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EVALUATING GENETIC AND PHENOTYPIC RELATIONSHIPS OF SIX TRAITS OTHER THAN PRODUCTION (TOP) IN DAIRY CATTLE PRIOR TO THEIR ADOPTION IN NEW ZEALAND

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SUMMARY

This study examined genetic and phenotypic correlations between six internationally recognised Traits Other than Production (TOP) with 12 existing TOP traits routinely scored in New Zealand dairy cattle. Scored on 1,386 first lactation Holstein-Friesian heifers, the aim was to assess whether evaluating these traits could provide additional information for breeding decisions. Of the six new traits, Body Depth (BD) and Udder Depth (UD) showed the greatest genetic variance and heritability, while Chest Width (CW) and Rear Legs Rear View (RLRV) had the lowest. All new traits were moderately to strongly correlated positively (>0.65; Central Ligament [CL], UD, CW and BD) or negatively (<-0.65; RLRV and Foot Angle [FA]) with at least one existing TOP trait. These findings suggest limited potential for capturing additional genetic information beyond what is already available, although some new traits may still serve as useful predictors due to their higher heritability.

INTRODUCTION

The routine scoring of Traits Other than Production (TOP) supports genetic evaluations in New Zealand's (NZ) dairy sector (DairyNZ 2024). Internationally recognised traits, including Central Ligament (CL), Udder Depth (UD), Chest Width (CW), Body Depth (BD), Rear Legs Rear View (RLRV), and Foot Angle (FA) (Brotherstone 1994; Interbull 2024; Williams *et al.* 2022), are not routinely scored in NZ. Incorporating these traits could improve the evaluation of conformation traits and enhance alignment with international genetic evaluation systems, facilitating data exchange with Interbull. This study evaluates the genetic and phenotypic correlations between these novel and established traits and assesses their potential value for inclusion in the TOP system.

MATERIALS AND METHODS

Individual TOP scores (for the traits described in Table 1) for 1,386 first lactation, Holstein-Friesian heifers from 15 herds were collected between 15/03/21 and 01/04/21 by trained inspectors. All traits were scored on a 1 to 9 linear scale. The 12 existing traits are described in DairyNZ (2023) and the six new traits are described in ICAR (2015). The Ruakura Animal Ethics Committee (Hamilton, NZ) approved this study and all manipulations (AE application: 14448).

Cattle were genotyped using Weatherbys (www.WeatherbysScientific.com) Illumina Versa 50K bovine panel and the resultant SNP data were stored in a Helical database for processing and extraction (Garrick *et al.* 2025). Any missing SNPs were imputed using findhap software (Van Raden *et al.* 2011). Only mapped SNPs assigned to chromosomes 1 through 29 and with a minor allele frequency >1% were included in the analysis (n=46,766).

Data were analysed in Julia 1.7.0 using the Julia for Whole-genome Analyses Software (JWAS v1.1.2) package (Cheng *et al.* 2018). Variance parameters were estimated using Markov-chain Monte Carlo (MCMC) approaches and inference was based on MCMC chains of 75,000 samples after a burn-in of 25,000 samples, retaining every 10th sample. Co(variance) components were estimated by fitting the below model equation pairwise:

$$Y = Xb + M\alpha + e$$

where: Y was the trait of interest (Table 1); X is the incidence matrix for fixed herd-visit day contemporary group effects (b); M is the matrix of additive covariates for 46,766 loci with effects (α) assumed independently and identically normally distributed with variance σ_α^2; and e is the residual effects independently and identically normally distributed with variance σ_e^2. Inference was based on the posterior means of the MCMC samples, their posterior variance, and their credibility intervals obtained directly from the samples. The upper and lower 90% credibility intervals were calculated by taking the 95th percentile of the MCMC samples as the upper bound and the 5th percentile as the lower bound.

RESULTS AND DISCUSSION

Heritability estimates for the udder traits were low to moderate and ranged from 0.16 for Fore Udder Attachment up to 0.34 for UD (Table 1). Heritability estimates were low for the two leg conformation traits (RLRV and Rear Legs Set [RLS]) and were low to moderate for the remaining body traits (0.13 to 0.39; Table 1). Estimates for both new and existing traits were aligned with values reported internationally (Brotherstone 1994; Berry *et al.* 2004; Williams *et al.* 2022).

Table 1. Descriptive statistics, genetic variances and heritability estimates of 12 existing and six new Traits Other Than Production (TOP) type traits. Genetic variances and heritability estimates are presented as posterior means with lower and upper 90% credibility intervals

Trait Name	Abbr.	Status	Mean ± SD	Genetic Variance	Heritability
Udder Traits					
Central Ligament	CL	New	6.09 ± 0.98	0.16 (0.10,0.23)	0.19 (0.12,0.27)
Fore Udder Attachment	FU	Existing	5.39 ± 1.02	0.15 (0.09,0.20)	0.16 (0.10,0.23)
Front Teat Placement	FT	Existing	4.82 ± 0.68	0.10 (0.07,0.14)	0.24 (0.16,0.32)
Rear Teat Placement	RT	Existing	7.00 ± 0.94	0.23 (0.16,0.30)	0.28 (0.20,0.36)
Rear Udder Attachment	RU	Existing	5.50 ± 0.88	0.09 (0.06,0.13)	0.15 (0.09,0.21)
Udder Depth	UD	New	6.19 ± 1.11	0.34 (0.26,0.43)	0.34 (0.26,0.42)
Udder Overall	UO	Existing	5.40 ± 0.88	0.12 (0.08,0.16)	0.18 (0.12,0.24)
Udder Support	US	Existing	5.97 ± 1.00	0.22 (0.14,0.29)	0.30 (0.20,0.40)
Body Traits					
Body Depth	BD	New	6.18 ± 1.04	0.40 (0.30,0.51)	0.39 (0.30,0.49)
Capacity	CA	Existing	6.21 ± 0.86	0.23 (0.17,0.30)	0.32 (0.24,0.41)
Chest Width	CW	New	5.57 ± 1.08	0.08 (0.04,0.12)	0.13 (0.07,0.19)
Dairy Conformation	DC	Existing	6.09 ± 0.96	0.19 (0.12,0.27)	0.22 (0.14,0.31)
Foot Angle	FA	New	5.36 ± 1.00	0.21 (0.14,0.29)	0.23 (0.15,0.30)
Rear Legs Rear View	RLRV	New	5.21 ± 0.90	0.04 (0.01,0.10)	0.06 (0.01,0.13)
Rear Legs Set	RLS	Existing	6.27 ± 0.59	0.03 (0.02,0.05)	0.10 (0.05,0.16)
Rump Angle	RA	Existing	4.14 ± 0.80	0.14 (0.09,0.19)	0.22 (0.15,0.31)
Rump Width	RW	Existing	5.43 ± 0.86	0.12 (0.07,0.18)	0.18 (0.11,0.27)
Stature	STAT	Existing	5.71 ± 0.85	0.18 (0.14,0.23)	0.38 (0.29,0.46)

The genetic correlations among the new and existing udder traits were higher than the phenotypic correlations (Table 2). Both the new udder traits (CL and UD) had at least one genetic correlation with an existing udder trait that was moderate to highly positive (Table 2). The genetic and phenotypic correlations between CL and UD was moderate at 0.31 (0.07, 0.52) and 0.35 (0.31, 0.39). In NZ, the existing Udder Support (US) trait is scored as a combination between CL and UD; unsurprisingly, the genetic correlation between US and UD was high at 0.79 and moderately high at 0.63 between US and CL (Table 2). The genetic correlations between CL and both front and rear teat placement traits were also high and positive (0.70 and 0.74; respectively); similar to Berry *et al.* (2004) who reported that a stronger central ligament was associated with closer teat placement.

Table 2. Posterior means (and 90% credibility intervals) of the genetic and phenotypic correlations between new and existing Traits Other Than Production (TOP) udder type traits. Trait abbreviations are defined in Table 1

Trait	US	FU	RU	FT	RT	UO
Genetic Correlations						
CL	0.63	0.31	0.31	0.70	0.74	0.35
	(0.44,0.77)	(-0.01,0.54)	(0.00,0.53)	(0.54,0.83)	(0.60,0.85)	(0.06,0.56)
UD	0.79	0.62	0.52	0.36	0.19	0.71
	(0.71,0.87)	(0.44,0.77)	(0.30,0.69)	(0.13,0.55)	(-0.04,0.39)	(0.58,0.82)
Phenotypic Correlations						
CL	0.42	0.20	0.29	0.26	0.37	0.34
	(0.38,0.46)	(0.15,0.24)	(0.25,0.33)	(0.21,0.30)	(0.33,0.41)	(0.30,0.38)
UD	0.45	0.29	0.34	0.11	0.11	0.40
	(0.41,0.48)	(0.25,0.33)	(0.29,0.37)	(0.07,0.16)	(0.06,0.15)	(0.36,0.43)

Table 3. Posterior means (and 90% credibility intervals) of the genetic and phenotypic correlations between new and existing Traits Other Than Production (TOP) body type traits. Trait abbreviations are defined in Table 1

Trait	STAT	CA	RA	RW	RLS	DC
Genetic Correlations						
CW	0.05	0.66	0.26	-0.02	-0.27	0.63
	(-0.25,0.29)	(0.48,0.80)	(-0.06,0.50)	(-0.35,0.27)	(-0.58,0.06)	(0.40,0.79)
BD	0.02	0.87	0.41	0.27	-0.10	0.87
	(-0.17,0.19)	(0.79,0.93)	(0.16,0.65)	(-0.02,0.56)	(-0.39,0.19)	(0.78,0.93)
RLRV	0.00	0.13	-0.24	-0.11	-0.65	0.12
	(-0.50,0.40)	(-0.43,0.54)	(-0.65,0.14)	(-0.63,0.31)	(-0.85,-0.33)	(-0.48,0.55)
FA	0.45	0.09	-0.32	-0.02	-0.89	0.19
	(0.22,0.68)	(-0.16,0.31)	(-0.54,-0.11)	(-0.31,0.26)	(-0.95,-0.80)	(-0.10,0.48)
Phenotypic Correlations						
CW	0.06	0.30	0.06	0.03	0.03	0.25
	(0.02,0.11)	(0.26,0.34)	(0.01,0.10)	(-0.02,0.07)	(-0.02,0.07)	(0.20,0.29)
BD	0.07	0.57	0.09	0.06	0.09	0.49
	(0.02,0.11)	(0.54,0.60)	(0.05,0.14)	(0.01,0.10)	(0.04,0.13)	(0.45,0.52)
RLRV	-0.02	0.11	0.02	-0.03	-0.01	0.14
	(-0.07,0.02)	(0.06,0.15)	(-0.03,0.06)	(-0.08,0.02)	(-0.06,0.03)	(0.09,0.18)
FA	0.12	0.07	0.00	0.01	-0.24	0.12
	(0.07,0.16)	(0.02,0.11)	(-0.04,0.05)	(-0.04,0.05)	(-0.29,-0.20)	(0.07,0.16)

Table 4. Posterior means (and 90% credibility intervals) of the genetic (below diagonal) and phenotypic (above diagonal) correlations between four new Traits Other Than Production (TOP) body type traits. Trait abbreviations are defined in Table 1

Trait	CW	BD	RLRV	FA
CW	1	0.29 (0.25,0.34)	0.18 (0.13,0.22)	0.07 (0.03,0.12)
BD	0.43 (0.08,0.69)	1	0.07 (0.02,0.11)	0.00 (-0.05,0.04)
RLRV	0.32 (-0.27,0.71)	0.16 (-0.13,0.48)	1	0.15 (0.10,0.19)
FA	0.17 (-0.14,0.47)	0.09 (-0.10,0.30)	0.18 (-0.21,0.63)	1

The existing body Capacity (CA) trait is scored as a combination between CW and BD, and expectedly, the genetic correlations between CA and BD or CW were high at 0.87 or moderately high at 0.66, respectively (Table 3). All four new body traits had at least one genetic correlation with an existing trait that was moderate to highly negative (<-0.65; RLRV and FA) or moderate to highly positive (>0.65; CW and BD). Brotherstone (1994) and Berry *et al.* (2004) also reported that FA and RLS had strong negative genetic correlations. Genetic correlations among the four new body traits ranged between 0.09 and 0.43 (Table 4), and were strongest between CW and BD.

The strong genetic correlations observed between the new traits and existing traits highlight their close genetic relationships, suggesting that these new traits may not capture novel genetic information. However, new traits that have strong genetic correlations with existing traits but more genetic variance or a higher heritability could provide value as a predictor trait. For example, while FA exhibited a strong negative genetic correlation with the existing trait RLS, its greater heritability (0.23 vs. 0.10) makes it a promising candidate as a predictor trait. Similarly, BD had strong genetic correlations (0.87) with both CA and DC, with a similar or greater heritability (0.39 vs. 0.32 and 0.22, respectively).

CONCLUSION

This study revealed strong genetic correlations between new body or udder traits and at least one existing TOP trait, indicating that the new traits may largely reflect genetic information already captured by existing traits. The body trait FA demonstrated a higher heritability compared with its correlated existing trait RLS, highlighting its potential utility as a predictor trait. While further research with larger datasets reflecting NZ's mixed-breed herds is needed to confirm these findings, this study provides a foundation for informed decision-making on the inclusion of new body and udder conformation traits into routine genetic evaluations.

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