

IMPROVING THE RELIABILITY OF FERTILITY BREEDING VALUES IN AUSTRALIAN DAIRY CATTLE

J.E. Pryce^{1,2}, M. Haile-Mariam^{1,2}, P. Bowman^{1,2}, T. Nguyen^{1,2}, K. Konstantinov^{1,2,3}, G.J. Nieuwhof^{1,2,3} and B.J. Hayes^{1,2}

¹DEPI, 5 Ring Road, La Trobe University, Bundoora, VIC, 3083, Australia

²Dairy Futures CRC, 5 Ring Road, Bundoora, VIC, 3083, Australia

³ADHIS Pty Ltd, 22 William St, Melbourne, VIC, 3000, Australia

jennie.pryce@depi.vic.gov.au

SUMMARY

Over several decades, a decline in fertility in dairy cattle has been observed around the world. Breeding values, known in Australia as ABVs were implemented for fertility in 2003 using a single trait model for calving interval and since then the genetic trend in fertility ABVs appears to have stabilised. In April 2013 a new fertility ABV calculated using a multi-trait model was introduced that includes the following predictors of 6 week in-calf rate: calving interval, lactation length, days to first service, non-return rate and pregnancy rate. The new multi-trait fertility model has increased the reliability of fertility ABVs (compared to the single-trait model it replaced) for bulls born since 2000 by 6.5% and 7.6% for Holsteins and Jerseys respectively. The limitation to realising the full potential of this model is the capture of data. For cows that have calving interval records, 93%, 28%, 21% and 24% have records used for lactation length, days to first mating, pregnancy result and non-return to first service used in ABV calculations (for records collected between 2008 and 2010). The Dairy Futures CRC in conjunction with ADHIS have recently embarked on a co-ordinated effort to capture many more mating and pregnancy records that are electronically recorded on-farm but currently do not contribute to fertility ABVs. We have also set up a genomic reference population of females through identifying herds that have very well recorded data. The introduction of genomic data has been shown to increase the reliability of fertility ABVs of first proof bulls by a further 3%, having a genomic reference population will aid in sustaining the reliability of fertility ABVs. The collection of extra phenotypic data in addition to genomics is expected to increase the response to selection in fertility in the Australian dairy herd.

INTRODUCTION

Fertility in dairy cattle has been declining. Over the last decade the genetic trend for protein yield has been favourable (+1 kg/year) and calving interval has been unfavourable (+0.5 days/year) (Haile-Mariam and Pryce 2012). Selection for fertility can help to stop the downward genetic trend.

To be fertile, a cow needs timely return to cyclicity, display of oestrus, conception and staying in-calf. Fertility is therefore a complex trait that benefits from multi-trait prediction (Haile-Mariam and Pryce 2012). There are several ways in which the reliability of fertility breeding values (known in Australia as ABVs) can be increased. In Australia, the strategies being used to increase the reliability of fertility ABVs include: 1) use a multi-trait model to estimate fertility breeding values that encapsulates as much of the underlying genetic variation as possible; 2) capturing phenotypic data that can be used to predict ABVs; 3) using genomics to increase the reliability; 4) setting up genomic reference populations of cows with excellent fertility records.

The new multi-trait fertility model was launched in April 2013 and includes the following predictors of 6 week in-calf rate: calving interval, lactation length, days to first service, non-return rate and pregnancy rate. The previous model was based on calving interval (CI). However, calving

interval suffers from censoring, because cows with the poorest fertility do not re-calve. A multi-trait prediction is expected to result in higher reliabilities, which is especially valuable for young bulls because first proofs are generally based on low numbers of daughters and are therefore more susceptible to biases introduced by censoring. Furthermore, using additional data should lead to better fertility breeding values that are available earlier. Until recently a limitation to extending the model used to calculate fertility ABVs from single-trait to multi-trait was data availability. The limitation to realising the full potential of this model is still the capture of data, which can be increased by actively seeking many more mating and pregnancy records that are electronically recorded on-farm but currently do not contribute to fertility ABVs. Furthermore, the very best of these herds could contribute further still through genotyping and becoming part of a “female” genomic reference population.

The main objectives of this research were: 1) to compare ABVs from the new multi-trait model to those from the old fertility ABV model; 2) benchmark the amount of fertility data currently used for genetic evaluations, so that the impact of a data collection project can be accurately quantified; 3) describe the process to identify cows for a genomic reference population.

MATERIALS AND METHODS

Multi-trait fertility model. The Australian Dairy Herd Improvement Scheme (ADHIS) calculated fertility ABVs for the “new” multi-trait model and the previous “old” model it replaced. The increase in the number of bulls with a publishable fertility ABV was calculated based on the April 2013 ABV run using only Australian data and conventional breeding values for bulls with first daughter born from 2000 onwards. The correlation between ABVs based on the new multi-trait and the current two-trait model was calculated for these animals.

Data capture. The aim of the data capture project is to increase the reliability of fertility ABVs through actively sourcing many more mating and pregnancy records that are electronically recorded on-farm, but currently do not contribute to fertility ABVs. To be able to assess the impact of this effort, the first step was to benchmark the amount of fertility data captured (required for the new fertility multi-trait model). Data were extracted in August 2012 from the ADHIS database for cows that calved between 2008 and 2011. Data editing rules specific to fertility data (Haile-Mariam and Pryce 2012) were applied to the data in addition to standard ADHIS rules; for example animals without sires, birth-dates or calving dates were excluded from the data extract. Data was extracted again in April 2013 and the increase in data quantified.

Genomic nucleus population. Cows with superior fertility data i.e. high proportions of calving dates, mating dates and pregnancy testing were identified using a scoring system where each cow was awarded points for data that qualified for ADHIS evaluations for an index on yield, fertility, workability, calving ease, cell count, conformation and survival. Extra points were awarded for repeated records. This strategy has already been used to identify cows with valuable data to include in the Australian genomic reference population and is also being applied to recruit the best 100 herds that wish to be part of the experiment (subject to geographical and breed spread) to become part of a genomic reference nucleus to increase the reliability of fertility breeding values further still.

RESULTS AND DISCUSSION

Multi-trait fertility model. The reliability of fertility ABVs for bulls born since 2000 has increased by 6.5%, 8.7% and 7.6% for Holsteins, Red breeds and Jerseys respectively (Table 1). This improvement is mainly because lactation length data is available for cows that did not have calving interval. The advantage of including additional fertility traits, such as pregnancy and calving to first service is principally to improve the timing of fertility ABVs for selection decisions i.e. rather than waiting for 2 consecutive calving dates. Another advantage of using a multi-trait

model is that the standard deviation of bull ABVs increases by about 13% overall (and 6% within the Holstein breed for bulls born since 2000). The threshold for publication of fertility ABVs set by ADHIS is 55% reliability and daughters in at least 10 herds. There are approximately double the number of domestic Holstein and Jersey bulls with publishable fertility ABVs compared to the old model (Table 2). The new fertility ABV has also passed Interbull genetic trend evaluation tests; this means that for the first time in Australia many foreign bulls now have publishable fertility ABVs. The total number of bulls with publishable fertility ABVs has increased 17 and 5 fold for Holsteins and Jerseys respectively (Table 2).

Table 1. Reliability of bulls born since 2000 for the old and new fertility ABV

Breed	Number of bulls	Reliability old ABV	Reliability new ABV	Difference	Correlation
Holstein	2,421	61.9	68.3	6.5	0.87
Red breeds	29	62.1	70.8	8.7	0.81
Jersey	498	62.4	70.0	7.6	0.86

Table 2. Number of Holstein and Jersey bulls with publishable (>55% reliability in at least 10 herds domestically and >55% for Interbull proofs)

	Holstein		Jersey	
	Old ABV	New ABV	Old ABV	New ABV
Domestic	3,711	7,038	746	1,350
Interbull	0	55,362	0	2,466
Total	3,711	62,400	746	3,816

Data capture. In Australia, data is transferred from farm to local Data Processing Centres and then to ADHIS. This works very well for fertility data stored in some software used on farms, but not for others. Tests of manual transfer of data have been successful and automation of this process is currently underway for one software provider. We anticipate this will have a positive impact on data available for ADHIS fertility ABV calculation in the future.

Currently, among cows that had calving interval records in 2008, 2009 or 2010 the average proportions with lactation length, days to first mating, pregnancy result and non-return to first service data used in ADHIS ABV calculations at August 2012 were 93%, 28%, 21% and 24% respectively. By March 2013, for exactly the same period of time (2008-2010 inclusive) the number of cows with data used by ADHIS for fertility ABV calculations has increased from 1,171,287 to 1,384,086, which is an 18% increase. Veterinary clinics are also part of the work being undertaken, veterinarians commonly use DairyData software (written and supported by Warrnambool Veterinary Clinic), and this is proving to be a valuable source of pregnancy test data. One of the challenges to maximise the benefit of data from veterinary clinics in particular is establishing ways in which data can be obtained from non-herd-testing herds.

Genomic nucleus population. The Australian genomic reference population for Holsteins (April, 2013) consists of 3,449 Holstein bulls (with Australian daughters) and 8,691 cows selected based on the quality and quantity of their phenotypes. The genomic reference population for Jerseys currently consists of 946 Jersey bulls (with Australian daughters) and 3,996 females. The contribution of genomic data has been shown to increase the reliability of fertility ABVs of first proof bulls by 5-10% for the old ABV and around 3% for the new ABV (Table 3). National genomic evaluations commenced in 2011.

Acknowledging and honouring the contribution of Dave Johnson to animal evaluation

Table 3. Reliability of conventional and genomic breeding values for 1791 Holstein and 361 Jersey bulls

Breed	Old ABV			New ABV		
	N	Conventional	Genomic	N	Conventional	Genomic
Holstein	1,048	54.3%	65.0%	1,791	70.0%	73.0%
Jersey	208	60.8%	64.6%	361	68.8%	72.3%

As genomic selection replaces progeny testing, the reliability of genomic breeding values is expected to decrease because the distance between the reference and predicted population increases (Lillehammer *et al.* 2010). Strategies to reduce the reduction in reliability include exchanging genotypes between countries, using denser or more informative SNP data and genotyping females to become part of the reference population. The research we are undertaking will attempt to use all 3 strategies, including setting up an industry-resource genomic reference population.

Future. Future research activities to increase the reliability of fertility ABVs include: 1) using sequence and genomic data to increase reliabilities through improved capture of genetic variants responsible for variation in fertility; 2) improving our understanding of non-additive and epistatic genomic effects; 3) testing other predictors of fertility to improve the ABV model: heifer fertility, body condition score, protein percentage and other novel measures; 4) exploring the impact of management on fertility ABVs e.g. synchrony and inductions.

CONCLUSION

A new multi-trait fertility model was introduced in April 2013 that has resulted in increased reliabilities of fertility ABVs and consequently the number of bulls with publishable fertility ABVs. To increase the reliability of fertility ABVs further, extra phenotypic data (especially on mating and pregnancy tests) is actively being sought. In conjunction with our other activities in genomics and more recently sequence data, it is expected that reliabilities of fertility ABVs will continue to improve, giving farmers better choice of bulls and increasing the response to selection of this important trait.

ACKNOWLEDGMENTS

Dairy Futures CRC and ADHIS are gratefully acknowledged for funding this research.

REFERENCES

- Haile-Mariam M. and Pryce J.E. (2012) *Proc. 5th Australasian Dairy Sci. Symp.* 298.
Lillehammer M., Meuwissen T.H.E. and Sonesson A.K. (2011) *J. Dairy Sci.* **94**: 493.