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Genetic parameters for feed intake and body weight in dairy cattle using high-throughput 3-dimensional cameras in Danish commercial farms

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ABSTRACT

Recording complex phenotypes on a large scale is becoming possible with the incorporation of recently developed new technologies. One of these new technologies is the use of 3-dimensional (3D) cameras on commercial farms to measure feed intake and body weight (BW) daily. Residual feed intake (RFI) has been proposed as a proxy for feed efficiency in several species, including cattle, pigs, and poultry. Dry matter intake (DMI) and BW records are required to calculate RFI, and the use of this new technology will help increase the number of individual records more efficiently. The aim of this study was to estimate genetic parameters (including genetic correlations) for DMI and BW obtained by 3D cameras from 6,000 cows in commercial farms from the breeds Danish Holstein, Jersey, and Nordic Red. Additionally, heritabilities per parity and genetic correlations among parities were estimated for DMI and BW in the 3 breeds. Data included 158,000 weekly records of DMI and BW obtained between 2019 and 2022 on 17 commercial farms. Estimated heritability for DMI ranged from 0.17 to 0.25, whereas for BW they ranged from 0.44 to 0.58. The genetic correlations between DMI and BW were moderately positive (0.58–0.65). Genetic correlations among parities in both traits were highly correlated in the 3 breeds, except for DMI between first parity and late parities in Holstein where they were down to 0.62. Based on these results, we conclude that DMI and BW phenotypes measured by 3D cameras are heritable for the 3 dairy breeds and their heritabilities are comparable to those obtained by traditional methods (scales and feed bins). The high heritabilities and correlations of 3D measurements with the true trait in previous studies demonstrate the potential of this new technology for measuring feed intake and BW in real time. In conclusion, 3D camera technology has the potential to become a valuable tool for automatic and continuous recording of feed intake and BW on commercial farms.

Key words: feed efficiency, 3-dimensional cameras phenotypes, dry matter intake, body weight

INTRODUCTION

Feed costs account for more than half of the total production cost of dairy cattle (Braae et al., 2021). Therefore, improving feed efficiency is a goal of the dairy industry. In the last decade, several countries, such as Australia, the Netherlands, the United States, and Canada, have included feed efficiency in their breeding goals (Pryce et al., 2015; CRV, 2022; Gaddis et al., 2021; Lactanet, 2021). Since 2020, the Nordic Cattle Genetic Evaluation (**NAV**) has included feed efficiency through the Saved Feed Index in the Nordic Total Merit Index (Lidauer et al., 2019; Stephansen et al., 2019). Residual feed intake (**RFI**) provides new information about feed efficiency beyond the existing traits. Feed efficiency is an important trait in all livestock species, including cattle, pigs, and poultry (Luiting, 1990; Berry and Crowley, 2013; Patience et al., 2015). Residual feed intake has many definitions; one widely accepted definition (originally for growing animals) is the difference between actual and predicted feed intake after considering variability in maintenance requirement and growth (Koch et al., 1963). For dairy cattle, Tempelman et al. (2015) defined RFI as an estimated residual derived from a multiple regression equation on energy sinks. Energy sinks usually include ECM, metabolic body weight, and body weight change. However, DMI and BW records used to calculate RFI are scarce, as they are labor intensive, expensive, and time consuming to measure. Currently, most DMI records are only available for research and nutrition experiments, mainly for the first and second lactation, and in many cases, only for a part of lactation (e.g., from 50 to 150 DIM). Some studies have shown the importance of recording DMI during the entire lactation (Manzanilla-Pech et al., 2014a,b; Li et al., 2016) and in multiple lactations (Khanal et al., 2022) to properly account for the ge-

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netic variation among lactation stages and parities. However, measuring full lactations in commercial data is not feasible, due to its costs and labor involved. In contrast, BW is recorded by different methods such as traditional weighting scales, walk-through scales, and scales attached to the automatic milking systems (e.g., Lely A3). Additionally, BW is also predicted by body size measurements as heart girth (Branton and Salisbury, 1946; Yan et al., 2009); however, there is not a consistent and continuous measurement method for BW, as we see in milk recording.

Recently, several technologies have been developed to facilitate precision phenotyping in livestock (Brito et al., 2020; Neethirajan and Kemp, 2021) for welfare, prediction, and diagnostic purposes. With these technologies, a new era of precision phenotyping has emerged. One of these technologies is the use of 3D cameras to predict individual feed intake and BW in commercial herds on a large scale. The Cattle Feed Intake System (**CFIT**; Lassen et al., 2018, 2023; Thomasen et al., 2018; Viking Genetics, 2022), which combines the use of 3D camera recordings and artificial intelligence, is an alternative tool for predicting individual DMI and BW compared with scale-based systems. The CFIT 3D cameras, located in barns, can identify individual cows and record individual DMI and BW for the entire herd using artificial intelligence algorithms (Borchersen et al., 2014, 2017; Lassen and Borchersen, 2020). One of the advantages of this new technology is that it allows us to predict feed intake and BW of every cow in the barn during the entire lactation and for all lactations. In comparison to traditional methods (feed bins) to record feed intake, recording with 3D cameras, located on the barn's roof, does not affect, or limit the feeding behavior of the animal. Furthermore, feed intake and BW are mainly recorded (fully or partially) on the first and second lactation, as most of the research on feed intake and feed efficiency, has been done using only early lactations. This has led to neglecting later (3+) lactations, whereas all commercial farms have cows in later lactations.

Finally, this methodology has been previously validated with crossed experiments using traditional methods and 3D cameras, the resulting squared correlation between traditional feed bins and 3D cameras had a value of 0.9 (Lassen et al., 2022). Additionally, Gebreyesus et al. (2023) presented prediction accuracies of 0.94 between the contour data (used to predict BW) and the actual BW measurements, with low prediction errors. However, as with every new phenotype, the genetic variation in these 3D traits (DMI and BW) needs to be quantified. This is the first study to report the heritability of 3D camera phenotypes for DMI and BW in dairy cattle. The objective of this study was to estimate the genetic parameters for DMI and BW (obtained by 3D cameras) from 6,000 Danish dairy cows from 3 different breeds, Holstein, Jersey, and Nordic Red, in commercial herds.

MATERIALS AND METHODS

Because this study was based on data collection without handling of animals, no ethical approval was needed.

Recording of the 3D Camera Phenotypes

The data were collected from 3D cameras installed in 17 commercial farms in Denmark during 2019 to 2021. The cameras were located above the feed bunk (attached to the roof) and the cows were recorded while eating (Lassen et al., 2018; Thomasen et al., 2018). The 3D camera was based on time-of-flight technology (Microsoft Xbox One Kinect v2) to create a 3D image, and the ear tags were read using a radio frequency identification reader (Agrident Sensor ASR550). A Dell T630 128-GB RAM server was installed in each herd with a 3090 RTX graphics card (NVIDIA) and used for data analysis. An algorithm based on artificial intelligence identifies cows and translates their 3D images into their phenotypes (DMI and BW). Lassen et al. (2018) and Thomasen et al. (2018) presented a description of the 3D camera methodology used to identify cows and measure individual feed intake. Feed intake was assigned after each cow visited the feed bunk. The cows were fed a total mixed ration diet consisting mainly of maize silage, grass silage, and concentrates. The last image of the feed before a cow begins a visit was stored. The cow puts down its head and is identified. The position in the barn and the starting point of the visit are saved. When the cow takes out its head again, the visit is over, and a new image of the feed is available. Differences in the 2 feed surfaces were determined, and the amount of feed removed was saved along with the end time of the visit. The position of the cow's head was used to distribute feed between 2 cows that could share feed and visits. A cow's head is in a virtual window and can eat feed from this window as well as from 2 corresponding windows to the left and 2 to the right, from the window in which its head is. If a cow eats alone from these 5 virtual windows, it will have all the feed distributed to her. If a virtual window is shared with another cow, the feed is distributed equally between the 2 cows. Body weight is also predicted using 3D images of the back of the cow while they pass a corridor leaving the milking parlor, from which the contours of the cow's back were obtained (Lassen et al., 2022; Gebreyesus et al., 2023). The images were standardized in terms of width and

Table 1. Cow distribution per farm (by farm identification [ID] no.) and breed, with number of records in parentheses, and total number of cows with phenotypes and genotypes per breed

Farm ID	Holstein	Farm ID	Jersey	Farm ID	Nordic Red
1	262 (4,220)	8	431 (22,874)	12	253 (10,915)
2	240 (1,401)	9	307 (14,308)	13	404 (7,690)
3	230 (2,887)	10	375 (11,210)	14	267 (3,372)
4	442 (9,236)	11	265 (7,189)	15	320 (6,167)
5	396 (13,096)		—	16	482 (7,790)
6	719 (24,396)		—	17	225 (1,754)
7	399 (10,396)		—		—
Total no. cows with phenotypes	2,688 (65,632)		1,378 (55,581)		1,951 (37,688)
Total no. cows with genotypes	1,824		1,107		1,679

length. Then, 100 points were taken from the spine of the cow, and 100 corresponding points identifying how far left and right the distance was to drop 3, 5, 10, and 15 cm from the spine. A prediction model was developed using the partial least squares method based on the scale measures of the cows (Lassen and Borchersen, 2020). Subsequently, weekly averages of DMI and BW were calculated based on daily records.

Data Editing

The data included records of DMI and BW obtained from 3D cameras in 6,000 cows from the breeds Danish Holstein, Jersey, and Nordic Red. Cow distribution per breed and parity is shown in Figure 1, whereas the number of records per lactation week, parity, and breed is shown in Supplemental Figure S1 (https://doi.org/10.7910/DVN/KP38VY). Furthermore, cow distribution per herd and breed with the number of records, and total number of cows with genotypes per breed is presented in Table 1. In total, 2,688 Holstein, 1,378 Jersey, and 1,951 Nordic Red cows were recorded between 2019 and 2022. Only data from the first to sixth parity from the first 330 d of lactation were used. Records were set to missing for values out of the range of mean ± 3 standard deviations. On average, cows had 1.3 lactations in this data set.

Pedigree and Genotypes

Three sets of genotypes and pedigrees were provided by SEGES (2023), one per breed for Holstein, Jersey,

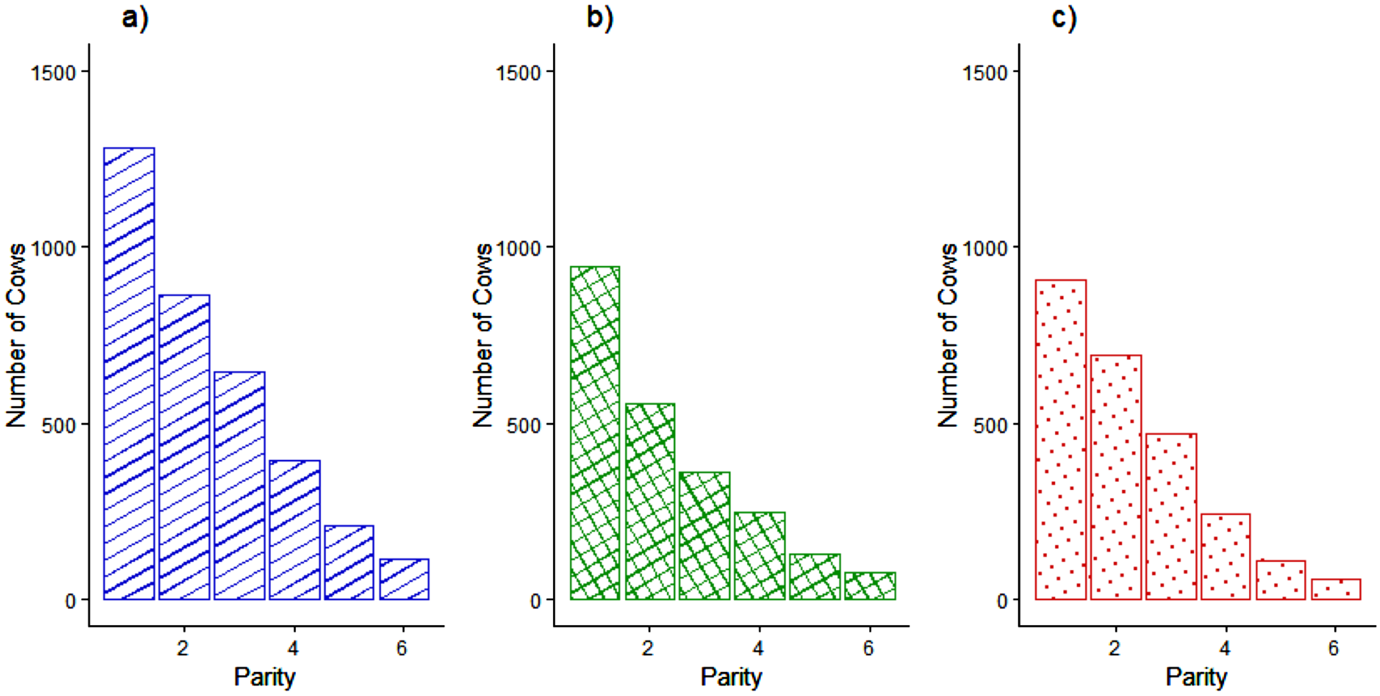

Figure 1. Distributions of cows in this study, per breed (a) Holstein, (b) Jersey, and (c) Nordic Red and parity (1 to 6).

and Nordic Red. The genotypes were either genotyped with 50k Illumina Bovine SNP50 or imputed from the LD chip panels. The genotype set for Holstein included 46,342 SNPs (1,824 cows), the genotype set for Jersey 41,897 SNPs (1,107 cows), and the genotype set for Nordic Red 46,914 SNPs (1,679 cows). The full pedigree for Holstein contained the identification of the cow, sire, and dam for around 675k individuals, whereas for Jersey 200k, and Nordic Red 440k individuals, it included all young bulls. After extracting the pedigree for animals with phenotypes and pruning for noninformative animals using DMU Trace (Madsen, 2012), 7,994 animals remained in the pedigree for Holstein, 5,489 for Jersey, and 9,534 for Nordic Red.

Statistical Analyses

Variance components for DMI and BW were estimated using the AI-REML algorithm with DMU software (Version 6, Release 5.4; Madsen and Jensen, 2014). Genetic and phenotypic correlations were estimated through bivariate analysis of traits using pedigree and genotypes. Heritability and correlations were calculated using pedigree BLUP and single-step genomic BLUP and are referred to as pedigree and genomic heritability and correlations. The genomic relationship matrix (**GRM**) was calculated according to VanRaden (2008) using the invgmatrix program (Su and Madsen, 2017).

The following model was used to estimate the variance components for both traits:

$$\mathbf{y} = \mathbf{X}\mathbf{b} + \mathbf{Z_1}\mathbf{a} + \mathbf{Z_2}\mathbf{c} + \mathbf{e}, \qquad [1]$$

where $\mathbf{y}$ is the vector of phenotypes; $\mathbf{b}$ represents the vector of fixed effects (age of cow at calving as linear regression, herd-year-season, week of lactation, year-season-lactation period nested within parity); $\mathbf{X}$ is the incidence matrix relating observations with fixed effects; $\mathbf{a}$ is the vector of direct additive genetic effects; $\mathbf{Z_1}$ is the incidence matrix relating observations with random genetic effects; $\mathbf{c}$ is the vector of permanent environmental effects; $\mathbf{Z_2}$ is the incidence matrix relating observations with random permanent environmental effects, and $\mathbf{e}$ is the vector of residual effects. Distributions of the random effects are var (a) $= \mathbf{A}\sigma_a^2$, where $\mathbf{A}$ is the pedigree relationship matrix (for the analyses using pedigree) and σ_a^2 is the additive genetic variance; var (a) $= \mathbf{H}\sigma_a^2$, where $\mathbf{H}$ is the combined pedigree and GRM (for the analyses including genomic information) and σ_a^2 is the additive genetic variance; var (c) $= \mathbf{I}\sigma_c^2$, where $\mathbf{I}$ is the identity matrix of order equal to the number of individuals with records and σ_c^2 is the permanent environmental variance; and var (e) $= \mathbf{I}\sigma_e^2$, where $\mathbf{I}$ is an identity matrix of order equal to the number of observations and σ_e^2 is the residual variance. The inverse of the $\mathbf{H}$ matrix, $\mathbf{H^{-1}}$ (Equation 2) was calculated using the following formula (Aguilar et al., 2010; Christensen and Lund, 2010):

$$\mathbf{H}^{-1} = \mathbf{A}^{-1} + \begin{bmatrix} 0 & 0 \\ 0 & \left(w\mathbf{G}^{-1} + (1-w)\mathbf{A}_{22}^{-1}\right) - \mathbf{A}_{22}^{-1} \end{bmatrix}, \qquad [2]$$

where $\mathbf{A}^{-1}$ is the inverse of the pedigree relationship matrix, $\mathbf{G^{-1}}$ is the inverse of the GRM, w is the relative weight of the polygenic effect ($w = 0.80$), and $\mathbf{A}_{22}^{-1}$ is the inverse of the pedigree relationship matrix among the genotyped animals.

Additionally, to determine whether DMI and BW heritability varies across parities, DMI and BW records were divided by parity 1, 2, 3, and 3+ (including records from third to sixth parity). The idea behind the use of parity 3+ was to group parities with small number of records and animals, instead of discarding them. Heritability estimates and genetic correlations were estimated using model [1] in univariate and bivariate analyses with pedigree and genomic data. Residual covariances between the parities were set to zero; consequently, it was not possible to estimate the phenotypic correlations between parities.

RESULTS AND DISCUSSION

Phenotypic Means

Descriptive statistics for DMI and BW in Holstein, Jersey, and Nordic Red cattle are presented in Table 2. The average DMI was 27.7 kg/d for Holstein (SD = 4.4) and Nordic Red (SD = 3.9), whereas Jersey was 23.2 kg/d (SD = 4.2). The DM content was assumed to be 40%. The averages for BW were 676 kg (SD = 75.6) for Holstein, 464 kg (SD = 42.5) for Jersey, and 641 kg (SD = 74.3) for Nordic Red. The average DMI for Holstein was higher than that previously reported by Li et al. (2016) (19.4 kg/d) for Danish Holstein cows from a research farm, but within the range (17 to 30 kg/d) reported by Tempelman et al. (2015) for a collection of several farms in the United States, the Netherlands, and the United Kingdom. Li et al. (2016) also reported a lower DMI for Jersey (15.8 kg/d) and Nordic Red (18.5 kg/d) in comparison with those in this study. Additionally, Difford et al. (2020) and Manzanilla-Pech et al. (2021) reported a lower average BW in Holstein cows. Similarly, Li et al. (2016) reported lower BW averages for Jersey (433 kg) and Nordic Red (575 kg) in primiparous Nordic cows measured within 32 weeks of lactation. This could also explain the differences, as

Table 2. Descriptive statistics for DMI and BW in Holstein, Jersey, and Nordic Red cows

Breed	Trait[1]	Number of records	Mean	SD	Minimum	Maximum	CV (%)
Holstein	DMI	65,393	27.7	4.4	12.7	40.9	16
	BW	65,293	675.8	75.6	448.4	905.0	11
Jersey	DMI	55,169	23.2	4.2	8.7	34.1	18
	BW	55,405	464.4	42.5	337.0	592.0	9
Nordic Red	DMI	37,487	27.7	3.9	15.3	38.4	14
	BW	37,576	641.5	74.3	340.0	909.0	11

[1] DMI is presented in kg/d; BW is presented in kg.

these are high-producing cows and some of them are from later lactations; they consume more feed and are heavier than research farm cows. Finally, the coefficient of variation (**CV**) for BW was lower (9–11) than that for DMI (14–18) in the 3 breeds.

Estimated Pedigree and Genomic Heritability

Estimated heritability and repeatability for DMI and BW in Holstein, Jersey, and Nordic Red cows are shown in Table 3. The estimated heritability values for DMI and BW phenotypes predicted using 3D cameras were moderate for the 3 breeds. Estimated pedigree heritability for DMI were 0.23 (SE = 0.02) for Holstein, 0.21 (SE = 0.04) for Jersey, and 0.20 (SE = 0.03) for Nordic Red, whereas permanent environmental ratio values were 0.26 (SE = 0.03) for Holstein, 0.49 (SE = 0.03) for Jersey, and 0.44 (SE = 0.02) for Nordic Red. Genomic heritability values for DMI in the 3 breeds were not different from pedigree heritability values (within 2 standard errors). Both heritability and repeatability for Nordic Red were slightly lower than those previously reported by Li et al. (2016, 2018) ranging from 0.25 to 0.37 for heritability and from 0.68 to 0.85 for repeatability. However, DMI heritability values for Holstein and Jersey were within the range (depending on the lactation week) reported by Li et al. (2016, 2018) for the 3 breeds (0.30–0.55 for Holstein; 0.17–0.52 for Jersey; and 0.20–0.48 for Nordic Red) in primiparous Nordic cows. Likewise, previous reports for Holstein cows reported similar heritability values for Holstein cows (Vallimont et al., 2010; Li et al., 2018; Difford et al., 2020; Manzanilla-Pech et al., 2021). The estimated pedigree heritability values for BW were 0.47 (SE = 0.05) for Holstein, 0.42 (SE = 0.05) for Jersey, and 0.53 (SE = 0.05) for Nordic Red. These values agreed with previously published heritability estimates (Li et al., 2018; Lidauer et al., 2019; Difford et al., 2020). Genomic heritability was slightly higher (with smaller SE) than pedigree heritability for BW among the 3 breeds. Additionally, heritability values for BW were within the range reported by Li et al. (2018) for the 3 breeds, ranging from 0.49 to 0.63 for Holsteins, and from 0.46 to 0.61 for Jersey cows, whereas for Nordic Red it was from 0.32 to 0.53. Furthermore, Mehtiö et al. (2021) reported heritability values between 0.44 and 0.56 for first to third lactation Nordic Red cows.

Estimated Genetic and Phenotypic Correlations

The genetic and phenotypic correlations between DMI and BW using pedigree and genomic information are presented in Table 4. The genetic correlation between DMI and BW was moderate to high in the 3 breeds, being 0.60 (SE = 0.06) for Holstein, 0.62 (SE = 0.08) for Jersey, and 0.69 (SE = 0.06) for Nordic Red. Genetic correlations, based on genomic information, were slightly lower among the 3 breeds. Moderate to high genetic correlations were estimated between DMI and BW, which were within the range of values previously

Table 3. Estimated genetic variances $\left(\sigma_a^2\right)$, heritabilities (h^2), and permanent environmental ratios (pe^2), with SE in parentheses, for DMI and BW for Holstein, Jersey, and Nordic Red cows using pedigree and genomic information[1]

		Pedigree			Genomic		
Breed	Trait	σ_a^2	h^2	pe^2	σ_a^2	h^2	pe^2
Holstein	DMI	1.8	0.23 (0.02)	0.26 (0.03)	1.9	0.25 (0.02)	0.25 (0.02)
	BW	1,255.4	0.47 (0.05)	0.40 (0.05)	1,598.9	0.51 (0.04)	0.37 (0.04)
Jersey	DMI	2.2	0.19 (0.04)	0.30 (0.03)	1.8	0.17 (0.03)	0.32 (0.02)
	BW	410.7	0.42 (0.05)	0.33 (0.05)	435.9	0.45 (0.04)	0.31 (0.04)
Nordic Red	DMI	1.3	0.20 (0.03)	0.24 (0.02)	1.1	0.18 (0.02)	0.25 (0.02)
	BW	1,765.2	0.53 (0.05)	0.36 (0.05)	1933.3	0.58 (0.04)	0.31 (0.04)

[1] DMI is presented in kg^2/d; BW is presented in kg^2.

Table 4. Estimated genetic (below diagonal) and phenotypic correlations (above diagonal) with SE in parentheses between DMI and BW for Holstein, Jersey, and Nordic Red cows using pedigree and genomic information

		Pedigree		Genomic	
Breed	Trait	DMI	BW	DMI	BW
Holstein	DMI		0.34 (0.01)		0.35 (0.01)
	BW	0.60 (0.06)		0.58 (0.05)	
Jersey	DMI		0.35 (0.02)		0.34 (0.02)
	BW	0.64 (0.08)		0.62 (0.07)	
Nordic Red	DMI		0.35 (0.01)		0.35 (0.01)
	BW	0.69 (0.06)		0.65 (0.06)	

reported (0.3–0.7) for Danish Holstein and Nordic Red cows across lactation stages using traditional methods (Li et al., 2018). Veerkamp and Brotherstone (1997), Hüttmann et al. (2009), and Manzanilla-Pech et al. (2014b) reported lower genetic correlations (0.31–0.43) between DMI and BW in Holstein cows. Furthermore, Vallimont et al. (2010) and Spurlock et al. (2012) reported similar correlations between the DMI and BW in Holstein cows. Liinamo et al. (2012) reported moderate genetic correlations (0.54; SE = 0.33) between DMI and BW in Nordic Red cows. Phenotypic correlations were similar (0.34–0.35; SE = 0.01–0.02) among the 3 breeds using pedigree and genomic information. Manafiazar et al. (2016) reported higher phenotypic correlations (0.51) for lifetime DMI and average BW in Holstein cows, whereas Vallimont et al. (2010) reported lower phenotypic correlations (0.19). For this part of the study, correlations of 1 were assumed between different lactations weeks and among parities (due to the current data available), which might not be totally correct based previous studies (Manzanilla-Pech et al., 2014a; Li et al., 2016, 2017; Khanal et al., 2022). Despite the incomplete lactation records, it was still feasible to divide the available data into separate parities and estimate the genetic parameters, including correlations among parities per trait and per breed.

Estimated Heritabilities and Genetic Correlations Between Parities

Estimated heritabilities for DMI and BW traits in Holstein, Jersey, and Nordic Red cattle per parity (1, 2, 3, and 3+) using pedigree and genomic information are presented in Table 5. Dry matter intake estimated (pedigree) heritabilities ranged from 0.20 (SE = 0.03) to 0.35 (SE = 0.05) among parities for Holstein, whereas, for Jersey were from 0.08 (SE = 0.04) to 0.24 (SE = 0.07), and for Nordic Red were from 0.15 (SE = 0.05) to 0.26 (SE = 0.03). Standard errors were in general larger for the third parity, due to the small number of animals with records for this parity (Table 5). Estimated (pedigree) heritabilities for BW ranged from 0.24 (SE = 0.06) to 0.47 (SE = 0.06) for Holstein, whereas, for Jersey were from 0.30 (SE = 0.07) to 0.60 (SE = 0.10), and for Nordic Red were from 0.41 (SE = 0.07) to 0.64 (SE = 0.07). Genomic estimated heritabilities for DMI and BW in all breeds were similar to the values estimated using pedigree. To the authors' knowledge, there is a limited number of studies that have reported heritabilities and genetic correlation per parity for DMI and BW for Holstein, Jersey, or Nordic Red cows. Tarekegn et al. (2021) reported previously similar heritabilities (0.20) for DMI in Holstein first parity and lower (0.17) for later parities. They also reported higher values (0.45) for heritabilities in Swedish Red (comparable to Nordic Red) in first parity and lower (0.10) in later parities. Estimated genetic correlations within parities with SE for DMI and BW in Holstein, Jersey, and Nordic Red cattle using pedigree and genomic information are presented in Table 6. Genetic correlations for DMI were highly correlated between first and second parity, 0.89 (SE = 0.08) for genomic and 0.86 (SE = 0.10) for pedigree. Genetic correlations for DMI among first and later parities were from moderate to highly correlated (above 0.63). Genetic correlations between second and third parity were highly correlated as well (0.82, SE = 0.09), as expected with consecutive parities. Tarekegn et al. (2021) reported genetic correlations for DMI first parity and later parities between 0.60 to 0.80 in Holstein. Similarly, Hardie et al. (2017) reported a genetic correlation of 0.78 between primiparous and multiparous Holstein cows. Unlike, Tarekegn et al. (2021) reported positive and negative genetic correlations (−0.80 to 0.80) for Swedish Red for DMI first parity and later parities. Genetic (pedigree) and genomic correlations for BW between parities were higher in Holstein and Nordic Red (0.88–0.99) than in Jersey (0.78–0.99). Nonetheless, higher correlations between parities in BW compared with DMI have been reported previously. Based on the high genetic correlations among parities for Jersey and Nordic Red, we expect that selection on DMI in first parity cows would

Table 5. Estimated heritabilities, with SE (in parentheses), for DMI and BW in Holstein, Jersey, and Nordic Red cows per parity[1] using pedigree and genomic information

				Pedigree		Genomic	
Breed	Parity	No. of records	No. of cows	h^2 DMI	h^2 BW	h^2 DMI	h^2 BW
Holstein	1	24,390	1,280	0.20 (0.03)	0.47 (0.06)	0.21 (0.03)	0.53 (0.04)
	2	16,301	862	0.22 (0.04)	0.24 (0.06)	0.25 (0.04)	0.37 (0.06)
	3	11,862	648	0.35 (0.05)	0.31 (0.08)	0.37 (0.05)	0.32 (0.07)
	3+	24,702	1,105	0.26 (0.03)	0.39 (0.06)	0.27 (0.03)	0.35 (0.05)
Jersey	1	21,736	943	0.14 (0.03)	0.40 (0.05)	0.13 (0.03)	0.40 (0.04)
	2	13,762	556	0.08 (0.04)	0.30 (0.07)	0.09 (0.03)	0.37 (0.06)
	3	8,953	361	0.24 (0.07)	0.60 (0.10)	0.18 (0.05)	0.55 (0.08)
	3+	19,671	501	0.24 (0.05)	0.47 (0.07)	0.21 (0.04)	0.40 (0.06)
Nordic Red	1	13,940	906	0.26 (0.03)	0.53 (0.05)	0.25 (0.03)	0.52 (0.05)
	2	10,768	695	0.19 (0.04)	0.64 (0.07)	0.19 (0.04)	0.64 (0.06)
	3	6,773	469	0.16 (0.07)	0.51 (0.10)	0.20 (0.05)	0.71 (0.07)
	3+	12,779	738	0.15 (0.05)	0.41 (0.07)	0.16 (0.03)	0.55 (0.06)

[1] Includes parities 3 to 6.

also improve DMI in later parities. This might not be the case for Holstein cows, where the genetic correlation between first and later parities is lower (0.63). However, given the reduced number of cows in later parities in the 3 breeds, these results should be taken cautiously, and it is advisable to repeat this study with larger number of animals per parity to confirm these results. If we assume that there are no residual covariances between parities, it could potentially lead to overestimation of the genetic correlations. Therefore, it is important to consider the possibility of residual covariances when estimating genetic correlations between parities. Hence, the necessity of permanent collection of data for DMI is extremely important, and this will be easier with the 3D cameras equipped in many commercial farms. This will help, in the future, to estimate genetic parameters per lactation week for different parities including late lactations that have never been studied before, and to determine whether DMI is genetically a different trait along and across lactation(s) in different breeds.

Implications and Further Research

To select animals that are more feed-efficient, we need records of DMI, BW, and milk production. The continuous recording of DMI and BW during and across lactation(s) has been a challenge for decades. Efforts to collate data across countries and experiments have

Table 6. Estimated genetic correlations among parities (1, 2, 3, and 3+[1]), with SE in parentheses, for DMI and BW in Holstein, Jersey, and Nordic Red cows using pedigree and genomic information

			Pedigree		Genomic	
Breed	Trait	Parity	1	2	1	2
Holstein	DMI	2	0.86 (0.10)		0.89 (0.08)	
		3	0.63 (0.15)	0.82 (0.09)	0.85 (0.11)	0.82 (0.08)
		3+	0.67 (0.17)	0.71 (0.12)	NE[2]	NE
	BW	2	0.95 (0.04)		0.97 (0.03)	
		3	0.88 (0.18)	0.95 (0.05)	0.95 (0.12)	0.97 (0.04)
		3+	0.88 (0.12)	0.91 (0.05)	NE	NE
Jersey	DMI	2	0.75 (0.20)		0.98 (0.05)	
		3	0.98 (0.20)	0.95 (0.13)	0.99 (0.18)	0.77 (0.17)
		3+	0.92 (0.18)	0.96 (0.13)	0.93 (0.17)	0.84 (0.16)
	BW	2	0.99 (0.03)		0.97 (0.03)	
		3	0.88 (0.08)	0.99 (0.05)	0.91 (0.05)	0.98 (0.04)
		3+	0.78 (0.11)	0.99 (0.05)	0.87 (0.07)	0.99 (0.04)
Nordic Red	DMI	2	0.85 (0.14)		0.76 (0.14)	
		3	0.99 (0.15)	0.89 (0.18)	0.85 (0.15)	0.88 (0.13)
		3+	0.92 (0.18)	0.90 (0.17)	0.86 (0.15)	0.98 (0.11)
	BW	2	0.93 (0.04)		0.88 (0.04)	
		3	0.94 (0.09)	0.97 (0.06)	0.97 (0.08)	0.99 (0.05)
		3+	0.98 (0.08)	0.98 (0.05)	0.99 (0.07)	0.95 (0.05)

[1] Parity 3+ includes parities 3 to 6.

[2] NE = not estimable.

been conducted to gather records to start a genetic evaluation (Banos et al., 2012; Veerkamp et al., 2012; Berry et al., 2014). However, merging data from different experiments and countries has presented some questions, such as, is feed intake the same trait across countries and production systems, such as grazing and indoor feeding? Furthermore, most of the collected data came from nutritional experiments in experimental (research) farms that did not record full lactation(s) or cows in late lactations. Therefore, the estimated breeding values were based on limited number of records per lactation and lactations per cow. Consequently, selection based on those breeding values would improve first lactation but not necessarily late lactations, similarly, as selection in early lactation cannot predict mid or late lactation (Liinamo et al., 2012; Li et al., 2018). Nowadays, with the development of technology, precision livestock farming has become possible. The CFIT system presented in this study is an example of this, allowing continuous recording of DMI and BW during the entire lactation period, including late lactations without disturbing the animal. Currently, DMI and BW phenotypes from 3D cameras are continuously collected in more than 20 farms in Denmark. However, this study is the first genetic study reporting heritability and correlations for DMI and BW in dairy cattle obtained by 3D cameras, and it aimed to establish the basis for future research on genetic analyses of new phenotyping methods in commercial farms. Recording more commercial farms and measuring a larger number of animals will allow us to estimate more accurate genetic parameters and breeding values for feed intake and feed efficiency. As we keep collecting data, we plan, in the future, to analyze DMI and BW per lactation week within parity using random regression to determine the variation across lactation weeks within parities, as several studies have pointed out the importance of consider this variation (Manzanilla-Pech et al., 2014b; Islam et al., 2020; Martin et al., 2021; Khanal et al., 2022). It would be beneficial to have complete lactation(s) data for all animals to accurately estimate residual covariances and correlations when calculating genetic and phenotypic correlations between parities. Furthermore, the CFIT system can potentially be used to measure other important traits related to health, behavior, and reproduction. An additional advantage of the CFIT system is that it allows the farmer access to the information in real time, which is crucial for on-time decision-making and problem solving in the production system. Schokker et al. (2022) has already discussed the benefits of a cloud solution including interactions among collaborators (e.g., animal and flexibility of computing power for preprocessing data or running statistical analyses).

CONCLUSIONS

This study's promising results endorse a new technique for recording feed intake and BW that is already in use on commercial farms. Our findings demonstrate that there is moderate heritability and genetic variation in DMI and BW phenotypes measured by 3D cameras. Moreover, estimated heritabilities and genetic correlations for both traits are similar to those reported using conventional measurement methods.

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