Assessing the impact of hormonal interventions on genetic evaluation of fertility in New Zealand

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Abstract

Reproductive efficiency is crucial for productivity and profitability in the New Zealand seasonal dairy system. It requires compact calving patterns to align lactation with pasture availability. Achieving a high 6-week in-calf rate is essential for maintaining a 365-day calving interval and optimising farm efficiency. Hormonal reproductive interventions are often being used to manage anoestrus cows, synchronise oestrus in cycling cows and heifers, and improve AI submission rates. Accurate genetic evaluation of fertility requires, therefore, reliable recording of hormonal synchronisation interventions. The aim of this study was to assess if the current level of reporting of fertility interventions is adequate for inclusion in the national genetic evaluation of cow fertility, and to evaluate alternative approaches for incorporating synchronisation information into genetic evaluation. After extensive data filtering requiring consistent synchrony reporting and herd continuity, a high-quality subset was created for variance component estimation. Adjusting fertility phenotypes for synchrony through either setting synchronised records to missing or applying a penalty substantially increased heritabilities, revealing additional additive genetic variation masked by intervention use. Synchronised cows consistently exhibited poorer fertility performance, with 1.5% lower 3-week submission rates and 11% lower 6-week in-calf rates compared to non-synchronised contemporaries. Use of synchronisation itself as a new trait showed heritability of 0.07–0.1, which is significantly higher than any fertility trait evaluated currently in New Zealand. Moderate to strong negative genetic correlations between synchrony use and fertility traits (ranging from -0.38 to -0.78) demonstrate that synchronisation captures biologically meaningful information about underlying reproductive merit. Overall, the study shows that intervention data can substantially improve fertility trait modelling and breeding value accuracy. However, only 7% of cows have treatment records available in recent years, which is not sufficient for implementation. Improved industry-wide synchrony recording is essential for integrating these findings into routine genetic evaluations.

Key words: fertility, genetic evaluation, dairy cows, reproductive interventions

Introduction

Dairy cow fertility has a major influence on farm production and profitability, particularly in seasonal grazing systems. In New Zealand, compact spring calving is needed to align lactation with pasture growth and helps minimise feed costs (Verkerk, 2003; Neal and Roche, 2019). In addition, maintaining a 365-day calving interval also requires cows to re-establish pregnancy within a maximum of 12 weeks. Mating season performance is commonly assessed using 3-week submission rate and 6-week in-calf rate, which correspond to fertility traits used in genetic evaluation (Stachowicz *et al*., 2023).

The current New Zealand fertility genetic evaluation includes heifer calving season day (CSD0 – number of days from planned start of calving to calving), presented for mating in the

first 21 days of the mating season (PM21 – binary, with 0 = not presented and 1 = presented), and pregnancy rate within the first 42 days of mating (PR42 – binary, with 0 = not pregnant and 1 = pregnant). PM21 and PR42 data from the first three parities are evaluated. The breeding value of PR42 is the only fertility trait included in the Breeding Worth Index (DairyNZ, 2026).

In New Zealand, anoestrus may affect a substantial proportion of lactating cows at the beginning of the breeding season, with estimates around 20% reported in earlier studies (Rhodes *et al*., 2003). The evaluated phenotypes are intended to capture genetic differences in fertility under comparable management conditions (Stachowicz *et al*., 2023). However, hormonal reproductive interventions are commonly used to treat cows that have not resumed cyclicity before mating, synchronise oestrus and/or ovulation in cycling animals, and improve early submission rates. As a result, these interventions can alter submission and pregnancy rate phenotypes by changing the timing of artificial insemination. If hormonal intervention records are unavailable for the genetic evaluation, phenotypes from treated cows introduce bias because the model effectively considers them as untreated animals.

The objective of this study was to assess whether the current level of reporting of fertility interventions is adequate for inclusion in the national genetic evaluation of cow fertility, and to evaluate alternative approaches for incorporating synchronisation information into fertility evaluation.

Materials and Methods

Data

Data for this study were derived from the national fertility genetic evaluation extracts combined with additional fertility treatment records provided by the Livestock Improvement Corporation (LIC). The hormonal treatment records were available from the LIC health treatment dataset, which contained records from 1997, although reporting increased substantially from the 2008–2010 seasons onward. Therefore, data from 2008 were included in this study. Treatment records were merged with pregnancy (PR42) and mating (PM21) phenotypes following the data pre-processing practice currently used in New Zealand for fertility genetic evaluation extracts.

A cow was marked as synchronised in a given season if she had a treatment record that included a fertility-related hormone product category and a health condition category recorded as Non-Cycling/Anoestrus. Fertility-related products included luteolytic hormones (e.g. prostaglandin), treatments associated with fixed-time insemination (e.g. CIDRs, DIBs and GnRH), and other reproductive hormones (e.g. FSH and oestradiol).

The full initial fertility genetic evaluation dataset for the 2008–2023 seasons contained 11.7 million cows from approximately 18,200 herds. For variance component estimation, multiple filtering steps were applied to ensure that included herds recorded calving and mating data in all seasons and the majority of cows had known parents in the pedigree. Herds were retained when synchronisation was reported in at least 6 of the 16 breeding seasons. This generated a dataset with synchronisation reporting levels closer to the rates reported by Laven *et al*. (2025).

The resulting filtered dataset contained 131,775 cows from 92 herds, representing approximately 1.1% of cows and 0.5% of herds in the full 2008–2023 genetic evaluation dataset. For further analyses, a random sample of 31,537 cows from 24 herds was used for variance component estimation. Within this random sample there were 1,150 sires represented. Results presented in this paper are based on this sample.

Alternative phenotype definitions

Three alternative definitions of PM21 and PR42 phenotypes were analysed. First, the current national genetic evaluation phenotype definitions were used. Second, phenotypes were set to missing when synchronisation was

reported. Third, records were penalised by setting PM21 and PR42 to 0 when synchronisation was reported. In addition, synchronisation use was analysed directly as binary phenotypes (0 = no, 1 = yes): PSYNC1, PSYNC2 and PSYNC3, indicating whether synchronisation was reported in parities 1, 2 and 3, respectively.

Variance components estimation models

Variance component estimation was carried out using ASReml 4.2 (Gilmour *et al*., 2023). Models were based on the current national fertility evaluation framework, with fixed effects for age at calving, contemporary group (herd-year), breed composition and heterosis. Seven-trait multivariate models were fitted including CSD0, PM21 and PR42 records from parity 1 to 3. Three variants were analysed: 1) the current definition of PM21 and PR42 phenotypes; 2) PM21 and PR42 phenotypes set to missing when synchronisation was reported; and 3) PM21 and PR42 phenotypes set to 0 when synchronisation was reported. Each parity was modelled as a separate trait, as in the current national fertility evaluation, and residuals between traits and parities were modelled as correlated.

Additionally, the 7-trait model (using the current definitions for PM21 and PR42) was expanded to a 10-trait model by adding synchronisation use (PSYNC) as three additional binary traits, one for each of parity. This model retained the current fertility trait definitions while allowing synchronisation use to be analysed as a correlated trait with CSD0, PM21 and PR42.

For EBV level comparisons data from bulls with at least 50 daughters with fertility and synchronisation phenotypes were used. There were 150 such sires available for analyses.

Results & Discussion

Data suitaility and phenotypic differences

The data quality assessment showed that reproductive intervention records were incomplete at the national level. Across all cows in the fertility extracts, 93% had no treatment records and 7% had between 1 and 44 treatments recorded per lactation. For stricter fertility treatment definitions based on health product and heath condition categories, only 1.7% of cows and 0.07% of heifers had synchronisation records. These percentages of hormonal treatment were lower than the expected level of intervention use reported by Laven *et al*. (2025).

According to these authors, 60% of New Zealand farmers used interventions, and 38% reported using them every year. Assuming representativeness of survey respondents, we can infer that in the dataset available for this study, hormonal interventions are very underreported, with only 10% of herds each year having any synchrony records. The subset of data created for variance component estimation had an average percentage of herds using synchrony of 70% (range 50-80% in 16 years), i.e. close to the value reported by Laven *et al*. (2025).

Laven *et al*. (2025) noted that approximately 20-30% of cows are not detected in oestrus before the start of the breeding season and may therefore be candidates for treatment. If 60% of farms use synchrony then we would expect treatment records for around 12-15% of cows on average. In the dataset used for variance component estimation, this average was 17% in lactation 1 and 2 and 13% in lactation 3. Therefore, the subset of data generated for variance component estimation seems to be of sufficient suitability.

Although individual level recording was inconsistent and incomplete, contemporary group (herd-year) level patterns indicated that after quality control data from 2008 to 2023 were suitable for exploratory analyses. The average percentage of cows with fertility

treatment records within reporting contemporary groups generally ranged from 15% to 25% in parities 1 and 2 and was slightly lower in parity 3. Heifer data were much less suitable for analysis because few contemporary groups contained usable on-farm intervention records.

The contrast between cow and heifer data was important. Heifer intervention records were too sparse to support reliable analysis, even though heifer synchronisation may be common for management purposes. The present analyses therefore focused on lactating cows, where reporting contemporary groups were numerous enough for exploratory work leading to a better understanding of bias due to fertility interventions. This distinction also means that the conclusions should not be extended directly to heifer fertility traits without improved heifer synchronisation recording by dairy producers.

The quality control strategy used created a dataset that resembled what was reported by Laven *et al*. (2025) and, therefore, suitable for variance component estimation, but it also highlighted a key implementation limitation. Herds retained for analysis were those with more consistent synchronisation recording, and therefore they were not expected to be a random sample of the population. Consequently, the subset was appropriate for testing whether synchronisation records contained useful information, but not sufficient by itself to support immediate national implementation, which requires consistent recording practices across producers.

Phenotypic comparisons showed that synchronised cows had poorer fertility performance than non-synchronised contemporaries (Table 1). In the filtered dataset, non-synchronised cows had higher average PM21 and PR42 phenotypes in parities 1-3. Differences between synchronised and non-synchronised cows were 0.02 to 0.08 for PM21 and 0.11 to 0.12 for PR42. This is consistent with reports of how treatment and synchronisation outcomes differ depending on cycling status and treatment protocol (McDougall, 2010).

Table 1: Average PM21 and PR42 phenotypes for synchronised and non-synchronised cows in the dataset filtered for synchrony reporting in at least 6 seasons

Trait	Non-synchro-nised	Synchro-nised	Difference
PM21, parity 1	0.86	0.84	0.03
PM21, parity 2	0.84	0.79	0.06
PM21, parity 3	0.86	0.78	0.08
PR42, parity 1	0.74	0.66	0.11
PR42, parity 2	0.74	0.65	0.12
PR42, parity 3	0.76	0.68	0.09

Phenotypic statistics of the dataset used for variance component estimation are presented in Table 2. Synchronisation was reported for 17% of cows in parities 1 and 2 and 13% in parity 3. The mean PM21 values were 0.84 to 0.86 across parities, while mean PR42 values were 0.74 to 0.76, indicating that the sampled dataset retained substantial variation in both submission and pregnancy phenotypes, respectively.

When PM21 and PR42 were set to missing due to synchronisation use being reported, the average PM21 changed only slightly, which indicates that similar proportion of synchronised cows was presented and not presented for mating in first 21 days of mating season (Table 2). The average PR42 increased by 2-4% after setting phenotypes of synchronised cows to missing. This indicates that cows that do not require synchronisation have better pregnancy rates than their synchronised contemporaries. On the other hand, a greater effect was observed applying the penalty approach, i.e. phenotype equal to zero, which resulted in PM21 and PR42 averages decreasing by 10-22% and 9-19%, respectively.

Table 2: Phenotypic means of data used for variance component estimation

Trait	Current pheno-type	Synchro-nised records set to missing	Synchro-nised records penalised
PM21, parity 1	0.86	0.86	0.72
PM21, parity 2	0.84	0.85	0.70
PM21, parity 3	0.86	0.86	0.75
PR42, parity 1	0.74	0.76	0.61
PR42, parity 2	0.74	0.76	0.61
PR42, parity 3	0.76	0.77	0.66

Seven-trait model variants for synchronisation adjustment

Heritabilities of PM21 and PR42 were lower than in the official national fertility evaluation, indicating that the subset was not fully representative of the national population. However, when PM21 and PR42 phenotypes were set to missing or penalised, heritabilities slightly increased and were 0.036-0.042 for PM21 and 0.033-0.045 for PR42 (Table 3). Penalising synchronised phenotypes resulted in the largest increase, with estimates approximately doubling for PM21 and PR42 in the 7-trait model (previously 0.07-0.088 for PM21 and 0.049-0.082 for PR42). These results indicate that penalising synchronised cows allows capturing more of the additive genetic variation in fertility phenotypes. Thus, proper recording of synchronisation would further lead to more accurate estimated breeding values for fertility and faster genetic progress for those traits.

Estimated genetic correlations among the seven fertility traits also changed when synchronised PM21 and PR42 records were penalised (Table 4). Genetic correlations between CSD0 and PM21 or PR42 became less negative in the penalised variant than in the current model. In contrast, correlations within and between the PM21 and PR42 trait groups increased when synchronised cows were penalised. For example, the correlation between first parity PM21 and PR42 increased from 0.71 to 0.81. This indicates that the penalised phenotype strengthened the genetic relationship between submission and pregnancy traits across parities, consistent with synchronisation records identifying cows with poorer underlying fertility performance. This might not be a desirable outcome as PM21 and PR42 represent different aspects of cows' fertility.

Ten-trait model with synchronisation trait

Synchronisation use itself had a measurable genetic component. In the 10-trait model, heritabilities for synchronisation use were 0.099, 0.078 and 0.057 for parities 1, 2 and 3, respectively (Table 5). These were higher than estimates for the individual fertility traits analysed in the same dataset indicating that synchronisation use contains important additive genetic signal that are relevant to fertility evaluation. Heritability of synchronisation use decreased from parity 1 to parity 3, from 0.099 to 0.057, indicating that the genetic variability captured by synchronisation use was greatest in first parity and declined across later parities.

Genetic correlations between synchronisation use and CSD0 were low and positive in all three parities (Table 5). Moreover, they were consistently negative with PM21 and PR42, with parity specific estimates

Table 3: Heritability estimates for the current 7-trait model and alternative phenotypes adjusted for synchronisation

Trait	Current phen-otype	Synchro-nised records set to missing	Synchro-nised records penalised
PM21, parity 1	0.022	0.038	0.085
PM21, parity 2	0.023	0.042	0.088
PM21, parity 3	0.025	0.036	0.070
PR42, parity 1	0.031	0.045	0.082
PR42, parity 2	0.027	0.033	0.070
PR42, parity 3	0.031	0.033	0.049

Table 4: Genetic correlations from 7-trait model variants. Current model correlations are above the diagonal; penalty-based model correlations are below the diagonal

Trait	CSD0	PM21 P1	PM21 P2	PM21 P3	PR42 P1	PR42 P2	PR42 P3
CSD0		-0.42	-0.32	-0.22	-0.50	-0.27	-0.14
PM21 P1	-0.31		0.62	0.55	0.71	0.59	0.20
PM21 P2	-0.26	0.88		0.57	0.94	0.75	0.54
PM21 P3	-0.10	0.80	0.86		0.40	0.48	0.24
PR42 P1	-0.37	0.81	0.86	0.71		0.67	0.50
PR42 P2	-0.31	0.84	0.79	0.80	0.90		0.53
PR42 P3	-0.04	0.62	0.72	0.62	0.80	0.83	

of -0.60, -0.78 and -0.61 between PSYNC and PM21, and -0.61, -0.62 and -0.43 between PSYNC and PR42 in parities 1, 2 and 3, respectively. These results indicate that cows with greater genetic propensity for synchronisation use tend to have lower genetic merit for submission and pregnancy rate traits, further supporting the need for proper recording of fertility interventions and their incorporation in the national fertility evaluation.

Using synchronisation as an additional correlated trait may be more practical under incomplete recording than directly adjusting PM21 or PR42 phenotypes. The 10-trait model retained the current fertility phenotypes while allowing synchronisation use to contribute correlated information. This approach avoids assigning an automatic missing or penalty to all synchronised cows, while still allowing the evaluation to use information from recorded interventions.

Table 5: Synchronisation trait heritabilities and parity specific genetic correlations with fertility traits in the 10-trait model

Estimate	Parity 1	Parity 2	Parity 3
Heritability of PSYNC	0.099	0.078	0.057
Genetic correlation: PSYNC with CSD0	0.17	0.22	0.08
Genetic correlation: PSYNC with PM21	-0.60	-0.78	-0.61
Genetic correlation: PSYNC with PR42	-0.61	-0.62	-0.43

A remaining interpretation issue is that synchronisation records do not always identify why an intervention was carried out. Treatment of anoestrous cows, synchronisation of cycling cows for compact mating, and heifer synchronisation for management efficiency may have different implications for genetic evaluation. Future recording systems would therefore need to distinguish intervention purpose, timing and animal physiological status as far as practical.

Overall, the results support the value of synchronisation data for understanding fertility phenotypes but also show that recording quality and consistency are the main barriers to implementation. Improvements in consistent herd-season reporting, sufficient coverage within contemporary groups, and clear definitions of treatment categories are needed before intervention records could be incorporated routinely into national evaluations.

Sire EBV correlations

The sire-level EBV correlations provided an initial indication of how alternative ways of accounting for synchronisation might affect ranking. The correlation between current PR42 EBV and PR42 EBV from the model with synchronisation set to missing was 0.95, indicating little reranking. In contrast, the correlation between current PR42 EBV and PR42 EBV with synchronisation penalty was 0.87, leading to a greater degree of sire reranking when synchronised records were penalised.

Conclusions

This study showed that the current level of reporting of fertility interventions is not adequate for direct inclusion in the national genetic evaluation of cow fertility. Incomplete and inconsistent recording means that intervention information is not reliably available across herds and seasons, creating a source of potential bias in the evaluation because treated animals are effectively analysed as untreated since synchronisation use is ignored.

Among the trait definitions and models tested, the 7-trait model with synchronised PM21 and PR42 records penalised, and the 10-trait model including synchronisation use as an additional correlated trait, appear to be the most suitable approaches for further exploration. The penalty approach captured additional additive genetic variation in fertility phenotypes, while the 10-trait model retained the current fertility definitions and used synchronisation as correlated information.

The next step should be a validation study to quantify the effect of unrecorded or unused fertility intervention information on the current evaluation. This should include assessment of recording completeness across herds and seasons, minimum data requirements for reliable use, sire re-ranking under alternative models, and separation of interventions used for poor fertility from those used for management convenience. Longer term work should focus on improving industry-wide recording standards and assessing whether synchronisation information, including the development of a synchronisation use (PSYNC) EBV and the estimation of all hormonal intervention costs, could be incorporated into the National Breeding Objective or a fertility sub-index.

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