Predicting the likelihood of conception to first insemination using milk mid-infrared spectroscopy: a model for FOSS instrument

P.N. Ho[1], A.J. Chamberlain[1,2], M. Haile-Mariam[1,2] and J.E. Pryce[1,2]

[1]Agriculture Victoria, AgriBio, Centre for AgriBioscience,
Bundoora, Victoria 3083, Australia
[2]School of Applied Systems Biology, La Trobe University,
Bundoora, Victoria 3083, Australia
Corresponding Author: phuong.ho@agriculture.vic.gov.au

Abstract

An ability to predict the likelihood of conception of dairy cows in early lactation would help farmers make informed breeding decisions. Cows predicted to be most fertile, for instance, could be inseminated with sexed or high premium semen while those predicted to be least fertile could be mated with beef semen. Previously, we developed such a model using data from commercial milk testing, which included milk yield, milk composition (fat, protein, and lactose percentages), somatic cell count, calving age, days in milk, days from calving to first insemination, and milk mid-infrared (MIR) spectra generated from a Bentley instrument. The model shows a good prediction accuracy and has been implemented by Australian herd-test centres who provide reports to farmers. This study extended the analysis to FOSS instrument, which is the other major instrument used for MIR in Australia. Firstly, we tested if the previously developed Bentley model would be applied directly to spectral data obtained from a FOSS machine. Secondly, a new model trained specifically using FOSS MIR data was developed and evaluated. Finally, various genomic and phenotypic measures were compared for cows predicted to have most and least likelihood of conception compared to herd average. A total of 9,120 records of milk MIR spectra, milk yield, milk composition, somatic cell count, calving age, days in milk and days from calving to first insemination of 3,518 cows from 31 dairy herds were used. The new model was developed in the same way as the Bentley model which included initial training on "extreme data" and then validating against field data. Specifically, the "extreme data" only include cows that conceived to first insemination ("good") and cows with no conception event recorded and had only one insemination ("poor"), whereas field data include all cows in the herd. The model performance was evaluated by first ranking the cows within a herd for their predicted likelihood of conception and then selecting the top and bottom 10% of records and compared to actual values. The accuracy was measured as the proportion of selected records being correct. When applying the Bentley model to FOSS data, the prediction accuracies of identifying the top and bottom 10% of cows were around 0.37 and 0.62, respectively. Such a poor prediction accuracy using the Bentley model implies the need to develop a separate model for FOSS. The new model was able to achieve an accuracy of around 0.53 and 0.77 when used to identify the top and bottom 10%, respectively, which is comparable to the published Bentley model. It could also correctly identify the top 10% of cows conceiving following two inseminations with an accuracy of 0.70. Compared to herd average, the top 10% of cows ranked by the model were significantly younger and had lower somatic cell cows while the opposite pattern was observed for cows in the bottom 10%. Interestingly, there was no significant differences in 305-day milk yield, milk composition, days from calving to first insemination, days in milk, and other breeding values and national selection indices. In conclusion, a model

for predicting the likelihood of conception to first insemination of Australian dairy cows using milk MIR spectra and other on-farm data has been developed and validated for further implementation for farmers who use FOSS instrument.

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Introduction

Along with genomic selection , numerous management tools have been developed to help farmers optimized their breeding decisions (Giordano *et al*., 2022). One important category of such models is those that aim to predict the potential outcome of insemination (Shahinfar *et al*., 2014, Hempstalk *et al*., 2015, Blavy *et al*., 2018, Ho and Pryce, 2020). The information used to develop these models vary from easy to obtain on-farm (e.g. milk production, milk composition, and milk mid-infrared (MIR) spectroscopy), to moderately easy to measure (e.g., milk progesterone) or comparatively difficult to measure (e.g., body weight and body condition score). In Australia, milk recording is routinely practiced by nearly half of Australian farmers with resulting data being utilized to support a range of management decisions such as culling or ending a cow's lactation (Newton *et al*., 2020). As such, the prediction models that make use of data from the current milk-testing program offer most advantage as this information is readily available on-farm. In 2019, Ho *et al*. (2019) developed a model for predicting the likelihood of a cow to get pregnant at first insemination with a good prediction accuracy (~0.76).

A potential application of this model is to rank cows within-herd for their probability of conception to subsequently prioritize them for insemination with different types of semen (sexed, beef or conventional semen). Newton *et al*. (2024) showed that MIR-fertility outperformed calving date when being applied to optimize semen allocation.

The model has been implemented by Australian herd-test centres who provide reports to farmers (DataGene, 2022). However, the current model is only available to farmers that have their milk tested with herd-test centres operating Bentley instrument, which means the other half of farmers who use FOSS instrument is missing (Peter Thurn, personal communication).

The major objective of this study was therefore to extend the analysis to FOSS instrument. First, the transferability of the current model trained using spectra generated by Bentley instruments was validated against data collected from FOSS brand. Then, a new model using FOSS MIR data was developed and evaluated. We also examined the differences in various genomic and phenotypic attributes between cows predicted to be most and least fertile compared to the herd average.

Materials and methods

Animal Data

All the data used for this study were obtained from DataGene (https://www.datagene.com.au/). Because the aim of this model is to predict how likely a cow is going to conceive to first insemination (i.e. a future event), only milk-testing records collected before the first insemination were retained. Accordingly, there were 9,120 records of insemination, calving date, days in milk (DIM) at herd-test, days from calving to first insemination (DAI), age at calving, herd-test day milk yield (MY), fat, protein, and lactose percentages, somatic cell count (SCC), and MIR spectra, from 3,518 cows of 31 commercial herds. The data were collected in the years of 2021 (n = 1,032) and 2022 (n = 7,989). Other information was also available on these cows, including 305-d milk yield, Banlance Performance Index (BPI), Health Weighted Index (HWI), and breeding values of milk, fat, protein, SCC and daughter fertility.

The cows were milked twice daily with milk samples (either a.m. or p.m.) being sent to the National Herd Development Co-Op Ltd (Cohuna, Victoria, Australia) and Dairy Express (Armidale, New South Wales, Australia) to be analyzed for fat, protein, and lactose concentrations and SCC using the MilkoScan FT+ spectrometer (Foss, Hillerød, Denmark). The corresponding spectra from the milk composition analysis were obtained for this study.

Data processing

The pregnancy was confirmed by a calving event in the subsequent lactation and was coded binarily as 1 (pregnant) or 0 (open). In addition, the inseminations that resulted in abortions were removed. Prior to modelling, several mathematical treatments were applied to the raw spectra. First, the spectral regions previously specified to be noisy or non-informative (regions between 1,710 and 1,600 cm−1, between 3,690 and 2,990 cm−1, and >3,822 cm−1) caused by a high-water absorption were eliminated, which led to 531 wavenumbers remained. Thereafter, a global Mahalanobis distance (GH) between each spectrum and the population average was calculated as an indicator of potential outliers. The spectra with GH > 3 were assumed to be outliers and excluded (n = 50). Lastly, first-order Saviztky–Golay derivative was applied to the reduced spectra. The final dataset included 9,070 records from 3,498 cows of 31 herds to be used for future analyses.

Model development and evaluation of performance

In the first scenario, we tested the transferability of the current Bentley model on the spectra generated from a FOSS instrument This was done by first matching each FOSS MIR wavenumber to the closest one generated from a Bentley machine. Then, the current Bentley model was applied directly to these spectra and other predictors including milk yield, milk composition, DIM, calving age, DAI, and SCC to derive predictions.

The second scenario included training and evaluating a new model specific to FOSS instrument, using the methodology described in Ho and Pryce (2020). Briefly, the model was first trained using only data from cows that conceived to first insemination (coded as 1) and cows with no conception event recorded and with only 1 insemination (coded as 0). A fresh dataset with all cow's data regardless of the conception statuses was used to test the ability of this newly developed model for identifying cows that conceived or did not conceive to first insemination. To do this, we first extracted the probability of conception from the model and used this to rank cows within each herd from highest to lowest (i.e. most and least fertile). Next, varying proportions of records from 5 to 40% were selected and validated against the actual observations.

In both scenarios, the model performance was evaluated as the proportion of selected records to be truly predicted. For example, if the purpose is to predict 10% of least fertile cows (i.e. potentially fail to get pregnant to first insemination) from a herd of 1000 cows, 100 of these will be selected from the bottom of the predicted list and compared with the actual values. The performance in this case will be calculated as the proportion of cows being non-pregnant over 100. For the scope of this study, we only reports the prediction accuracy obtained from the external herd-by-herd validation, which has been concluded to provide realistic performance compared to random cross-validation (Wang and Bovenhuis, 2019). In this validation approach, for each round, data of a given herd was excluded to be subsequently used as a validation set against the model trained using the data of the remaining herds (i.e. 30 herds), and this process was continued until all herds have been validated once.

Finally, to further understand the model's behaviour, we extracted and compared various genomic and phenotypic characteristics of cows ranked as top and bottom 10% in comparison to the herd average. The comparisons were done using 1-way ANOVA tests with pairwise comparisons. All analyses in this study were performed using R statistical software version 3.6.1 (R Development Core Team, 2020).

Results and discussion

When applying the Bentley model directly to the FOSS data, regardless of the proportions selected, the prediction accuracies for all three categories (conceived to first insemination, conceived following two inseminations, and open to first insemination) were around 0.37, 0.49, and 0.62, respectively (Tabe 1). The corresponding figures of model performance reported by Ho and Pryce (2020) were 0.48, 0.76 and 0.69. The poor performance obtained in the current study implies the need to develop a separate model for farmers that milk-test their herds with herd-test centres operating FOSS instrument.

On the new model, good performance was obtained and the results were comparable with that of Bentley model (Ho and Pryce, 2020). The prediction accuracies of the model to rank and identify cows that conceived to first and second insemination, and cows not conceived to first insemination ranged between 0.49–0.54, 0.66–0.72, and 0.75–0.81, respectively. Also, the higher the selected proportions, the lower the model performance. However, the prediction accuracies of this FOSS model were considerably variable (the standard deviation of around 0.20) indicating that more data is needed to improve the robustness of the model, as also concluded by Pralle and White (2020).

To further understand the model's behaviour, we examined various phenotypic and genomic features of cows that were predicted to be high and low fertility compared to the herd average. This is an important step as it gives farmers confidence in using

Table 1. Accuracy of models (mean ± standard deviation) for identifying cows with good likelihood of conception to first and second insemination and cows with poor likelihood of conception to first insemination.

Proportions	Cows with good likelihood of conception at first insemination	Cows with good likelihood of conception at second insemination	Cows with poor likelihood of conception at first insemination
Scenario 1: Bentley model applied to FOSS data			
5	0.31 ± 0.34	0.39 ± 0.36	0.59 ± 0.29
10	0.31 ± 0.32	0.40 ± 0.35	0.58 ± 0.26
15	0.32 ± 0.32	0.41 ± 0.35	0.56 ± 0.24
20	0.32 ± 0.32	0.41 ± 0.35	0.55 ± 0.24
25	0.32 ± 0.32	0.41 ± 0.35	0.54 ± 0.24
30	0.32 ± 0.32	0.41 ± 0.35	0.54 ± 0.23
Scenario 2: new FOSS model			
5	0.54 ± 0.25	0.72 ± 0.21	0.81 ± 0.27
10	0.52 ± 0.20	0.68 ± 0.18	0.77 ± 0.26
15	0.49 ± 0.21	0.68 ± 0.16	0.76 ± 0.23
20	0.49 ± 0.20	0.67 ± 0.17	0.76 ± 0.20
25	0.48 ± 0.19	0.66 ± 0.16	0.76 ± 0.22
30	0.49 ± 0.13	0.66 ± 0.14	0.75 ± 0.23

Table 2. Mean and standard deviation of genomic and phenotypic traits for predicted high fertility subgroup, herd-average, and predicted low fertility subgroups.*

	Top 10%	Herd average	Bottom 10%
MY305 (kg)	6,548 ± 1,270	6,880 ± 1,355	7,107 ± 1,427
Fat percent	3.95 ± 0.51	4.00 ± 0.43	4.05 ± 0.53
Protein percent	3.27 ± 0.28	3.22 ± 0.26	3.20 ± 0.36
SCC	63.7 ± 49.3^{a}	164.5 ± 103.3^{b}	676.4 ± 716.5^{c}
MY24 (kg)	24.0 ± 4.2^{a}	27.2 ± 4.5^{b}	27.5 ± 6.1^{b}
DIM	47.2 ± 26.6^{a}	55.6 ± 21.6^{b}	66.7 ± 28.4^{b}
Calving age (month)	32.3 ± 8.9^{a}	49.9 ± 10.1^{b}	77.1 ± 20.3^{c}
Calving to first AI	95.5 ± 22.8^{a}	108.9 ± 29.3^{ab}	124.7 ± 39.5^{b}
Conception to first AI	0.47 ± 0.19^{a}	0.40 ± 0.16^{a}	0.23 ± 0.22^{b}
BPI	157 ± 100	152 ± 66	136 ± 69
HWI	161 ± 99	154 ± 64	133 ± 55
ABV_{milk}	58.2 ± 161	73.1 ± 64	74 ± 242
ABV_{fat}	11.1 ± 12.1	12.1 ± 7.5	12.3 ± 9.3
$ABV_{protein}$	7.2 ± 5.6	7.2 ± 5.1	6.9 ± 7.3
ABV_{scc}	129.8 ± 19.4	126.7 ± 12.1	122.2 ± 10.1
$ABV_{daughter\_fertility}$	104.1 ± 3.3	103.6 ± 2.5	102.8 ± 2.5

[*] The results are similar for other selected proportions (i.e. 5%, 15%, 20%, 25%, and 30%), only those that obtained when 10% of records were selected being presented here.

MY305 = 305d milk yield (kg), SCC = somatic cell count, MY24 = 24 hours milk yield on the herd-test day (kg), DIM = days in milk at herd-test, BPI = Balance Performance Index, HWI = Health Weighted Index.

the model to make breeding and management decisions. For example, in conjunction with BPI or daughter fertility, the cows predicted to have high likelihood of conception could be inseminated with sexed or premium semen. In this context, it is essential to make sure that the fertile cows are not the low milk producers. Because the results are similar when other proportions of cows being selected, we only present here the statistics for the top and bottom 10% of cows selected to compare with that of herd average. In general, the results were similar to our previous analysis on the Bentley model (Bird *et al*., 2023). Compared to the herd average, cows predicted to be most fertile by the model were significantly younger and had a lower somatic cell count while the opposite patterns were observed for cows that were predicted to be least fertile. These results might partially explain for the higher conception rate to first insemination of the top-ranking cows compared to herd average and bottom-ranking individuals (0.47, 0.40, and 0.23, respectively). Numerous previous publications have reported the negative association between the cow's age as well as SCC and their health and reproductive performance (Lomander *et al*., 2013, Golder *et al*., 2021). Interestingly, while 24-hrs milk yield was significantly between the three groups, MY305 were not, which would be explained by the difference in DIM, i.e. predicted fertile cows were milked earlier while the infertile cows were milked later than all cows within the herd (47.2, 66.7 versus 55.6, respectively). In addition, predicted high fertility cows had a decreased calving to first insemination interval compared to the herd average and low fertility cows (Table 2). This is highly desirable especially in the pasture-based and seasonal calving system, for example, in Australia, because this allows farmers to match the cow's high energy requirements in early lactation to the peak pasture growth rate (Shalloo *et al*., 2014).

While there were no statistically significant differences between the three groups regarding the genomic features, it is interesting to note that the cows predicted to be most fertile had higher BPI and daughter fertility breeding values. These results are consistent with the previous analysis of Bird *et al*. (2023).

Conclusions

This study shows that the MIR-fertility prediction model developed using data from a Bentley instrument could not be transferred directly to the spectra generated from a FOSS instrument. Further, we have successfully developed a new model specific to FOSS instrument with good prediction accuracy. However, more data is needed to improve the robustness of the model.

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