Breeding Focus 2016 – Improving Welfare

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Preface

The inaugural 'Breeding Focus' workshop was held in 2014 to outline and discuss avenues for genetic improvement of resilience. The Breeding Focus workshop was developed to provide a forum for exchange between industry and research across livestock and aquaculture industries. The objective of Breeding Focus is to cross-foster ideas and to encourage discussion between representatives from different industries because the challenges faced by individual breeding organisations are similar across species. This book accompanies the Breeding Focus 2016 workshop. The topic of this workshop is 'Breeding Focus 2016 - Improving welfare'.

> *"Animal welfare means how an animal is coping with the conditions in which it lives. An animal is in a good state of welfare if (as indicated by scientific evidence) it is healthy, comfortable, well nourished, safe, able to express innate behaviour, and if it is not suffering from unpleasant states such as pain, fear, and distress. Good animal welfare requires disease prevention and veterinary treatment, appropriate shelter, management, nutrition, humane handling and humane slaughter/killing. Animal welfare refers to the state of the animal; the treatment that an animal receives is covered by other terms such as animal care, animal husbandry, and humane treatment."* (World Organisation for Animal Health 2008).

Animal breeding offers opportunities to improve the state of animals. Existing methodologies and technologies used in animal breeding can be used to improve welfare of animals on farm while maintaining productivity. Welfare and productivity are not necessarily in opposition because several welfare measures are genetically independent from productivity traits. Further, it is often economically beneficial to improve welfare traits. These aspects provide ample opportunities to improve both welfare and productivity through selective breeding.

The chapters of this book describe existing frameworks to define welfare of animals and outline examples of genetic improvement of welfare of farm animals. A reflection on ethical issues of animal breeding and welfare is presented and further avenues for genetic improvement of welfare are discussed.

We thank all authors for their contributions to this book and their presentations at the Breeding Focus 2016 workshop in Armidale. Each manuscript was subject to peer review by two referees. We thank all reviewers who generously gave their time to referee each book chapter. A special thank you goes to Kathy Dobos for looking after all details of organising this workshop and for her meticulous work on putting this book together.

Susanne Hermesch and Sonja Dominik

Armidale, September 2016.

Breeding for welfare traits in dairy cattle

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Abstract

Between 1990/91 and 2013/14 the average amount of milk produced by milk recorded cows in Australia has increased from 4,245 litres/year to 6,709 litres/year and genetic selection accounts for around 30% gain. As farm revenue is directly linked to milk production, they are and will continue to be key dairy selection objectives. However, from the mid-1990s, it was recognised that narrow breeding goals, focused on only production traits, has had negative consequences for fitness traits which has negatively impacted animal welfare. Notably, the deterioration in female fertility as a consequence of unfavourable genetic correlations with milk production traits has been observed worldwide. Since then, breeding goals have been extended and realised selection responses for traits such as fertility show that genetic selection can improve even low heritability traits. Multi-trait selection indices optimised for local conditions, such as Balanced Performance Index (BPI) in Australia, Economic Breeding Index (EBI) in Ireland, Breeding Worth (BW) in New Zealand, Profitable Lifetime Index (PLI) in the UK, Net Merit (NM) in USA etc. ensure simultaneous improvement in several traits that encompass farm revenue and costs. However, dairy cattle breeding goals are now becoming more complex in order to meet challenges set by consumers and society. For example, farmer preferences are accounted for in the development of national selection indices for dairy in several countries. Research to broaden breeding goals further still to include other traits important for animal welfare and farm profitability is underway worldwide. Genomic selection is already being used to develop breeding values for some of these traits and is proving to be especially useful for expensive or difficult to measure traits.

Introduction

Selection for milk production has been very successful in dairy cattle breeding. In 1950-1955, the average annual milk volume of Australian dairy cows was 2,284 litres, in 2013-14 the average yield was 6,709 litres. Since the 1990s, milk yield has increased by on average 106 litres/year (Figure 1) (source ADHIS.com.au accessed April 2016) at the same time Australian Breeding Values (ABVs) for milk yield have increased by 31.7 litres per year (between 1990 and 2014). It can be concluded that around 30% of the gain in milk yield over approximately the last 20 years is due to genetics. Over the same time herd-size has almost doubled. These two factors have impacted cow health and welfare through: 1. Increased metabolic load required to produce large volumes of milk impacting directly on cow health and fertility and 2. Larger herds have led to changes in cow management and cow social structures. In this paper, we will focus on the impact of historic selection strategies on health and fertility and strategies to improve animal welfare through breeding goals that encompass animal welfare and farmer opinions.

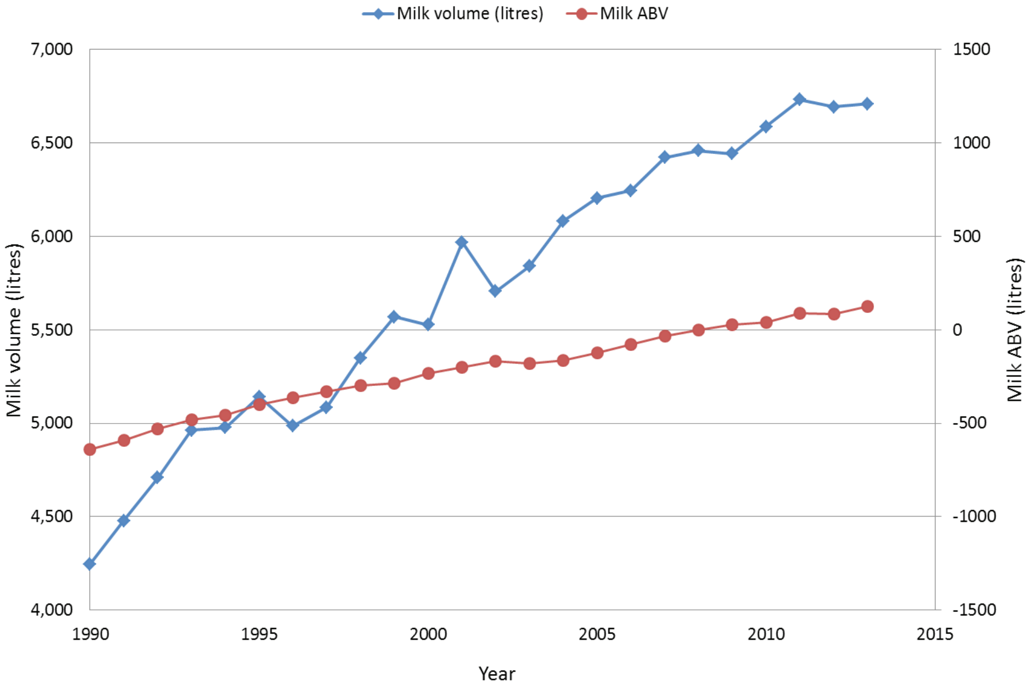

Figure 1. Average milk volume per cow by year of production and milk Australian Breeding Value (ABV) by year of birth from 1990/91-2013/14 (www.ADHIS.com.au)

Selection objectives

By the 1980s and 1990s evidence was starting to build that single-trait selection for milk production traits had led to unwanted consequences in other traits of importance, notably unfavourable genetic correlations between fertility and milk production traits (Pryce and Veerkamp 1999), but there was also evidence that other traits associated with health and animal welfare (e.g. mastitis resistance, lameness, reproductive and metabolic disorders), were also starting to deteriorate (Rauw *et al.* 1998). Pryce *et al.* (2014) used data collated by the World Holstein Federation to show that phenotypic calving interval appears to have reached a plateau by 2007. Between 1990 and 2000 calving interval increased “worldwide” by 1.25d/year phenotypically (Pryce *et al*., 2014). The introduction of fertility breeding values is leading to improvements in fertility. Evidence that selecting for improved fertility will result in phenotypic improvement is building. The daughters of sires with higher breeding values for daughter fertility have markedly better reproductive performance than daughters of sires with lower daughter fertility (Figure 2). The story of cow fertility has led to valuable lessons that have been learnt by dairy geneticists in the dangers of narrow breeding goals. In addition to sustaining selection on fertility, welfare and disease resistance traits in particular are becoming key areas where breeding values are being developed for future breeding goals.

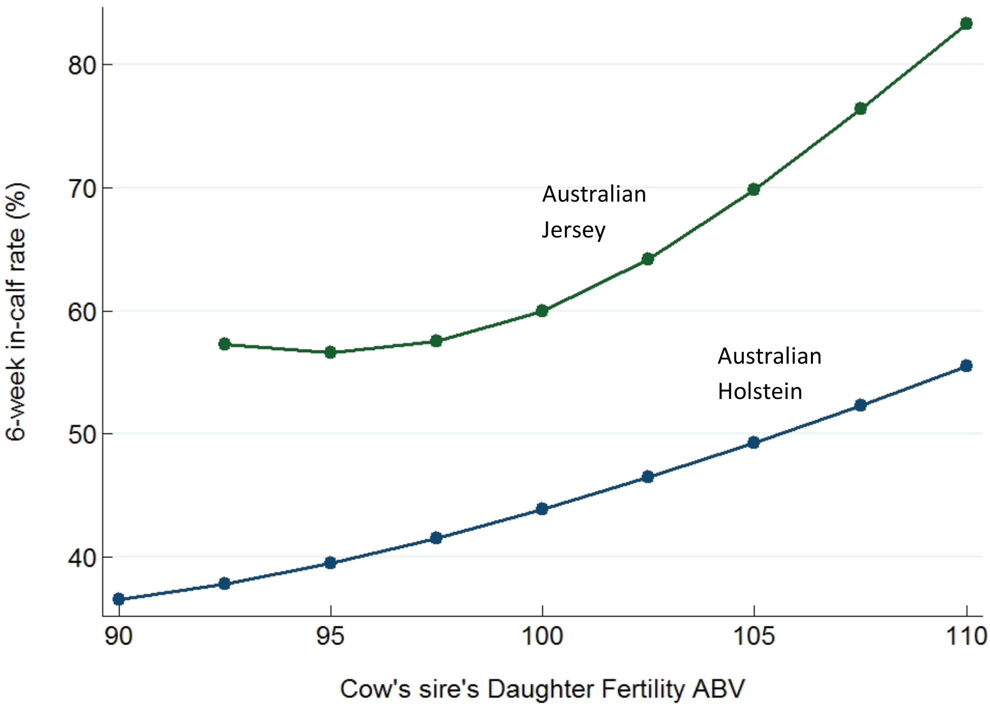

Figure 2. Phenotypic performance in 6 week in-calf rate versus the cow’s sire’s daughter fertility breeding values for Australian Jerseys (upper line) and Holsteins (lower line) estimated using data from 60,000 Holstein and 3000 Jersey cow lactations from 74 herds with high quality reproductive data (figure courtesy of Dr John Morton, Jemora Pty Limited, Geelong, Victoria, Australia).

The best way to ensure that all (measured) traits contributing to profitability are included in selection decisions is to select the sires of the next generation using the local national selection index, examples include: Balanced Performance Index (BPI), Health Weighted Index (HWI) and Type Weighted Index (TWI) in Australia, Breeding Worth (BW) in New Zealand, Profitable Lifetime Index (PLI) in the UK, Net Merit (NM) in USA, Economic Breeding Index (EBI) in

Ireland etc. An index is constructed by calculating appropriate weights for each of the breeding values included in the index. The first step is to calculate economic values for each trait, commonly with a bio-economic model, where the economic value is the increase in revenue from a unit change of a trait while everything else is held constant. The next step is to calculate the index weights and expected rate of genetic gain. Selection index theory (Hazel 1943) was developed to calculate the most appropriate index weights and responses to selection for a set of traits, their genetic and phenotypic (co)variances and the economic values of traits in the index. Provided genetic parameters are known with reasonable accuracy, this is the most appropriate way to calculate responses to selection. One common misconception is that by adding more and more traits to an index, selection is somehow diluted. This is true if the traits do not contribute anything economically, however if each trait has monetary value, then the net result of multi-trait selection is reduced gain in each component trait, but greater gain in the overall breeding objective. In fact, many countries now have more than 6 trait categories (milk production, type, longevity, udder health, fertility, other) in their national selection objectives (Egger-Danner *et al.* 2015).

More recently, there has been interest in devising non-market values to apply to traits under selection (Nielsen *et al.* 2005). These take into consideration consumer willingness to pay for aspects of traits that have perceived societal or animal welfare value. As breeding objectives are now becoming more complex in order to meet challenges set by consumers and society (Boichard and Brochard 2012). Other aspects affecting breeding objectives will some become more important, for example, as the growing human population places more pressure on limited resources and global changes leading to hotter and drier conditions to manage livestock, there is also a need to recognise increased consumer awareness of animal welfare and farming conditions. So, future breeding goals need to adapt to these considerations by including economic, societal and environmental considerations simultaneously.

Selection indices for Australian dairy cattle

Martin-Collado *et al.* (2015) used the “1000 minds” methodology to add objectivity to perceived non-market values through a survey, where questions on perceived values are assessed through a series of comparisons that are of similar actual value. The idea being that if opinions are canvassed from many farmers (hence the “1000 minds” name), then the comparative value of a trait to groups of farmers with similar philosophies can be quantified. This approach was the foundation to determine farmer preferences for three national selection indices being developed in Australia.

Highlights of the responses from farmers included: 1) There is a continuum of breeding preferences rather than distinct and separate groups of farmers; 2) Differences in preferences are only moderately linked to production system drivers such as calving pattern and feeding system; 3) Improved udders and type were important to a broad section of farmers, regardless of the proportion of the herd registered with a breed society.

Farmer preferences for the improvement of key traits were assessed by the degree of which farmer's perceived value deviated most from the trait's economic value (Martin-Collado *et al.* 2015) and the ranking was as follows: 1) mastitis; 2) longevity; 3) fertility; 4) mammary system; 5) lameness; 6) protein yield; 7) type; 8) feed efficiency; 9) calving ease; 10) temperament; 11) lactation persistence; 12) liveweight. Clearly functional traits, such as mastitis resistance, longevity, fertility and lameness are traits that farmers would like to select for.

Although farmer preferences were the focus of the research, it was clear that animal welfare (with 3 traits ranked in the top 5 associated with health) and improving the functional ability of dairy cows was at the forefront of farmers' desires for future generations of their herds. To provide selection tools that gave farmers of different philosophies an index that best suited their needs, in April 2015, ADHIS released 3 indices, the Balanced Performance Index, which is focused on profitability and designed to be in line with farmer preferences, the Health Weighted Index, which has additional selection emphasis on health, fertility and survival traits and the Type Weighted Index, which places additional selection pressure on conformation traits. The correlations between BPI and the TWI and HWI were 0.94 and 0.98, respectively, when reported on a list of published Holstein bulls born between 1990 and 2009 (N=5,213) (Byrne *et al.* 2016).

Table 1. Predicted key trait responses to selection required to achieve 100 units (AUS$) gain in the BPI index, with selection on the BPI, TWI and HWI indexes (adapted from Byrne et al., 2016)

	Index		
Trait	BPI	TWI	HWI
Milk protein (kg)	6.50	5.84	4.80
Milk volume (litres)	121.29	126.54	81.91
Milk fat (kg)	9.25	8.19	6.89
Somatic cell count (cell counts score ml-1)	8.86	9.06	10.47
Fertility (% calving in first 42 days)	0.82	0.35	1.16
Feed saved (kg/year)	4.49	-4.35	20.30
Survival (% survival from one parity to next)	2.09	2.20	2.26
Milking speed (% Milking speed ABV)	1.00	1.07	1.00
Temperament (% Temperament ABV)	0.72	0.82	0.67
Overall type (% of Overall type score)	1.56	2.90	1.52
Mammary System (Mammary system ABV)	1.73	2.99	1.81
Feed saved (kg/year)	4.49	-4.35	20.30
Total economic gain (AUS$)	100.00	94.36	98.44

Responses to selection were calculated for each index using Australian breeding values (ABVs) from bulls born between 1990 and 2009 (N=5,213), from NASIS (i.e. National Artificial Breeding Sire Identification Scheme) and are shown in Table 1. Individual trait changes were calculated by regressing each trait on the BPI, the HWI, and TWI, respectively. Responses are for a level of selection intensity that would achieve 100 units (AUS$) of change in the BPI (Table 1; Byrne *et al.*, 2016). Responses in the HWI and the TWI relative to the BPI were calculated by multiplying individual trait responses, by the index weights in the BPI. The HWI provides an increase in response to selection in somatic cell count (+18% increase when compared to the BPI), fertility (+41%), survival (+8%), and mammary system (+5%). The TWI provides an increase in response to selection in type traits; overall type (+86%) increase when compared to the BPI) and mammary system (+73%).

Breeding values for new traits

Over the last couple of decades we have already seen a rapid evolution in the number of traits that are available for farmers to select on. Almost without exception the breeding values that are currently available rely on large amounts of field data that are freely available through current recording systems. However, not all important traits are well recorded and we are likely to see increased use of data (to estimate breeding values) that originates from research herds or commercial herds with much more in depth phenotyping than has been possible before.

Most, if not all, traits are heritable to some degree. Some traits, such as health and fertility traits have relatively low heritability estimates (<5%) (Egger-Danner *et al.* 2015) while others, such as milk production, stature and liveweight have higher heritabilities (typically greater than 30%). However, the coefficient of genetic variation appears to be reasonably consistent between traits (Berry *et al.* 2014). Meaning that even for traits with low heritability there is sufficient genetic variation to make selection feasible.

There is an opportunity for genomics to bring rapid progress to the dairy industry for traits that generally have a large current or future impact on the industry but are too difficult or too costly to measure on thousands of herds across the country. This also opens prospects to work with "phenotype developers" i.e. researchers who have small-scale predictors of traits that could be scaled up to genomic or mid-infrared analysis (MIR) predictions. While some breeding values will still be developed using national data, there is an opportunity to use dedicated reference populations of genotyped females for the prediction and development of novel trait breeding values. This idea is starting to get traction in Australia, through the establishment of Ginfo, a genomic information nucleus. The best model is likely to be that for cheap and easy to measure phenotypes, reference populations will comprise of genotyped bulls with progeny groups. For traits that are expensive to measure, or where data is sparse, the best option is to obtain phenotypes on dedicated reference populations of genotyped cows (Chesnais *et al.* 2016).

Genomic information nucleus

The Ginfo population that is used in national evaluations comprises around 25,000 genotyped females many of which have been added to the genomic reference population. The Ginfo cows are Holsteins, Jerseys and their crosses from around 100 herds, selected because of the high quality phenotype data they collect. They have increased the size of the Australian reference population by 44% and 38% for Holsteins and Jerseys respectively. The April 2016 Australian Breeding Value (ABV) release was the first time Ginfo data has been incorporated in published genomic ABVs, known as ABV(g)s and breeding indices. In preparation for this, an interim ABV(g) run was conducted in February 2016. The interim run showed a substantial increase in reliability across all traits solely from adding the Ginfo cows. For example, the reliability of the Balanced Performance Index (BPI) increased by 5.8% in Holstein genotyped animals; the reliability of the fertility ABV(g)s improved by 4.5% and overall type improved by 7.1% (unpublished results). These are substantial improvements and pave the way for extending the number of traits evaluated, as the future Ginfo population is expected to be a rich resource in phenotypes for “new” traits.

Breeding values for health traits

The incidences of electronically-recorded health disorders in Australia are less than paper records, implying that only the most severe cases are recorded (e.g. only cows requiring treatment are recorded electronically). This means that any breeding values that are developed using clinical cases of disease will help to breed for a reduction in the most severe and most costly manifestations of disease. Comprehensive health data records are also only available from some herds and the Ginfo population has demonstrated to be a rich resource in this regard. However, there are also opportunities to use more widely recorded data to predict sub-clinical disease, for example somatic cell count (SCC) is available for all herds that participate in herd-recording.

The Health Data for Healthy Cows (HDHC) project (funded by the Gardiner Foundation, Melbourne, Australia), provided the platform for future development of breeding values for health traits. Genetic, parameters for health traits have been estimated using health records from ~90,000 cows collected from the 100 Ginfo herds. Preliminary results on the prevalence and genetic control of common diseases show that health traits are heritable (less than 5%). Based on incidence and genetic variation the focus should be primarily on developing breeding values for mastitis and lameness. Provided these traits are included in the national breeding objective, this will lead to permanent and cumulative improvement of health and vitality traits.

Heat tolerance

Animals have a comfort zone where body heat is effectively dissipated and the physiological state is maintained. When environmental parameters (e.g. temperature, humidity, radiation solar and wind speed) go beyond this thermo-neutral zone (threshold), animals will start to experience heat load, if this becomes acute, then heat stress will occur. Inability of animals to regulate body temperature under heat stress can result in loss of production, decrease in feed efficiency potentially leading to decreased reproductive performance (Hansen 2007). Differences in the ability to cope with heat stress are influenced by several factors varying from animal characteristics (e.g. age, level of production) and physical properties (e.g. size, skin, coat) to environmental and herd management (e.g. feeding, housing, heat duration and abatement techniques).

In Australia, it is projected that major dairying regions will experience an increase in daily average temperatures as well as more frequent heat waves. Therefore, developing strategies to mitigate the impacts of the warming climate on animal performance is of great importance. In fact, several efforts have been made to reduce the impacts of heat stress in Australian dairy cattle, such as the Cool Cows initiative of Dairy Australia (http://www.coolcows.com.au/). There are also promising opportunities to use genetics to alleviate heat stress. For example, breed differences have already been identified, as Holsteins appear to exhibit greater reductions in milk yield in hotter climates than Jerseys or crossbreds (Bryant *et al.* 2007). In fact, reductions in yield start when temperatures exceed 21 and 25 respectively at 75% humidity for Holsteins and Jerseys respectively (Bryant *et al.* 2007). Nguyen *et al.* (2016) used the decline in milk, fat and protein yields as THI increases as indicators of heat stress. The study found that using high density SNP genotypes, heat tolerance genomic breeding values can be predicted at the accuracy of 0.42 – 0.61. Heat tolerance genomic breeding values had unfavourable correlations with production traits, but favourable correlations with fertility (Nguyen *et al.* 2016). Genomically predicted heat susceptible and predicted heat tolerant animals show significantly difference in milk yield losses, rectal and intra-vaginal temperatures when experiencing a mild simulated heat wave (Garner *et al*. personal communication).

Mid-infra-red spectral data

One of the most promising ways of evaluating subclinical disease is the mid-infrared analysis (MIR) of milk samples. In addition to traditional traits (i.e., fat, protein, casein, lactose and urea contents), MIR analysis of milk has been used to predict other milk characteristics such as fatty acid composition, milk protein composition, milk coagulation properties, milk acidity, mineral composition and ketone bodies (De Marchi *et al.* 2014). MIR can be used for predicting diseases such as subclinical ketosis (Gengler *et al.* 2016). Circulating beta-hydroxybutyrate (BHBA) in blood is deemed to be the gold-standard of way of diagnosing subclinical ketosis (McArt *et al.* 2012). However, blood sampling on a large scale is likely to be impractical for many farms. It would be much more convenient if BHBA could be quantified in milk using data collected at routine monthly milk recording. The accuracy of predicting BHBA using MIR has been tested in several studies (Koeck 2015; Grelet *et al.* 2016). Breeding values for ketosis that include MIR data are already available in some countries e.g. Canada (Koeck 2015). Although a promising alternative is to use MIR to predict energy balance (McParland *et al.* 2014), as cows that are ketotic are generally in negative energy balance.

Inbreeding

Extensive use of artificial insemination and very similar selection objectives worldwide has led to high international usage of a relatively small number of bulls. Therefore, it is almost impossible to find dairy animals without genetic ties to certain key ancestor bulls. This has led to an increase in inbreeding reported in most dairy populations (Miglior *et al.* 1995; Wiggans *et al.* 1995; VanRaden *et al.* 2011).

As inbreeding increases, the risk of homozygous lethal recessives existing also increases. There are examples of genetic diseases that are lethal recessives, such as Complex Vertebral Malformation (CVM), Bovine Leucocyte Adhesion Deficiency (BLAD) and Deficiency of Uridine Monophosphate Synthase (DUMPS) in Holsteins. Most of these diseases are the result of reasonably recent (rare) mutations. For example complex vertebral malformation, or CVM, can be traced to two former elite Holstein sires, because of their widespread use, the sires appeared on both sides of the pedigree of affected calves (Agerholm *et al.* 2001). The occurrence of these diseases highlights the importance of managing rates of inbreeding, which arises as a result of the co-occurrence of common ancestor(s) in maternal and paternal pedigrees.

Genomic data can be used to control of monitor inbreeding in a population by quantifying genomic relationships between animals (Pryce *et al.* 2012). One of the advantages in using genomic, rather than pedigree relationships, is that it is a more accurate estimate of identity by descent, because it does not suffer from lack of depth of pedigree data and pedigree errors.

Gene editing

An opportunity to use genetics to improve animal welfare is through new technologies, such as gene editing. Gene editing techniques can be used to precisely alter the genome through inserting, editing or DNA sequences (Hsu *et al.* 2014). Gene editing is very precise, and makes it possible to change or disable a single gene without changing the "meaning" of the rest of the genome. So, undesired effects such as accidentally turning off a useful gene are less likely than with previous genome modification (GM) techniques. This way the desired gene is introduced rapidly in a population. However, there are regulatory issues associated with applying gene editing to livestock that need to be dealt with before practical applications are made. Provided these can be overcome, there are many applications that could have major implications for animal welfare, an example is introgression of the polled gene into dairy cattle.

Most dairy heifers are disbudded or dehorned at an early age. The procedure is generally done using heat cauterisation, often without the use of anaesthetic and is therefore considered an animal welfare issue. The gene for polled is a single dominant gene. Therefore, mating a homozygous polled bull (PP) to a herd of non-polled cows (hh) will result in all the offspring being polled (Ph). If the bull is heterozygous (Ph) and the cows are horned (hh), then half the offspring will be polled (Ph). Two mutations that prevent development of horns in certain breeds of cattle have been mapped on the bovine genome (Medugorac *et al.* 2012). Breeding for hornless cattle would certainly be preferable, however introgression of the polled gene through conventional selection would lead to a trade-off in genetic merit, as carriers of the polled mutation are generally inferior in genetic merit, recovery of genetic merit could take several generations. Gene editing is an obvious solution and has already been used to generate live polled calves (Fahrenkrug and Carlson 2014).

Conclusions

- Narrow breeding goals (i.e. selection for milk production only) leads to a deterioration of welfare related traits e.g. dairy cow fertility.

- There is sufficient genetic variation in traits associated with animal welfare, such as health traits to make genetic progress in these traits feasible.

- The most practical way to make genetic progress is to use the local national selection index e.g. BPI, HWI and TWI in Australia, EBI in Ireland, BW in New Zealand, PLI in the UK, NM in USA etc.

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References

Agerholm, JS, Bendixen, C, Andersen, O, Arnbjerg, J (2001) Complex vertebral malformation in Holstein calves. *Journal of Veterinary Diagnostic Investigation* **13**, 283-289.

Berry, D, Wall, E, Pryce, J (2014) Genetics and genomics of reproductive performance in dairy and beef cattle. *Animal* **8**, 105-121.

Boichard, D, Brochard, M (2012) New phenotypes for new breeding goals in dairy cattle. *Animal* **6**, 544-550.

Bryant, J, López-Villalobos, N, Pryce, J, Holmes, C, Johnson, D (2007) Quantifying the effect of thermal environment on production traits in three breeds of dairy cattle in New Zealand. *New Zealand Journal of Agricultural Research* **50**, 327-338.

Byrne, T, Santos, B, Amer, P, Martin-Collado, D, Pryce, J, Axford, M (2016) New Breeding Objectives and Selection Indices for the Australian Dairy Industry. *Journal of Dairy Science* **In Press**, Chesnais, J, Cooper, T, Wiggans, G, Sargolzaei, M, Pryce, J, Miglior, F (2016) Using genomics to enhance selection of novel traits in North American dairy cattle. *Journal of Dairy Science*

De Marchi, M, Toffanin, V, Cassandro, M, Penasa, M (2014) Invited review: Mid-infrared spectroscopy as phenotyping tool for milk traits. *Journal of Dairy Science* **97**, 1171-1186.

Egger-Danner, C, Cole, J, Pryce, J, Gengler, N, Heringstad, B, Bradley, A, Stock, K (2015) Invited review: overview of new traits and phenotyping strategies in dairy cattle with a focus on functional traits. *Animal* **9**, 191-207.

Fahrenkrug, SC, Carlson, DF (2014) Hornless livestock. Google Patents,

Gengler, N, Soyeurt, H, Dehareng, F, Bastin, C, Colinet, F, Hammami, H, Vanrobays, M-L, Lainé, A, Vanderick, S, Grelet, C (2016) Capitalizing on fine milk composition for breeding and management of dairy cows. *Journal of Dairy Science*

Grelet, C, Bastin, C, Gelé, M, Davière, J-B, Johan, M, Werner, A, Reding, R, Pierna, JF, Colinet, F, Dardenne, P (2016) Development of Fourier transform mid-infrared calibrations to predict acetone, β-hydroxybutyrate, and citrate contents in bovine milk through a European dairy network. *Journal of Dairy Science*

Hansen, P (2007) Exploitation of genetic and physiological determinants of embryonic resistance to elevated temperature to improve embryonic survival in dairy cattle during heat stress. *Theriogenology* **68**, S242-S249.

Hazel, LN (1943) The genetic basis for constructing selection indexes. *Genetics* **28**, 476-490.

Hsu, PD, Lander, ES, Zhang, F (2014) Development and applications of CRISPR-Cas9 for genome engineering. *Cell* **157**, 1262-1278.

Koeck, A (2015) Development of genetic evaluations for metabolic disease traits for Canadian dairy cattle. *Interbull Bulletin*

Martin-Collado, D, Byrne, T, Amer, P, Santos, B, Axford, M, Pryce, J (2015) Analyzing the heterogeneity of farmers' preferences for improvements in dairy cow traits using farmer typologies. *Journal of Dairy Science* **98**, 4148-4161.

McArt, JAA, Nydam, DV, Oetzel, GR (2012) Epidemiology of subclinical ketosis in early lactation dairy cattle. *Journal of Dairy Science* **95**, 5056-5066.

McParland, S, Lewis, E, Kennedy, E, Moore, S, McCarthy, B, O'Donovan, M, Butler, S, Pryce, J, Berry, D (2014) Mid-infrared spectrometry of milk as a predictor of energy intake and efficiency in lactating dairy cows. *Journal of Dairy Science* **97**, 5863-5871.

Medugorac, I, Seichter, D, Graf, A, Russ, I, Blum, H, Göpel, KH, Rothammer, S, Förster, M, Krebs, S (2012) Bovine polledness–an autosomal dominant trait with allelic heterogeneity. *PLoS One* **7**, e39477.

Miglior, F, Burnside, EB, Kennedy, BW (1995) Production traits of Holstein cattle: estimation of nonadditive genetic variance components and inbreeding depression. *J Dairy Sci* **78**, 1174-80.

Nguyen, TT, Bowman, PJ, Haile-Mariam, M, Pryce, JE, Hayes, BJ (2016) Genomic selection for tolerance to heat stress in Australian dairy cattle. *Journal of Dairy Science* **99**, 2849-2862.

Nielsen, H-M, Christensen, LG, Groen, A (2005) Derivation of sustainable breeding goals for dairy cattle using selection index theory. *Journal of Dairy Science* **88**, 1882-1890.

Pryce, J, Hayes, B, Goddard, M (2012) Novel strategies to minimize progeny inbreeding while maximizing genetic gain using genomic information. *Journal of Dairy Science* **95**, 377-388.

Pryce, J, Veerkamp, R (1999) The incorporation of fertility indices in genetic improvement programmes.

Pryce, JE, Woolaston, R, Berry, DP, Wall, E, Winters, M, Butler, R, Shaffer, M (2014) World Trends in Dairy Cow Fertility. *Proceedings, 10th World Congress of Genetics Applied to Livestock Production* **In press**,

Rauw, W, Kanis, E, Noordhuizen-Stassen, E, Grommers, F (1998) Undesirable side effects of selection for high production efficiency in farm animals: a review. *Livestock Production Science* **56**, 15-33.

VanRaden, PM, Olson, KM, Wiggans, GR, Cole, JB, Tooker, ME (2011) Genomic inbreeding and relationships among Holsteins, Jerseys, and Brown Swiss. *J Dairy Sci* **94**, 5673-82.

Wiggans, GR, VanRaden, PM, Zuurbier, J (1995) Calculation and use of inbreeding coefficients for genetic evaluation of United States dairy cattle. *J Dairy Sci* **78**, 1584-90.