

## **APPLYING NEXT GENERATION PHENOTYPING STRATEGIES FOR GENETIC GAIN IN DAIRY CATTLE**

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### **SUMMARY**

Genomic selection is changing how we selectively breed animals and, more recently, for the traits we select. In addition to providing genomic breeding values for traits that were traditionally evaluated through progeny-testing of Australian dairy cattle, genomic breeding values have already been provided for two novel traits. Feed Saved, and Heat Tolerance, were released in 2015 and 2017, respectively. Our focus for dairy cattle breeding is now on traits associated with animal health, fertility and impacts on the environment. This is being achieved by directly selecting measurable phenotypic traits, or indirectly using tools such as mid-infrared spectral data and automated sensor devices to identify predictors of these traits. Greater collaboration between scientific disciplines and countries is likely to facilitate development of data-sets that will serve as better reference populations for genomic selection of new traits into the future.

### **INTRODUCTION**

Genomic selection has transformed worldwide livestock and plant breeding. While genomic selection has changed how we select, it has not substantially changed the traits we select for. Having said this, there are recent examples of traits that are now being selected for that would not be possible without genomic selection. In this paper we describe two examples of how genomic selection has enabled the next generation of breeding values for dairy cattle. In addition, we will explore new opportunities that leverage off advances in phenotyping.

### **GENOMIC REFERENCE POPULATIONS**

For most traits evaluated in dairy breeding, the genomic reference population is usually composed of bulls with large daughter groups. Often published breeding values include information from the animal's pedigree, including progeny and ancestors, in addition to the genomic component. However, for expensive or difficult to measure traits, it is not cost effective to phenotype large daughter groups. Instead the reference population can be genotyped females that have the desired phenotype measured directly. The Australian **Genomic Information Nucleus** (Ginfo) started in 2013 with around 100 herds and 30,000 cows and has contributed to the increase of reliabilities of genomic ABVs and played a key role in development of genomic breeding values of novel traits.

### **TECHNOLOGICAL ADVANCES**

The use of fully automated phenotyping in animal breeding is still in its infancy. Many precision farming technologies, such as pedometers, automatic temperature devices, automated oestrus detection, daily body condition scoring and bodyweight scales are becoming more common on modern dairy farms (Egger-Danner *et al.* 2014). To make substantial advances in low and moderately heritable traits, it is important to measure phenotypes on a large number (>10,000) of animals. Generating

quality phenotypes from large amounts of data is a challenge that requires expertise in interpretation of data and how it can be used for selection. It is important to consider the effect of any new breeding objective on other traits in the breeding goal.

**Sensors.** The use of sensor technology alongside genomic selection could lead to a further improvement in the prediction of complex traits, such as fertility, as the data obtained is likely to be more objective than other sources and potentially provide new information. For example, Talukder *et al.* (2015) compared gold standard progesterone-evaluated oestrus detection, infrared thermography, heat and rumination tags (e.g. Hi Tag, SCR Engineers, Israel) and visual assessment of mounting indicators. The mounting indicators had 100% positive predictive values, while prediction using thermography was poor. The sensor tags performed reasonably well with 70% positive predictive values.

**Mid-infrared spectroscopy (MIR).** Mid-infrared spectroscopy involves passing a beam of light through a milk sample to provide data in the form of spectra (absorbance or reflectance at specific wavelengths). Farmers currently receive regular reports from their herd test centres with information on milk volume and fat and protein concentration generated from MIR. Analysis of milk MIR has been used to predict other milk characteristics such as milk fatty acids, milk protein composition, milk coagulation properties, milk acidity, mineral composition and ketone bodies with reasonable accuracy (De Marchi *et al.* 2014).

Mid-infrared prediction equations are already showing promise to aid management decisions regarding complex traits. A good example is beta-hydroxy-butyrate (BHB) concentration, where most MIR prediction equations are calculated using the concentration of BHB in milk (Grelet *et al.* 2016). The BHB concentration in milk can also be used to predict the BHB concentration in blood (Luke *et al.* 2019). This is important as sub-clinical ketosis in dairy cattle is often diagnosed using the concentration of BHB in blood, hence using MIR in milk to predict metabolites measured in blood is likely to be a suitable practical approach to manage metabolic disease. The way in which MIR can be used for selection purposes may differ from management purposes i.e. it may not enhance genomic prediction. However, it has already been shown to be a powerful tool to identify genetic variants associated with milk composition (Benedet *et al.* 2019).

**Multi-omics.** There may also be opportunities to use information from multiple sources. Examples include direct measurements, the metagenome (e.g. rumen, reproductive etc), the proteome/metabolome (protein and metabolite structure and function) and functional genomic assays (e.g., methylation, transcriptomics etc.). When these techniques are used in conjunction with sequencing technologies, causal variants can be identified, which should lead to better responses to selection. Ultimately, multi-omics approaches could enhance selection of existing and novel traits.

## FEED SAVED AND GREENHOUSE GAS EMISSIONS

The Feed Saved Australian Breeding Value (ABV) comprises the energy required for maintenance, through liveweight breeding values calculated from conformation scores (Haile-Mariam *et al.*, 2014) and residual feed intake (RFI) as a genomic prediction evaluated in heifers and cows. The reference population for RFI comprises around 2000 Australian heifers and cows and European Holstein cows (Pryce *et al.* 2015). The current reliability of Feed Saved is 35-40%.

Maintenance of this breeding value requires additional data from cows that are contemporaries of the current national population. One way to increase the accuracy of genomic breeding values is to increase the size of the reference population through large international collaborations. An example of this is the global dry matter initiative (gDMI) where a reference population of around 10,000 cows (Berry *et al.* 2014). More recently, the Efficient Dairy Genome Project, which is a multi-national research initiative led by Canada and it currently (April 2019) has collated feed intake records from 4,779 cows (T. Chud, personal communication). Each partner has free access to the database that includes

feed intake, production and liveweight phenotypes in addition to pedigree and genomic information.

Technological advances to measure feed intake in commercial cows are occurring rapidly. For example, in dairy cattle in confined systems, cameras are being used to estimate volume changes along a feed lane before and after feeding to estimate the change in volume of feed (Bloch *et al.* 2019). In grazing environments, bite meters can be used to measure feeding behaviour discriminating between time spent biting, chewing and ruminating. It is more challenging to measure the volume of each bite and the nutrient concentrations of the pasture eaten. If this can be overcome, then individual feed intake records might become more common, especially if the sensors have multiple functions, so that farmers are motivated to purchase them.

In recent times, there has been a push to share phenotypes on individual cow methane emissions. Methane production is an expensive phenotype to measure and again, international cooperation is an attractive way to develop a dataset that is large enough for genomic prediction. There are many ways to measure methane emissions, some of which measure the total methane emitted by an individual cow in a day (Deighton *et al.* 2014). Others measure the methane emitted only at certain times or locations (Hegarty 2013). Therefore, there has been a requirement to develop statistical ways to combine heterogeneous data (Haas *et al.* 2018). In addition to multi-country reference populations, there may also be a benefit to bringing together data on different breeds, such as beef breeds.

### **HEAT TOLERANCE**

Worldwide, heat stress is a concern for many livestock production systems as it affects animal welfare and reduces productivity. In December 2017 genomic estimated breeding values (GEBV) for heat tolerance in dairy cattle were released for the first time in Australia. The dataset was constructed by merging herd-test production records with weather station data. Heat tolerance phenotypes were defined as the rates of decline in milk, fat and protein yield after a heat stress event (i.e. temperature-humidity index exceeds 60) and were estimated using a reaction norm model (Nguyen *et al.* 2016). The GEBV has been validated using divergent lines managed in controlled hot weather events (Garner *et al.* 2016). Although the reliability of heat tolerance is moderate (on average around 38%), it is expected that this will improve as the size of reference populations are increased. The genetic trend for heat tolerance has worsened, the genetic correlation with the Australian national selection index (Balanced Performance Index; BPI) is -0.20. Including heat tolerance in the BPI could improve farm profitability.

There are other ways that heat impacts dairy cows. For example, Dahl *et al.* (2016) stated that heat stress reduces dry matter intake, which in turn reduces yield and compromises immune function and if heat events are experienced in late gestation calf survival and performance is affected. Therefore, there is a need for further research on the impacts of heat stress on other traits to develop a multi-faceted heat tolerance breeding value.

### **HEALTH TRAITS**

Most genomic breeding values associated with health of dairy cattle have either been developed using records of “clinical cases” collected from farms, or by using predictor traits. For example, Abdelsayed *et al.* (2017) obtained clinical disease data from >150k cows in 90 Ginfo herds, concluding that many health traits have sufficient genetic variation for selection purposes.

The problem with farmer recorded data is that it is often inconsistent, incomplete, or sparse and generally only works well when electronic record keeping is mandatory for other purposes. However, there are opportunities to improve the reliability of genomic breeding values through the use of predictor traits, such as conformation traits, e.g. udder conformation for mastitis resistance and feet and leg traits for lameness. Technological advances in phenotyping, described earlier, could offer potential solutions for genetic selection.

## **FERTILITY**

Currently, most fertility breeding values around the world consider calving, mating and pregnancy data usually recorded by farmers. More extensive use of mid-infrared (MIR) spectroscopy (generated through machines used in routine commercial herd-testing), advanced phenotyping (using sensor technology etc) and genes identified to explain some of the genetic variation in fertility are under study and to expected deliver more precise genomic breeding values of fertility by getting closer to the biology of this complex trait.

## **CONCLUSIONS**

New technologies will generate large amounts of data that can be used for selection purposes and it is expected these will improve the way we select for current and future breeding objectives. As the emphasis of genetic evaluations changes from increasing output to reducing production costs and environmental footprints and improving animal welfare, access to quality data will be a challenge. This can be met by collaboration including with international partners and with farmers and research working in other disciplines to ensure expensive data is used for many purposes.

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