (EBV/GEBV) and simultaneous optimisation of environmental conditions, in accordance with Interbull recommendations for national genetic evaluation programmes for conformation in dairy breeds.

The relatively small effective population size (n = 2,956) compared to reference studies results in wider confidence intervals for heritability estimates. Additionally, the use of multiple classifiers may have introduced systematic variability, particularly for subjectively scored traits such as teat length. Future research should incorporate genealogical data analysis to clarify the unusually high heritability of rump width, and extend the dataset to improve estimation precision.

CONCLUSIONS

The results obtained provide a useful scientific basis for both farmers and breed improvers involved in enhancing exterior conformation in the Romanian Black and White breed. For farmers, knowledge of traits with high variability and low genetic determination - such as feet and legs traits and teat placement and length - guides management decisions towards optimising housing conditions, with more immediate and accessible effects than direct genetic selection.

For breed improvers, rump width - pin bones stands out as the most promising trait for inclusion in selection indices, due to its high genetic determination, which guarantees a predictable and rapid response to selection. Udder traits, despite their low heritability, justify sustained long-term selection given their documented role in maintaining udder health, reducing mastitis incidence and extending productive longevity - factors with a direct impact on farm profitability.

Overall, the results of this study can be used in breeding programmes to consolidate and improve the exterior conformation of the Romanian Black and White breed in line with the international standards of the Holstein breed.

REFERENCES

Brotherstone S. (1994). Genetic and phenotypic correlations between linear type traits and production traits in Holstein-Friesian dairy cattle. *Animal Production, 59(*2), 183-187.

Brotherstone, S., & Hill, W.G. (1990). Estimation of genetic parameters for linear and miscellaneous type traits in Holstein-Friesian dairy cattle. *Livestock Production Science, 26*(3-4), 177-192.

Campos, R.V., Cobuci, J.A., Kern, E.L., Costa, C.N., & McManus, C.M. (2015). Genetic parameters for linear type traits and milk, fat, and protein production in Holstein cows in Brazil. *Asian-Australasian Journal of Animal Sciences, 28*(4), 476-484.

Falconer, D.S., & Mackay, T.F.C. (1996). *Introduction to Quantitative Genetics* (4th ed.). Essex, UK: Longman Publishing House.

Foster, W.W., Freeman, A.E., Berger, P.J., & Kuck, A. (1989). Association of type traits scored linearly with production and herd life of Holsteins. *Journal of Dairy Science, 72*(10), 2651-2664.

Harris, B.L., Freeman, A.E., & Metzger, E. (1992). Genetic and phenotypic parameters for type and production in Guernsey dairy cows. *Journal of Dairy Science, 75*(4), 1147-1153.

Hazel, L.N. (1943). The genetic basis for constructing selection indexes. *Genetics, 28*(6), 476-490.

Kőrösi, Z.J., Benec, S.A., Bognár, L., & Szabó, F. (2025). Heritability and trends in selected udder traits and their relation to milk production in Holstein-Friesian cows. *Animals, 15*(9), 1276.

Lactanet (2021). *Genetic parameters for conformation traits in Holstein cattle*. Lactanet Canada Technical Report.

Miglior, F., Muir, B.L., & Van Doormaal, B.J., (2005). Selection indices in Holstein cattle of various countries. *Journal of Dairy Science, 88*(3), 1255-1263.

Misztal, I., Lawlor, T.J., Short, T.H., & VanRaden, P.M. (1992). Multiple-trait estimation of variance components of yield and type traits using an animal model. *Journal of Dairy Science, 75*(2), 544-551.

Němcová, E., Štípková, M., & Zavadilová, L. (2011). Genetic parameters for linear type traits in Czech Holstein cattle. *Czech Journal of Animal Science, 56*(4), 157-162.

Short, T.H., & Lawlor, T.J. (1992). Genetic parameters of conformation traits, milk yield, and herd life in Holsteins. *Journal of Dairy Science, 75*(7), 1987-1998.

Sousa Junior, L.P.B., Pinto, L.F.B., Cruz, V.A.R., Oliveira Junior, G.A., Oliveira, H.R., Chud T.S., Pedrosa, V.B., Miglior, F., Schenkel, F.S., & Brito, L.F. (2024). Genome-wide association and functional genomic analyses for body conformation traits in North American Holstein cattle. *Frontiers in Genetics, 15*, 1478788.

Williams, M., Sleator, R.D., Murphy, C.P., McCarthy, J., & Williams, D.P. (2022). Re-assessing the importance of linear type traits in predicting genetic merit for survival in an aging Holstein-Friesian dairy cow population. *Journal of Dairy Science, 105*(9), 7550-7563.