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Can wearable technology improve selection for fertility in New Zealand dairy cows?

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Introduction

Poor fertility can result in delayed calving, shortened lactation lengths, and reduced overall productivity. In fact, failure to conceive is responsible for 33.4% of total culls in New Zealand dairy herds (Kerslake *et al*., 2018).

In New Zealand's seasonal dairy system, the primary goal of reproductive management is to achieve high pregnancy rates shortly after the planned start of mating, to maintain a compact calving distribution for the following season (Xu *et al*., 1998). Pregnancy rate within the first 42 days of the herd's mating period (PR42) is the most important measure of fertility in this system, because it reflects both the inherent fertility of the cow and the effectiveness of heat detection and mating strategies (Xu and Burton, 2003). Herds with very similar genetics have large variation in PR42, highlighting the influence of farm management practices and importance of accurate heat detection and timely breeding decisions (Xu and Burton, 2003, Hemming *et al*., 2018).

Genetic improvement of fertility traits is constrained by their low heritability (i.e., < 0.05) (Harris *et al*., 2006; Jayawardana *et al*., 2023). This low heritability is largely due to the binary nature of these traits, meaning that most of the observed variation is caused by environmental and management factors. As a result, the reliability of fertility breeding values is limited (Veerkamp and Beerda, 2007; Sun *et al*., 2010).

The interval from calving to first ovulation based on milk progesterone has been identified has having significantly higher heritability than traditional reproductive traits, with reported heritabilities ranging from 0.12 to 0.33 (Royal *et al*., 2002; Häggman *et al*., 2019). The challenge to adopting genetic evaluation of this trait has been the difficulty and expense of collecting suitable phenotypes for routine use beyond research settings.

The interval from calving to first high activity (CFHA) is another alternative phenotype that can be developed from wearable sensor technologies. In 2023 16% of New Zealand farmers were using some kind of wearable technology (DairyNZ, 2023), and that proportion continues to increase. This trait has heritability estimates of 0.05 and 0.16 (Ismael *et al*., 2015; Heringstad and Wethal, 2023). Moreover, CFHA also has a strong genetic correlation with the interval from calving to first insemination (0.87 to 0.96), indicating that including CFHA in the genetic evaluation of female cow fertility could improve the effectiveness of selection (Ismael *et al*., 2015; Ismael *et al*., 2017). Therefore, the objective of this study is to investigate the genetic parameters and genetic correlation between CFHA generated from wearables and the traditional PR42 based on mating data in New Zealand dairy cow population.

Materials & Methods

Heat detection events were collected from the Livestock Improvement Corporation (LIC) database (MINDA). Heat detection alerts were available for 517 commercial herds from 5 different manufacturers (Halter®, NEW Zealand; DataMars Livestock, New Zealand;

CowManager®, Netherlands; Affimilk Ltd, Israel; Nedap, Groenlo, Netherlands). In total, there were 1,792,585 heat alerts available for 346,007 cows between October 2021 to January 2025. Duplicate events were removed. Only heat alerts between 16 to 100 d postpartum, and records from cows in parities 1 to 3 were included. Calving dates were used to define CFHA as the number of days from calving to first heat alert. After editing, the final CFHA dataset included 167,303 records from 143,363 cows. PR42 was defined as a binary trait indicating whether a cow conceived within the first 42 d from the start of the mating period (coded as 1 for conception, 0 otherwise). These records were obtained from the Livestock Improvement Corporation (LIC) animal evaluation database. Cows with unknown sires were excluded from the analysis. The final dataset for PR42 comprised 1,445,436 records from 1,149,769 cows. The pedigree was built using a sire-dam structure, traced back 5 generations and include 4,621,116 animals.

Statistical analysis. All genetic analysis was performed using the average information REML algorithm in the APEX – Linear Model Suite statistical package. Bivariate analysis was performed to estimate variance components and heritability for each trait and genetic correlations between traits. The basic model was a repeatability animal model as follows:

$$\mathbf{y = X\beta + Za + Zpe + e} \quad (1)$$

where y is the vector of observations for each trait; β is the vector of fixed effects including the overall mean, herd-calving year-lactation contemporary group, calving week, heat detection supplier (CFHA), calving system (seasonal or split calving) for CFHA, age at calving standardized within lactation (PR42), fixed covariates of the pedigree inbreeding coefficient, breed proportions (Jersey, Holstein, Friesian, Ayrshire), heterosis effects (Friesian × Jersey, Friesian × Ayrshire, Friesian × Other, Friesian × Holstein, Jersey × Ayrshire, Jersey × Holstein, Ayrshire × Holstein), and genetic groups effects (2 genetic groups); **a** is the random additive genetic effect; **pe** is the vector of the random permanent environmental effect of the individual animal; **X** and **Z** are incidence matrices of the fixed and random effects of the vector of phenotypes y; and e is the random residual deviations of individual animals. The variance-covariance structure for the multi-trait model were:

$$\begin{bmatrix} a1 \\ a2 \end{bmatrix} \sim N \begin{bmatrix} A\sigma^2_{a1} & A\sigma_{a1,a2} \\ A\sigma_{a1,a2} & A\sigma^2_{a2} \end{bmatrix},$$

$$\begin{bmatrix} pe1 \\ pe2 \end{bmatrix} \sim N \begin{bmatrix} I\sigma^2_{pe1} & I\sigma_{pe1,pe2} \\ I\sigma_{pe1,pe2} & I\sigma^2_{pe2} \end{bmatrix},$$

$$\begin{bmatrix} e1 \\ e2 \end{bmatrix} \sim N \begin{bmatrix} I\sigma^2_{e1} & I\sigma_{e1,e2} \\ I\sigma_{e1,e2} & I\sigma^2_{e2} \end{bmatrix} \quad (2)$$

Where a1 and a2 represents the breeding values for CFHA, PR42; σ^2_{a1} and σ^2_{a2} represents the additive genetic variances for CFHA and PR42, $\sigma_{a1,a2}$ represents the additive genetic covariances among traits; pe1 and pe2 represents the permanent environmental effects for each trait; σ^2_{pe1} and σ^2_{pe2} represents the permanent environmental variance for each trait, $\sigma_{pe1,pe2}$ represents the permanent environmental covariances among traits; e1 and e2 represents the residuals for each trait; σ^2_{e1}, σ^2_{e2} represents the residual variance for each trait and $\sigma_{e1,e2}$ represents the residual covariances among the traits.

Results & Discussion

Overall summary statistics for CFHA and PR42 are shown in Table 1. The mean interval from calving to first heat was 51.4 d, which is slightly higher than the average CFHA reported in previous studies with CFHA ranged between 44 d to 49.5 d in Danish Holstein population

(Løvendahl and Chagunda, 2009; Ismael *et al*., 2015). The average pregnancy rate at 42 d from the start of the herd's mating period (PR42) was 78%.

Table1. Number of sires, number of records, number of cows and the summary statistics of CFHA and PR42

Trait	No. of records	No. of cows	No. of sires	Mean	SD	Min	Max
CFHA[1]	167,303	143,363	3,647	51.43	21.45	16	100
PR42[2]	1,445,436	1,149,769	8,945	0.78	0.42	0	1

[1] CHFA= Interval from calving to first high activity.
[2] PR42= Cow pregnancy rate within the first 42 d of the herd's mating period.

The genetic parameters estimated for traits are shown in Table 2. The heritability for CFHA was 0.11, which was slightly lower than those obtained in previous studies (Løvendahl and Chagunda, 2009; Ismael *et al*., 2015), where the heritability of CFHA ranged between 0.14 and 0.18. Heritability estimates for PR42 in the present study were very low (0.027) and consistent with the previously reported estimates for PR42 (Jayawardana *et al*., 2023). The higher heritability for CFHA compared to PR42 indicates that the trait is less affected by environmental factors and management decisions than PR42.
The phenotypic correlation between CFHA and PR42 was weak (rp = -0.09), but the genetic correlation was strong and negative (rg = -0.64), indicating that cows with shorter interval from calving to first estrus are more likely to conceive within 6-weeks of the start of the breeding period. It also means that selection for shorter CFHA would indirectly improve PR42 in dairy cows. Previous studies reported similar relationship between the interval from calving to first service (CFS) (i.e., a proxy of the time from calving to first estrus). For example, Jayawardana *et al*. (2023) reported a genetic correlation of -0.14 between the interval from calving to first service (CFS) and PR42 in New Zealand dairy cattle. The current findings indicate that including CFHA in addition to PR42 in a breeding program would increase the genetic gain for PR42. There is also an advantage in the timing of the phenotype collection, with CFHA available as heats occur, whilst PR42 is not confirmed until calving. Furthermore, the data from wearables could be used to study other traits such as the number pre-mating heats, or inter-estrus intervals which are not currently measured in all breeding programs.

Table 2. Additive genetic variance (σ_a^2) permanent environmental variance (σ_{pe}^2), residual variance (σ_e^2), heritability (h^2), genetic correlations between traits (*rg*) and phenotypic correlations between traits (*rp*).

Trait	σ_a^2	σ_{pe}^2	σ_e^2	h^2	*rg*	*rp*
CFHA[1]	31.56	33.13	217.2	0.11 (0.005)	-0.64 (0.02)	-0.09
PR42[2]	0.004	0.012	0.14	0.027 (0.001)		

[1] CHFA= Interval from calving to first high activity.
[2] PR42= Cow pregnancy rate within the first 42 d of the herd's mating period.
$h^2 = \sigma_a^2 / (\sigma_a^2 + \sigma_{pe}^2 + \sigma_e^2)$

Conclusions

Data from wearables could be used to develop fertility indicator traits that are less affected by environmental and management factors. Estimated heritabilities for CFHA were significantly higher than traditional fertility measures. The high heritability of CFHA and the strong genetic correlation with PR42 in the current study suggest that CFHA should be included in the current animal evaluation for fertility in New Zealand.

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References
Dairy N.Z. 2023. Available at: https://www.dairynz.co.nz/media/55lbd2cw/technology-survey-report-2023-v51.pdf , visited on: 23/01/2026.
Häggman J., Christensen J.M., Mäntysaari E.A., *et al*. (2019) Animal 13:248–255. https://doi:10.1017/S1751731118001386
Harris B. L., Pryce J.E., Xu Z.Z., *et al*. (2006) In: Proc. N.Z. Soc. Anim. Prod., Napier. p.107–112.
Hemming N.V., McNaughton, L.R., and Couldrey C. (2018) In: Proc. N.Z. Soc. Anim. Prod, Lincoln. p.170–172.
Heringstad B., and Wethal K.B. (2023). JDS Communications. 4:99–100. https://doi.org/10.3168/jdsc.2022-0251
Ismael A., Løvendahl P., Fogh A., *et al*. (2017) J. Dairy Sci. 100:8188–8196. https://doi:10.3168/jds.2017-13122
Ismael A., Strandberg E., Kargo M., *et al*. (2015) J. Dairy Sci. 98:3470–3477. https://doi:10.3168/jds.2014-8940
Jayawardana J., Lopez-Villalobos N., Hickson, R.E., *et al*. (2023) J. Dairy Sci. 106:364–380. https://doi.org/10.3168/jds.2022-22053
Kerslake J. I., Amer P.R., O'Neill P.L., *et al*. (2018) J. Dairy Sci. 101:1795–1803. https://doi:10.3168/jds.2017-13124
Løvendahl P., and Chagunda M.G.G. (2009) J. Dairy Sci. 92:4683–4688. https://doi.org/10.3168/jds.2008-1736
Royal M. D., Flint A.P.F., and Woolliams J.A. (2002) J. Dairy Sci. 85:958–967. https://doi.org/10.3168/jds.S0022-0302(02)74155-6
Sun C., Madsen P., Lund M.S., *et al*. (2010) J. Anim. Sci. 88:871–878 https://doi:10.2527/jas.2009-1912
Veerkamp R. F., and Beerda B. (2007) Theriogenology. 68, Supple:S266–S273. https://doi.org/10.1016/j.theriogenology.2007.04.034
Xu Z. Z., and Burton L.J. (2003) Occas. Publ. LIC, Hamilton, New Zealand, pp. 4-33.
Xu Z. Z., McKnight D.J., Vishwanath R., *et al*. (1998) J. Dairy Sci. 81:2890–2896. https://doi.org/10.3168/jds.S0022-0302(98)75849-7