Breeding for Reproductive Traits - Dairy

ATTRIBUTES OF LACTATING COWS RANKED DIVERGENTLY FOR FERTILITY USING A MILK MID-INFRARED SPECTROSCOPY BASED PREDICTION MODEL

A.R. Bird¹, J.E. Newton² and P.N. Ho²

¹ University of Melbourne, Parkville, Victoria 3052, Australia
 ² Agriculture Victoria, AgriBio, Centre for AgriBioscience, Bundoora, Victoria 3083, Australia

SUMMARY

Predicting the fertility of dairy cows is a powerful tool for the dairy sector, giving farmers more confidence in making breeding and culling decisions. This study aimed to determine how animals ranked as high probability of conception to first insemination by a previously published model (i.e., MIR fertility model) differed from that of low-ranking individuals for various phenotypic and genotypic traits.

Data including MIR spectral data, herd test data, and genotypic breeding values were obtained for 18,831 cows located in Australia. Cows were ranked based on the probability of conception estimated by the MIR fertility model, and subsets of animals were created from the top and bottom 10% of animals. The mean values for phenotypic and genotypic traits of each group were compared using two-way t-tests. High MIR-predicted fertility (MFERT) cows were found to have significantly better reproductive performance and reduced somatic cell counts. High MFERT animals were found to have lower 305-day milk, fat, and protein yields compared to average, but this difference was reduced by correcting for parity. Conversely, high MFERT cows had higher milk production ABVs compared to average. Finally, high MFERT cows showed improved balanced performance index and health weighted index scores compared to the data average, and the low MFERT cows. Future studies should investigate how high and low MFERT cows differ in terms of other health traits, and how the model performs in conjunction with other breeding and management tools.

INTRODUCTION

Historical selection for milk production has resulted in poor fertility among the Australian dairy herd, with factors such as nutritional subfertility, where a cow must dedicate her energy resources either to her current calf through milk production or her future calf by maintaining body condition, as one of the possible contributors (Friggens *et al.* 2010). Whilst genetic selection has allowed for improvement in fertility, predicting the likelihood of pregnancy early on in the joining period would be helpful for farmers in making informed breeding decisions. Ho *et al.* (2019) developed an MIR model as a means of predicting an animal's likelihood of conception to first insemination. To offer more insight into the predicted outcomes of using the MIR model, this study aimed to determine the phenotypic and genotypic differences between animals with a high likelihood of conception.

MATERIALS AND METHODS

Data collection. Data from 18,831 cows, collected between 2016 and 2020, from 50 farms in Victoria, Tasmania, and New South Wales were obtained from DataGene (Bundoora, Victoria, Australia). Herd size ranged from 69 to 1,217 head. Breed proportions were 59.80% Holstein, 4.88% Jersey, and 35.32% other breeds. Data included milk production parameters from 1st herd test after calving and 305-day cumulative lactation estimates, calving age, calving to first AI interval, calving date, pregnancy outcomes and date of birth, BPI, HWI, and Australian breeding values (ABVs) for milk production traits, overall type, condition score, survival, calving ease, somatic cell count, daughter fertility, feed saved, heat tolerance, and gestation length. MIR spectral data were obtained

directly from herd test centres. For animals with multiple previous lactations prior to the insemination event, data from the first record were used.

Data analysis. The MIR fertility model uses MIR spectral data and other herd testing data to derive a fertility prediction (pMIR) for each cow. Further details of this model have been described by Ho et al. (2019), but briefly, a training population of cows were categorised as having good or poor fertility based on whether they conceived to their first insemination. This training population was then used to train the model using partial least squares discriminant analysis. The model was used to assign the pMIR values. Data were split into 96 herd-year groupings to minimise the potential effects of environmental and management factors. Within each herd-year, cows were ranked on pMIR, and the most fertile top 5, 10, or 20% of animals and least fertile, bottom 5, 10, and 20% of animals were placed in subgroups. The mean and standard deviations of the ABVs, indices and phenotypic traits for each of the subgroups, as well as the overall dataset were calculated. To compare potential biological differences between cows predicted to have poor and good fertility, two-way t-tests were conducted in R (R Core Team 2021) between the top subgroups and the average, the bottom subgroups and the average, and the top and bottom subgroups. Results with a p-value of less than 0.05 were deemed statistically significant. Similar differences between the high fertility and low fertility animals were seen regardless of what proportion of the population was selected. Therefore, data for the top and bottom 10% of animals are presented here, as this proportion has the highest prediction accuracy (Ho and Pryce 2020).

RESULTS AND DISCUSSION

This study found that groups of dairy cows predicted as having a high likelihood of conception by the MIR fertility model (high MFERT) differed from animals predicted as having a low likelihood of conception (low MFERT) on several traits.

Relationship between MIR fertility ranking and phenotypic performance. High MFERT animals had significantly higher mean pregnancy rates compared to the population average whereas low MFERT cows had significantly lower mean pregnancy rates (Table 1), indicating that high MFERT cows had a higher chance of reproductive success. This is consistent with the findings of Ho *et al.* (2019) when the model was first developed and tested. High MFERT cows also had decreased calving to first and second AI intervals compared to the average (Table 1). This is highly desirable in a seasonal production system as these traits allow cows to become pregnant early in the joining season and subsequently calve early in the season (Berry *et al.* 2013).

Table 1.	Mean and	l standard o	leviation of	phenotypi	c traits re	lated to t	fertility for	high Ml	FERT
subgrou	p, average	e (all anima	ls) and low	MFERT s	ubgroup				

	High	Average	Low
Pregnant after joining period rate	$0.84\pm0.37^{\rm a}$	$0.75\pm0.43^{\rm b}$	$0.53\pm0.5^{\circ}$
Pregnant after 1st AI rate	$0.48\pm0.5^{\rm a}$	$0.42\pm0.49^{\rm b}$	$0.30\pm0.46^{\circ}$
Pregnant after 2nd AI rate	$0.71\pm0.46^{\rm a}$	$0.63\pm0.48^{\rm b}$	$0.43\pm0.5^{\circ}$
Calving to first AI interval (days)	$81.46\pm26.05^{\rm a}$	$93.68\pm49.93^{\mathrm{b}}$	$114.72\pm82.8^{\rm c}$
Calving to last AI interval (days)	$125.1\pm90.04^{\rm a}$	$143.46 \pm 105.53^{\text{b}}$	$163.29\pm122.4^{\circ}$

a,b,c denotes where means are significantly different (P<0.05)

Low MFERT cows had a significantly elevated SCC (774,640 \pm 1,560,500 cells/mL, P<0.001) compared to the average (176,840 \pm 594,300 cells/mL), whereas high MFERT cows had a significantly lower SCC (56,890 \pm 83,700, P<0.001). Lomander *et al.* (2013) reported an increased calving to first AI interval of cows with high SCC compared to their contemporaries, corresponding with the findings above.

Breeding for Reproductive Traits - Dairy

There was no significant difference between the 305-day milk, and milk fat and protein yields for low MFERT cows and the average, whereas high MFERT animals had a significantly lower 305day yield compared to the data average. However, these differences were no longer significant after correcting the data for parity.

Table 2. Mean and standard deviation of phenotypic traits related to milk production for	high
MFERT subgroup, average and low MFERT subgroups	

	High	Average	Low	
305-day milk yield (litres)	$6304.6\pm 2007.8^{\rm a}$	6794.3 ± 2138.0^{ab}	7094.7 ± 2122.9^{b}	
305-day fat yield (kg)	$256.1\pm73.8^{\rm a}$	270.06 ± 80.05^{ab}	$282.84 \pm 81.36^{\rm b}$	
305-day protein yield (kg)	$220.1\pm67.4^{\rm a}$	$231.6\pm70.6^{\rm ab}$	$238.5\pm69.0^{\mathrm{b}}$	
a = b = denotes where means are significantly different ($r < 0.05$)				

a,b,c denotes where means are significantly different (p < 0.05)

Relationship between MIR fertility ranking and genetic merit. Apart from comparing the phenotypic performance of high versus low MFERT cows, we also analysed how genetic merit differed. There was no significant difference in daughter fertility ABV in any of the subgroups, which may be due to the low heritability of fertility (Tenghe *et al.* 2015). However, high MFERT cows were found to have a significantly lower gestation length ABV (-0.84 \pm 2.24, P<0.05) than average (-0.55 \pm 2.28), and low MFERT animals had a higher gestation length ABV (-0.16 \pm 2.19, P<0.001) compared to the average. The gestation length BV has been shown to be correlated with rate of conception to first AI (Vieira-Neto *et al.* 2017), which was the value being predicted by the MIR fertility model.

High MFERT cows were shown to have a significantly increased SCC ABV (119.9 \pm 16.85, P<0.001) compared to average (115.3 \pm 17.99), whereas low MFERT cows had a significantly lower SCC ABV (107.73 \pm 17.11, P<0.001) than average, consistent with the phenotypic SCC values presented above. Favourable genetic relationships have been previously shown between SCC and various fertility traits, including calving interval and days to first service (Wall *et al.* 2003), which are closely related to rate of conception to first AI.

High MFERT cows were found to have significantly higher production ABVs compared to average, whereas low MFERT cows had significantly lower production values compared to average (Table 3). This demonstrates genetic potential for the high MFERT cows to produce a high quality and quantity of milk, which further demonstrates that the phenotypic differences in production presented above are more likely the result of differences in parity. The ASI, which combines protein, fat, and milk yield ABVs based on their economic value, was also included in the analysis. High MFERT cows in were found to have a significantly higher ASI than the average, whereas low MFERT cows had a significantly lower ASI.

 Table 3. Mean and standard deviation of breeding values related to milk production for high

 MFERT subgroup, average (all animals) and low MFERT subgroups

	High	Average	Low
Milk ABV	$107.3\pm460.8^{\rm a}$	$89\pm453.12^{\rm a}$	36.32 ± 453.17^{b}
Fat ABV	$12.88\pm15.01^{\mathtt{a}}$	$7.56 \pm 15.38^{\mathrm{b}}$	$4.08\pm15.39^{\circ}$
Protein ABV	$11.39\pm10.42^{\rm a}$	$7.51\pm10.89^{\mathrm{b}}$	$4.55 \pm 11.29^{\circ}$
ASI	$91.11\pm71.31^{\mathtt{a}}$	56.67 ± 73.89^{b}	$35.09\pm74.24^\circ$

a,b,c denotes where means are significantly different (p<0.05)

Australia's two main selection indices were used to look at the combined effects of health, fertility, and production ABVs on the genetic merit of high and low MFERT cows. This study found

that high MFERT cows had a significantly higher mean BPI (123.6 ± 79.16 , P<0.001) compared to the average (82.9 ± 82.58), whereas the BPI for low MFERT animals was significantly lower than average (45.6 ± 78.59 , P<0.001). Animals with increased BPIs have been shown to live longer productive lives and have greater chance of conception which lowers AI costs (Newton *et al.* 2017). As a result, cows in the high MFERT group could generate an average additional profit of \$41 per cow per year compared to the average. High MFERT animals also had a significantly higher mean HWI value of 91.35 ± 61.41 (P<0.001) compared to the average (64.28 ± 63.04). The low MFERT animals had a mean HWI of 35.81 ± 58.96 , which was significantly lower than the data average (P<0.001). This was expected due to the heavy weighting of health and fertility in the HWI, but was included in the study to quantify the difference in profitability of low and high MFERT cows.

Applications. These findings should give farmers confidence to use the MIR fertility model along with other existing tools (e.g., daughter fertility breeding values or BPI) to make decisions on farm, particularly to improve fertility without affecting milk production. For example, the model can be used as an additional tool to support optimised semen allocation, where high predicted fertility cows can be assigned sexed semen, and low predicted fertility cows can be assigned beef or conventional semen (Newton *et al.* 2021). Additionally, farmers could use the model to identify high BPI cows with low predicted fertility, and implement management strategies such as nutritional adjustments to improve the profitability of these cows before the mating period starts.

CONCLUSIONS

This study shows that high MFERT cows as ranked by the MIR fertility model had improved reproductive performance, lower SCCs, and higher BPI, ASI, and HWI values, showing potential for improved lifetime profitability. There were no significant differences in milk production between groups, but high MFERT cows had above average milk solid percentages. Further studies should be undertaken into how the model can be used in conjunction with other commonly used breeding and management tools, as well as how high and low MFERT animals differ with regard to other health traits.

ACKNOWLEDGEMENTS

This study was undertaken as part of the DairyBio research program, which is funded by Dairy Australia (Melbourne, Australia), the Gardiner Foundation (Melbourne, Australia), and Agriculture Victoria (Melbourne, Australia). It formed part of A. Bird's MAgSc at University of Melbourne.

REFERENCES

Axford M., Santos B., Stachowicz K., Quinton C., Pryce J.E. and Amer P. (2021) Anim. Prod. Sci. 61: 1940.

Berry D.P., Kearney J.F., Twomey K. and Evans R.D. (2013) Irish. Agr. Food Res. 52: 1

Friggens N., Disenhaus C. and Petit, H. (2010) Animal 4: 1197.

Ho P., Bonfatti V., Luke T. and Pryce J. (2019) J. Dairy Sci. 102: 10460.

Ho P. and Pryce J. (2020) J. Dairy Sci. 103: 11535.

- Lomander H., Svensson C., Hallén-Sandgren C., Gustafsson H. and Frössling J. (2013) J. Dairy Sci. 96: 6315.
- Newton J.E., Ho P.N. and Pryce J.E. (2021) Proc. Assoc. Advmt. Anim. Breed. Genet. 24: 263.
- Tenghe A., Bouwman A., Berglund B., Strandberg E., Blom J. and Veerkamp R. (2015) *J. Dairy Sci.* **98:** 5763.

Vieira-Neto A., Galvão K., Thatcher W. and Santos J. (2017) J. Dairy Sci. 100: 316.

Wall E., Brotherstone S., Woolliams J.A., Banos G. and Coffey M.P. (2003) J. Dairy Sci. 86: 4093.