Breeding Focus 2021 - Improving Reproduction

Edited by

Susanne Hermesch

Animal Genetics and Breeding Unit, University of New England, Armidale, Australia

Sonja Dominik

CSIRO Agriculture and Food, Armidale, Australia

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Preface

“Breeding Focus 2021 – Improving reproduction” is the fourth workshop in the series. The Breeding Focus series was developed to provide an opportunity for exchange between industry and research across a number of agricultural industry sectors. With this goal in mind, workshops have included presentations across multiple agriculturally relevant animal species to take participants outside their area of expertise and encourage them to think outside the box. Reproduction is a main driver for profitability and genetic gain. We will discuss existing knowledge, identify gaps and explore genetic and management strategies to improve reproduction further in multiple species.

Successful reproduction is a complex characteristic comprising the formation of reproductive cells, successful mating and fertilisation, embryonic and fetal growth and eventually a successful birthing event. In livestock species, reproduction traits have mostly low heritabilities, which makes it challenging to improve reproduction as part of a multiple trait breeding objective. The complexity arises not just from the cascade of processes required to result in successful reproduction, but the relevant traits are different in males and females and they are influenced through health and fitness, nutrition, climate and other environmental and management factors.

Challenges to the improvement of reproduction can vary widely for different species. For less domesticated species such as abalone, the ability to produce and reproduce the animals in captivity presents a major challenge. In bees, reproduction has not been given great attention and little research has been undertaken to understand the underlying genetics of drone and queen reproduction. However, in all industries reproduction is recognised as the basis for genetic and economic gain. It directly influences the selection intensity that can be applied. It also determines how many animals are not required for replacement and can be sold. In all industries, irrespective of the challenge, cost-effective and easy to measure phenotypes of reasonable heritability are central. New technologies and approaches enable the development of novel phenotypes for genetic improvement which will be combined with a growing amount of genomic data in livestock species and together these developments provide new and exciting opportunities to improve reproduction further.

We would like to thank everyone who has contributed to this event for their time and effort: the authors for their contributions to the book and presentations, the reviewers who all readily agreed to critique the manuscripts. We would like to express a special thanks to Kathy Dobos for her contributions into the organisation of this workshop and the publication. Thank you!

Susanne Hermesch and Sonja Dominik

Armidale, May 2021

New phenotypes for genetic improvement of fertility in dairy cows

Irene van den Berg[1], Melissa Stephen[2], Phuong N. Ho[1], Mekonnen Haile-Mariam[1], Claire Phyn[2], Susanne Meier[2], Chris Burke[2], Nicole Steele[2] and Jennie E. Pryce[1,3]

[1]Agriculture Victoria Research, AgriBio, Centre for AgriBioscience, 5 Ring Road, Bundoora, Victoria 3083, Australia

[2]DairyNZ Ltd, Hamilton, New Zealand

[3]School of Applied Systems Biology, La Trobe University, Bundoora, Victoria 3083, Australia

Abstract

While the inclusion of fertility in dairy cattle breeding programmes has improved the genetic trend for fertility, further increases are desirable, especially in pasture-based systems such as those in New Zealand (NZ) and Australia, where maintaining compact, seasonal calving intervals is an important objective to match pasture growth to feed requirements of the cow. There is interest in the use of novel traits to aid the improvement of fertility, because traditional phenotypes derived using mating and calving data have low heritabilities. Potential novel traits include mid-infrared spectroscopy predicted fertility (MFERT), age of puberty, serum biomarkers, traits derived from sensor technology, body condition score and conformation. In this chapter, we focus on MFERT (using Australian data) and age of puberty (using NZ data), because these traits can potentially be available on large numbers of animals comparatively early in life. We estimated the heritability of MFERT (0.18 ± 0.04), the heritability of traditional fertility traits (ranging from 0.02 ± 0.00 to 0.04 ± 0.00) and the genetic correlations between MFERT and traditional fertility phenotypes (0.06 ± 0.15 to -0.53 ± 0.10). Based on our estimates of genetic parameters for MFERT and the number of records currently available, including MFERT in the fertility index is unlikely to increase the response to selection, but this may change when more records for MFERT become available. Age of puberty has been recently measured in approximately 5,000 NZ Holstein-Friesian heifers. Preliminary analysis of age of puberty, obtained by monthly blood progesterone testing, indicates that the heritability is between 0.20 and 0.30. Both MFERT and age at puberty have heritabilities higher than most traditional measures and may be useful for the development of fertility Estimated Breeding Values that use multiple sources of information, including traditional fertility traits.

Introduction

Fertility is a trait of great importance to most dairy farmers. After all, lactation is dependent on parturition (i.e., reproduction). In broad terms, "fertility" is defined as the ability to produce offspring. In the dairy industry, female fertility refers to the ability of a cow to conceive and maintain pregnancy within a specific time period; where the preferred time period is determined by the particular production system in use. The relevance of certain fertility parameters may therefore differ between production systems, and evaluations of female fertility data have to account for these differences. Variation exists, however, in the relative importance of fertility in national breeding objectives. In some countries, it is economically more valuable to produce extra milk rather than improve fertility, while in others there is a strong link between pasture production profiles and milk lactation profiles (Berry et al., 2014; Pryce et al., 2014). To optimize pasture usage, calving patterns need to align with the initiation of grass growth and, therefore, good fertility is essential.

Female fertility is a complex trait with low heritability because it is a combination of several traits. For example, it is desirable to have a cow that returns to cyclicity soon after calving, shows strong signs of oestrus, has a high probability of becoming pregnant when inseminated, has no or few fertility disorders and has the ability to keep the embryo/foetus for the entire gestation period. For heifers, all characteristics except the first are essential. Multiple physiological functions are involved including hormone systems, defence mechanisms and metabolism, so a larger number of parameters may affect fertility function or dysfunction.

Historically, selection for increased milk production contributed to a decrease in fertility in dairy cattle due to the unfavourable genetic correlation between milk production and fertility (Haile-Mariam and Pryce, 2019). To counter this decline, fertility has been included in most dairy cattle breeding programmes around the world (Berry et al., 2014; Ma et al., 2019). In Australia the first dairy female fertility Estimated Breeding Values (EBVs) were released in the early 2000s, with six-week-in-calf rate derived from calving interval, lactation length, pregnancy rate, first service non-return rate and calving to first service interval. At a similar time, New Zealand introduced a fertility EBV also focused on six week in-calf rate, but including resumption of cyclicity (Harris et al., 2005). While this has led to an increase in the genetic trend of female fertility (Figure 1), further genetic improvements of fertility are desirable. Fertility still remains the most common culling reason in the Australian dairy industry (Workie et al., 2019), and pregnancy losses are costly (de Vries, 2006). Therefore, continuous selection for and further improvement in fertility is an important objective for the dairy industry.

In this chapter, we give an overview of traditional fertility phenotypes and novel fertility phenotypes, focussing on mid-infrared spectroscopy and age at puberty as case studies.

Traditional fertility phenotypes

Various measures of fertility exist, and the appropriate phenotype for selection depends on the production environment and the breeding objective. Traditionally used fertility traits include the interval from calving to first insemination, days open, calving interval, conception rate, non-return rate, interval from first insemination to conception and the number of inseminations. In Australia, the fertility breeding objective includes six-week-in-calf rate mainly derived from calving interval. Calving interval was chosen because it 1) has an abundance of data, as farmers generally always collect calving data and 2) it captures both aspects of fertility, i.e., conception and submission for insemination. However, it is censored, as only the most fertile cows re-calve. In New Zealand, the current breeding objective is six-week in-calf rate (that is, the likelihood of a cow to calve within the first six weeks of the calving period as a three-year-old). Three-week submission for mating rate as a two-year-old is used as a predictor trait (Harris et al., 2005). The breeding objective in NZ will soon be replaced by a continuous version, known as calving season day, defined as the difference in days between calving and the planned start of calving (PSC) (Amer et al., 2016). PSC is defined as the average calving date of the first 3 to 10 percent of calvings observed within herd and season, minus three days (Bowley et al., 2015).

While traditional fertility phenotypes (from mating and calving records) are cheap and easy to record, they are strongly influenced by environmental factors such as management decisions and poor oestrus detection, resulting in low heritabilities (Haile-Mariam and Pryce, 2019). Even though heritabilities of these fertility traits are low, the amount of genetic variance is sufficient for genetic improvement (Pryce and Veerkamp, 2001; Berry et al., 2014), as demonstrated by the reversal of the genetic trend for fertility. To obtain accurate breeding values, it is recommended that bulls have at least 100 daughters with fertility records (Philipsson and Lindhé, 2003). In practice, however, this is often not the case, limiting the accuracy of fertility breeding values and thereby the response to selection. New phenotypes could help improve the response to selection, either by more accurately defining the fertility breeding objective, or serving as indicator traits for fertility.

The introduction of genomic selection has benefited low reliability traits, such as fertility. Genomic only proofs (i.e., available at birth) in Australia have average reliabilities of 45%, bulls with small daughter groups (~n=70) and genomic information have average reliabilities of fertility proofs of 86%, while larger groups have reliabilities of about 93% (DataGene, April 2020 Australian Breeding Value (ABV) run). As expected, the relationship between genomic ABVs (at birth) and ABVs of the same set of bulls when evaluated using their daughters is similar to the published genomic reliability, i.e., explaining about 46% of the variation, with little bias (Figure 2).

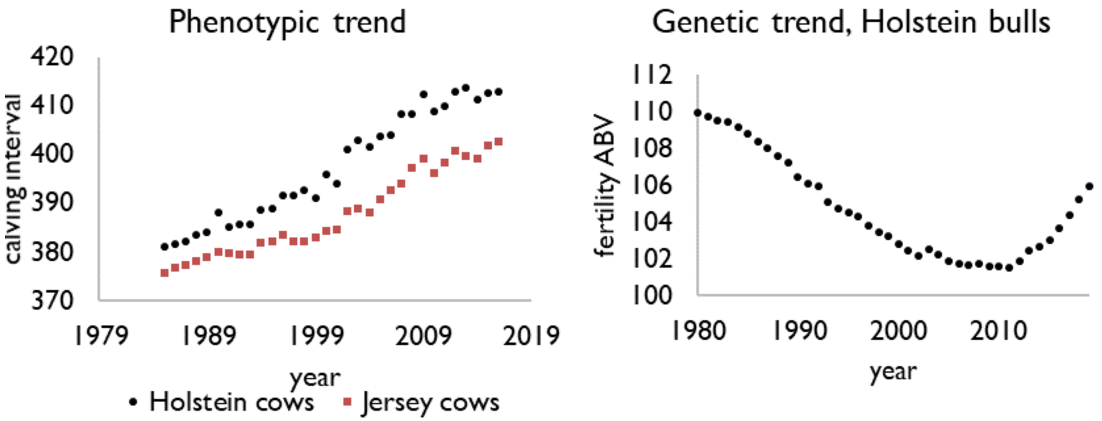

Figure 1. Phenotypic trend of calving interval in Australian Holstein and Jersey cows (left) and genetic trend of fertility Australian Breeding Value (ABV) in Holstein bulls (right)

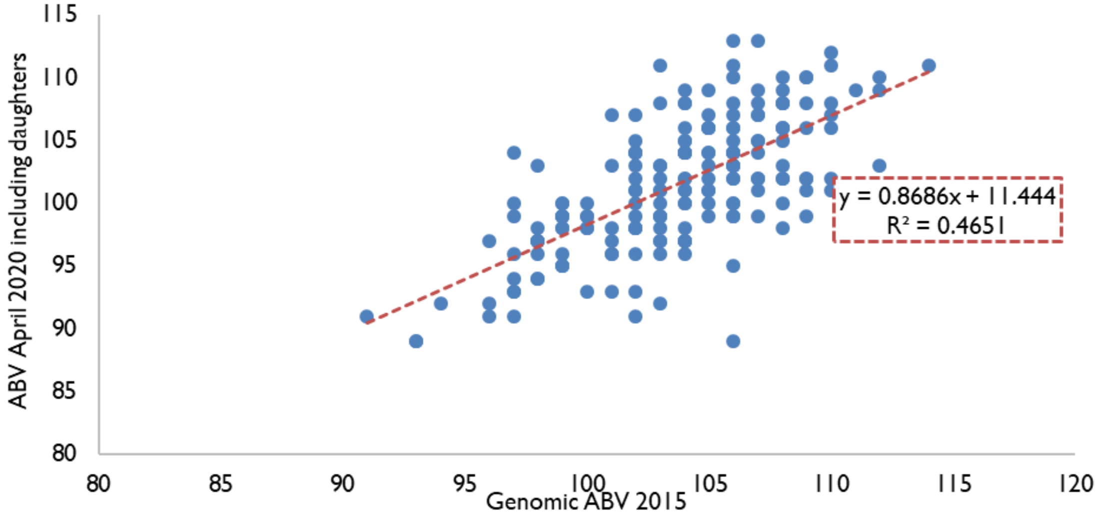

Figure 2. Genomic only Australian Breeding Values (ABVs) of bulls in 2015 and their ABVs in 2020 with (>50) daughters (DataGene, April 2020). The red line shows the regression of GEBV on ABV

New phenotypes

To increase the response to selection for fertility, new phenotypes for fertility should be 1) genetically correlated with the desired fertility breeding objective, 2) heritable, and 3) available on a large number of individuals. Various novel traits have been proposed and investigated for their use as indicator traits to improve fertility, including mid-infrared (MIR) spectroscopy predicted fertility (Ho et al., 2019), age of puberty (Fortes et al., 2012), serum biomarkers (Luke et al., 2019), traits derived using sensor technology (Ismael et al., 2015), body condition score and confirmation traits (González-Recio et al., 2016).

Here, we use two case studies of potential selection criteria that could improve fertility of dairy cows, one from Australia describing the potential use of mid-infrared spectroscopy and the other from New Zealand, describing age at puberty. Finally, we discuss the opportunities to use other novel phenotypes.

Mid-infrared spectroscopy (Australian case study)

Material outline

Recently, Ho et al. (2019) demonstrated how MIR spectroscopy can be used to phenotypically predict whether a cow conceives at the first insemination and accurately distinguish between high and low fertile cows. Because MIR spectroscopy uses a milk sample, MIR predicted fertility (MFERT) would potentially be available on all cows with milk records in the first weeks of lactation, hence earlier and on a much larger number of cows than the current fertility traits. However, genetic parameters of MFERT are unknown. Therefore, we estimated the heritability of MFERT and genetic correlations between MFERT and traditional fertility phenotypes (calving interval (CI), lactation length (LL), calving to first service (CFS) and pregnancy rate (PREG; a binary trait, coded 1 if a cow conceived within the mating period and 0 if she did not conceive)).

Phenotypes from up to 618,856 Holstein cows were used to analyse CI, LL, CFS, PREG and MFERT (Table 1). Milk samples collected between 2016 and 2018 from 29 commercial Australian dairy herds were used to obtained MIR spectra at Hico Pty Ltd (Maffra, Victoria, Australia), TasHerd Pty Ltd (Hadspen, Tasmania, Australia) and DairyExpress (Armidale, New South Wales, Australia) using Bentley Instruments NexGen Series FTS Combi machines. Subsequently, partial least squares discriminant analysis was used to develop prediction equations for MFERT using the mixOmics R package of Lê Cao et al. (2011). More details on the derivation of MFERT are described by Ho et al. (2019). Heritabilities of and genetic correlations among traits were estimated with an animal model and the AIREMLF90 software (Misztal et al., 2014), using three generations of pedigree to estimate genetic relationships between animals. Fixed effects included in the model were herd-year-season, age-parity and month of calving.

To assess the potential benefits of including MFERT in a fertility index, we compared the accuracy of two indices: one with only traditional fertility traits, and one with traditional fertility traits and MFERT. For both indices, CI was the main objective. We assumed there were always 60 progeny records available for MFERT, but varied the number records for the traditional fertility traits, with 0, 10, 30 and 60 progeny records for each of the traditional fertility traits (CI, LL, CFS and PREG).

Genetic parameters

Heritabilities for traditional fertility traits were low, varying from 0.02 for PREG to 0.04 for CI and LL (Table 1), which is consistent with previously published fertility heritabilities (Haile-Mariam et al., 2013). The heritability of MFERT was larger than that of the traditional fertility traits (0.18). However, the relatively large standard error (0.04) indicates the uncertainty of the estimate and the importance of a larger dataset to estimate genetic parameters more precisely.

The genetic correlations and standard errors between MFERT and traditional fertility traits are presented in Table 1. Correlations were low to moderate, varying from -0.53 for CFS to 0.06 for PREG, with relatively large standard errors for all traits (0.10-0.15) in comparison to other dairy traits. Genetic correlations between MFERT and CI, LL and CFS were significantly different from zero, indicating the potential of using MFERT as an indicator trait for fertility. However, a larger dataset of MFERT is required to provide more accurate estimates of genetic correlations.

Table 1. Number of records (n), heritabilities (h^2) and genetic correlation (r_g) between calving interval (CI), lactation length (LL), calving to first service (CFS), pregnancy rate (PREG) and fertility predicted using mid-infrared spectroscopy (MFERT); se = standard error

Parameter	CI	LL	CFS	PREG	MFERT
n	618,856	598,732	357,110	302,069	4,124
h^2 ± se	0.04 ± 0.00	0.04 ± 0.00	0.03 ± 0.00	0.02 ± 0.00	0.18 ± 0.04
r_g ± se	-0.35 ± 0.12	-0.32 ± 0.13	-0.53 ± 0.10	0.06 ± 0.15	-

Accuracy of selection indices

The accuracies of the different indices including only traditional fertility traits (TFERT) or traditional fertility traits and MFERT (TFERT+MFERT) are presented in Figure 3. When the number of progeny records for MFERT is much larger than the number of records for TFERT (60 records for MFERT and 10 for TFERT), including MFERT in the fertility index increased the accuracy from 0.34 to 0.43. An index based on 60 MFERT records and no TFERT records yielded an accuracy of 0.30, which was slightly lower than an accuracy using 10 TFERT records. When the number of traditional fertility records increases, the benefit of including MFERT in the index decreases, and when the number of records for traditional fertility traits equals that of MFERT, there is no benefit due to the inclusion of MFERT in the index.

Based on our estimates of genetic parameters for MFERT and the number of records currently available, including MFERT in the fertility index is unlikely to increase the response to selection. This may, however, change when the number of MFERT records surpasses the number of fertility records. In Australia, this is not the case and the benefits of including MFERT in the fertility index are currently limited because MIR data has not been routinely stored until recently. However, because of the usefulness of MIR for prediction of multiple other important phenotypes such as energy balance, metabolic profiles and milk fatty acids, the number of cows with MIR records and thus MFERT is expected to increase and may eventually surpass the number of records for traditional fertility traits. When this happens, genetic parameters can be estimated more accurately, and MFERT could potentially be used to increase the response to selection for fertility.

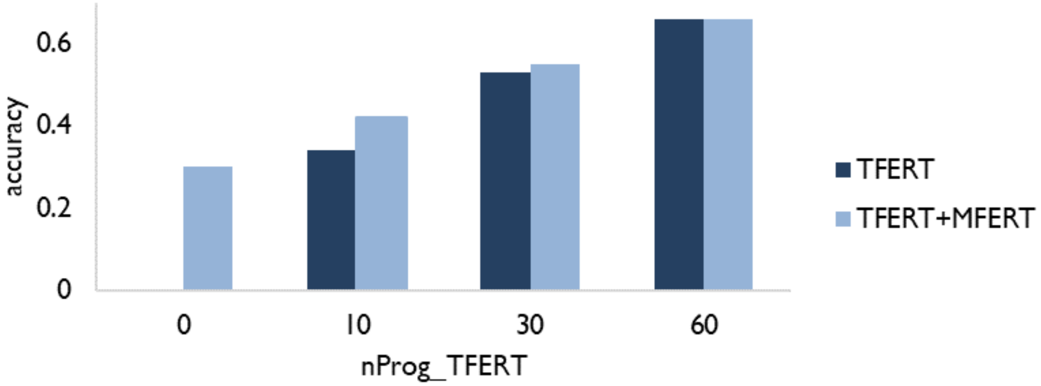

Figure 3. Accuracy of selection indices containing only traditional fertility traits (TFERT) or traditional fertility traits and MIR predicted fertility (TFERT+MFERT). We assumed 60 progeny records for MFERT and 0, 10, 30 or 60 progeny records for traditional fertility traits (nProg_TFERT)

Age of Puberty in heifers (New Zealand case study)

Age of puberty was initially measured in a purpose-bred herd of 500 Holstein-Friesian heifers with extremely divergent fertility EBVs. Weekly blood sampling was performed to detect elevated plasma progesterone concentrations (> 1 ng/mL), which indicated that a heifer had reached puberty. Heifers with positive fertility EBVs (n = 250) were found to reach puberty at a younger age (358 vs. 385 days; SD 6 days), a lighter liveweight (274 vs. 294 kg; SD 4.3 kg), and at a lower percentage of predicted mature liveweight (51 vs. 55%) than their herd mates with negative fertility EBVs (n = 250) (Meier et al., 2021). This finding suggests that age of puberty may be predictive of a cow's reproductive performance later in life. Subsequently, a second large-scale data collection initiative was carried out, where the age of puberty trait was estimated in approximately 5,000 Holstein-Friesian heifers, farmed at 54 locations throughout 3 regions of New Zealand. The objectives of this large-scale study were to: 1) establish a feasible method for measuring age of puberty at scale, 2) quantify the heritability of the trait 'age of puberty' in a large NZ dairy cattle population and 3) quantify the genetic correlation between 'age of puberty' and reproductive performance later in life.

Establish a feasible method for measuring age of puberty at scale

Age of puberty was obtained using two methods. The first method involved blood sampling the animals to measure their plasma progesterone concentrations. Animals were deemed to have reached puberty when their plasma progesterone concentrations were elevated, indicating that they had ovulated. All 5,000 animals enrolled in the study were blood sampled on three occasions at approximately 10, 11 and 12 months of age. This approach, while feasible for a proof-of-concept study of this size, would be difficult to implement at a national scale. Therefore, genetic analysis of these progesterone data will include investigating the merit of fewer blood tests per cow. The second method involved monitoring animal activity (using pedometer sensors attached to one hind leg to measure step counts and lying/standing behaviours) of a subset of approximately 2,000 heifers in 17 herds over a 10-week period. A period of increased activity can indicate an oestrus event, which may provide a suitable method for estimating timing of puberty at a larger scale. Activity data can also inform a wide range of animal health monitoring and management decisions on-farm and going forward it is possible that the collection of early-in-life activity data becomes routine within commercial farming operations. With this in mind, an age of puberty phenotype based on activity data could be a viable approach at a national scale in future years.

Heritability of age of puberty

Existing literature indicates heritabilities for age of puberty ranging from 0.10 to 0.56, depending upon the methodologies used (Smith et al., 1989; Fortes et al., 2012). Preliminary analysis of age of puberty obtained in our population by monthly blood testing indicates that the heritability of age of puberty is between 0.20 and 0.30 (Stephen et al., unpublished results). We are yet to complete the analysis of age of puberty obtained via activity monitoring. However, the continuous capture of data may provide a more heritable measure of timing of puberty relative to monthly blood testing.

Genetic correlation between age of puberty and reproductive performance later in life

The 5,000 animals involved in this study will complete their first lactation by June 2021. Reproduction traits such as intervals to first mating date and conception date, and submission, pregnancy and subsequent re-calving rates, will be obtained for our analysis to determine the value of age at puberty as a suitable predictor for improving genetic gain in fertility. In addition to these somewhat routinely recorded reproduction phenotypes, a subset of approximately 2,000 animals will wear activity monitoring devices from calving through to the end of mating. We will use these data to determine oestrus behaviour-based traits such as the interval to their first post-calving oestrus event, oestrous cycle length, and strength and duration of their oestrus events. If promising results are achieved, then further research will examine age of puberty and other novel traits across crossbred and Jersey breeds and determine relationships with reproductive performance in second or greater lactations.

Serum biomarkers

Using improved biological knowledge of the processes underlying fertility may help to define more precise phenotypes, that could have a higher heritability than traditional fertility traits. Serum biomarkers involved in reproductive processes may be potential indicator traits for fertility. For example, Anti-Müllerian hormone is involved in ovarian growth and has a moderate heritability of 0.36 and may be a promising biomarker for fertility (Nawaz et al., 2018). Other serum biomarkers such as beta-hydroxybutyric acid, fatty acids and urea have been associated with fertility, health, and production (Ospina et al., 2010; Raboisson et al., 2017). Recently, formulae have been developed to predict these serum biomarkers using MIR spectroscopy (Luke et al., 2019). Especially for urea, genetic correlations between MIR predicted urea and measured urea were not significantly different from 1, ranging from 0.96 to 0.98 depending on the model used (van den Berg et al., 2021). While our preliminary analyses of Australian Holstein cows did not find significant genetic correlations between urea and fertility traits (van den Berg et al., unpublished results), it may be worth re-estimating these correlations on a larger dataset to assess the potential use of urea as an indicator trait for fertility, as it could be available on all cows with milk samples. Furthermore, applying metabolomic finger-printing approaches such as regressing nuclear magnetic resonance against known health/fertility biomarkers may reveal novel biomarkers that could be of use for identifying cows in negative energy balance (Luke et al., 2020) or other aspects of fertility. In addition, bringing together sophisticated molecular phenotyping approaches with genomic sequence data may help to identify variants to help improve genomic prediction.

Sensor technologies

Submission rate traits, such as display of oestrus, could be automated to a large degree. Sensor technology may offer opportunities to improve the accuracy of oestrus detection. Possible sensors include activity tags, infrared thermography and visual assessments of mounting indicators. Ismael et al. (2015) reported heritabilities ranging from 0.02 to 0.16 for oestrus traits derived using electronic activity tags fitted on cow neckbands to measure cow activity. The highest heritability was obtained for interval from calving to first high activity, which had a genetic correlation of 0.96 with the traditional phenotype interval from calving to first insemination. Stevenson et al. (2014) showed the potential of automated activity monitor to predict ovulation. While sensor technologies show potential as indicator traits, it may be challenging, at least in the short term, to obtain a large enough reference population with sensor phenotypes.

Body condition score and conformation

Body condition score (BCS), angularity and several conformation traits are genetically correlated with fertility and may be used as indicator traits for fertility, as is currently the case in New Zealand. De Jong (2005) and Harris et al. (2005) reported heritabilities of 0.43 and 0.19 of BCS, respectively, and genetic correlations between BCS and various fertility traits ranging from -0.43 to 0.49. Biffani et al. (2005) showed the potential of angularity as indicator trait for fertility, with a heritability of 0.17 and genetic correlation with fertility traits between 0.03 and 0.38. González-Recio et al. (2016) used udder texture, bone quality, angularity and body condition score to derive energy status, that was subsequently tested in a multi trait fertility index. Inclusion of the energy status trait in the index increased the reliability of the fertility breeding value by 30%.

Conclusions

There is a wide range of traits that are genetically correlated with fertility and have a higher heritability than traditional fertility phenotypes. In practice, the benefits of the inclusion of such traits depends on the number of records available, the cost involved to record them, their genetic correlation with the fertility trait in the breeding objective, their heritability and the age at which they are recorded. Phenotypes available at younger age shorten the generation interval and consequently increase the response to selection. Both MFERT and age of puberty have a higher heritability and are available earlier in life than traditional fertility traits. On top of this, MFERT would potentially be available on all cows with an early herd test, which is approximately 50% of the Australian dairy cattle population. With genomic prediction, breeding values for both MFERT and age of puberty would be available on all genotyped individuals earlier in life, which could aid further improvement of fertility.

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