DEVELOPING SELECTION INDEXES & ESTIMATION OF GENETIC PARAMETERS FOR TRAITS OF ECONOMIC IMPORTANCE IN DAIRY CATTLE UNDER ONCE-A-DAY MILKING

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Abstract

Developing Selection Indexes & Estimation of Genetic Parameters for Traits of Economic Importance in Dairy Cattle under Once-a-Day Milking.
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In New Zealand, about 5% of dairy herds are milked once-a-day (OAD). The cows are inseminated using sires from the twice-a-day milking system (TAD) evaluated on breeding worth (BW) or an OAD selection index. Testing for sire-by-milking frequency (MF) interaction (S×MF) could reveal if developing an OAD-specific selection scheme is justified. In this thesis production records were analysed from herds milked OAD and an equivalent TAD population provided by Livestock Improvement Corporation. Across MF, heritabilities (h^2) and genetic correlations were similar for milk yields (h^2: 0.21-0.36), although they tended to be greater in TAD. Genetic correlations were 0.35-0.40 between milk and fat yields, 0.85 between milk and protein yields and 0.54-0.60 between fat and protein yields. Observed rank correlation between OAD and TAD EBVs of the sires were moderate to high for milk yields, being greater in Jersey (J) (0.74-0.84) sires compared to Holstein-Friesian (F) and F×J crossbred (0.55-0.77) sires. Those values were greater than their critical values of the expected correlations (5th percentile), indicating that S×MF was not significant. Data from a university herd indicated that J cows were more efficient at production of milk solids (MS; fat + protein) per 100 kg of live weight than F or F×J cows milked OAD. In comparison, data from commercial herds milked either OAD or TAD indicated that F cows milked OAD had 19%-25% lower milk yields, whilst the reduction in yields from F×J and J cows was around 15%-19%. Breed effects (F-J) were lower on OAD compared to TAD systems, but heterosis effects were similar across MF (4.1%-7.6%). Under a progeny testing selection scheme for herds milked OAD, estimated genetic gains ranged from 3.3 to 3.7 kg/year for MS. Nevertheless, genetic gain resulting from the selection of bulls generated in TAD systems and dedicated to OAD herds would results in a similar increase compared with a separate scheme (only 11%-13% less of MS), indicating that there is little advantage in the implementation of a separate selection scheme. The main conclusion was that the S×MF interaction was not significant and farmers operating under OAD milking achieve similar genetic gain using sires from the TAD milking selection scheme but ranked on an OAD-selection index.

This thesis is dedicated to my dear wife Macarena, my son Pedro Felipe, and to the memory of my late father, Jorge.

Declaration

This thesis contains no material that has been accepted for a degree or diploma by the University or any other institution. To the best of knowledge no material previously published or written by another person has been used, expect where due acknowledgement has been made in text.

This thesis has been written with chapters formatted as papers for publication. Therefore there is some repetition of introduction and methods sections. Each chapter contains a full discussion, with the final general discussion chapter providing a succinct discussion of key findings of this thesis.

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List of Abbreviations

MF = Milking frequency
OAD = Once-a-day
TAD = Twice-a-day
F = Holstein-Friesian
J = Jersey
F×J = Holstein-Friesian × Jersey crossbred
MY = Milk yield
FY = Fat yield
PY = Protein yield
SCS = Somatic cell score
MS = Milk solids
PL = Production level
BW = Breeding Worth
EBVs = Estimated breeding values
G×E = Genotype by environment interaction
S×MF = Sire by milking frequency interaction

CHAPTER 1

General introduction

The standard milking frequency (MF) in the New Zealand dairy industry is twice-a-day (TAD). Nevertheless, approximately 3% to 5% of farmers have chosen to reduce MF to once-a-day (OAD) for the whole lactation (Davis et al. 1999). Currently, those farmers operating under OAD can only select sires tested in TAD systems, because there is no selection program designed specifically for the OAD cow population. Sires evaluated in New Zealand will have progeny distributed in both MF. This represents an opportunity to investigate if the ranking of sires available as parents is affected by the MF environment.

In the New Zealand dairy industry, the genetic merit of an animal is evaluated according to the breeding worth index (BW) (López-Villalobos & Garrick 2005). This index is calculated by weighting estimated breeding values (EBVs) for lactation yields of milk, fat and protein, somatic cell score, live weight, fertility, and residual survival, with their respective economic values. This index ranks sires and cows according to their expected ability to produce more profitable replacements, quantified in terms of marginal changes to profit per 5 tonnes of consumed dry matter. The BW index is the main tool that is used to select sires for the generation of future replacements. For the population milked OAD, Livestock Improvement Corporation (LIC) developed a specific OAD selection index (Stelwagen et al. 2013). The EBVs for sires in this index, however, are predicted with data from cows milked TAD. For this reason, testing for sire×MF needs consideration. To meet this goal, the main objective of this thesis is to determine the effect of MF environments on the genetic evaluation of dairy sires with progeny milked either OAD or TAD in grazing systems.

A selection scheme for the cattle population milked OAD has not been implemented given the small proportion of herds milked OAD in New Zealand (~3.0%). However, it might be foreseen, that if the popularity of OAD systems increases (Bewsell et al. 2008) dairy farmers might demand either a specific OAD index or a separate selection scheme if there is evidence for significant sire×MF and if there is a large enough population of cows in this system. Therefore, it is also a primary goal of this thesis to design and compare specific selection schemes for the population milked OAD, if the interaction due to MF is significant. The design of a separate OAD-selection scheme requires the estimation of genetic parameters, and the definition of a selection objective for predicting genetic gain.

In an experimental study carried out in New Zealand, Clark et al. (2006) reported significant interactions between Holstein-Friesian (F) and Jersey (J) breeds for milk yield traits when milked OAD or TAD. Holstein-Friesian and J cows milked OAD yielded 30% and 19% less milk solids (MS, fat + protein) than cows of the same breeds milked TAD. Nevertheless, that study reported yield differences in cows milked TAD with cows recently switched to OAD. Therefore, the results of that study can be interpreted that transition from TAD to OAD systems is easier for J cows, but not necessarily meaning that J cows are better than F (and crossbred F×J) cows for a permanent switch to OAD. In consequence, it is important to investigate if the apparent advantage of J cows under OAD systems observed under research conditions is sustained in commercial herds under several seasons operating OAD.

Although the literature indicates that J cows are preferred under OAD systems (Stelwagen et al. 2013), comparisons regarding feed conversion and gross efficiencies (Davis 2005; Prendiville et al. 2009), and expression of breed and heterosis effects for milk production traits in cows milked OAD have not been quantified in New Zealand. Those topics are worthy of deeper investigation since a) traits related to efficiencies are critical to economical profitability in dairy systems (Davis 2005); and b) crossbreeding has brought favourable heterosis for production, fertility and survival traits, resulting in increased overall farm profitability in New Zealand (López-Villalobos et al. 2000). The latter is reflected in the statistics that 45.6% of the national herd was comprised of F×J cows (LIC & Dairy NZ 2015) in 2014. Therefore, a third goal of this research was to investigate production, efficiencies and crossbreeding parameters for traits of economic importance under OAD, pasture-based systems.

To achieve these goals, this thesis addresses five specific objectives:

1. A comprehensive review of literature about pasture-based systems of dairy cattle milked OAD (Chapter 2).
2. To investigate feed conversion and gross efficiencies (Chapter 3), production performances (Chapter 4) and crossbreeding parameters for traits of economic importance under OAD pasture-based systems (Chapter 5).
3. To estimate genetic parameters (heritability, genetic correlations and genetic variances) of milk production traits for OAD milking (Chapter 6).

4. To formally test for evidence of sire re-ranking for milk production traits across MF in grazing systems (Chapter 7).
5. To evaluate alternative selection schemes by estimating genetic progress in the traits of different selection objectives for New Zealand dairy herds milked OAD (Chapter 8).

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CHAPTER 2

Literature review

Introduction

Dairy production in New Zealand is typically a spring-calving, pasture-based system. This seasonal system is largely determined by the pattern of pasture growth, where calving of cows precedes a period of rapid pasture growth and cows are dried-off in late-autumn when pasture growth decreases (Holmes et al. 2002). In this context, dairy farming has been mostly undertaken using twice-a-day (TAD) milking. Many farmers have chosen to reduce milking frequency (MF) to once-a-day milking (OAD), either as partial (early or late) lactation management, or as a strategy for the whole lactation (Davis 2005). The popularity of OAD milking increased during the early 2000s (Bewsell et al. 2008), but the number of herds milked OAD has been stable in recent seasons. Currently, up to 5% of herds in New Zealand are milked OAD for the whole season (Stachowicz et al. 2014).

Reducing MF has several benefits including: reduced costs, increased labour productivity, improved life style, alleviation of nutritional stress of cows during periods of feed shortage, improved cow body condition in late lactation, improved reproductive performance of the herd, reduced heat stress of cows and reduced incidence of lameness of the herd (Davis et al. 1999; Stelwagen et al. 2013).

Once-a-day milking for the whole herd and season is a relatively new management strategy which has attracted considerable research over the last 25 years. However, the economic viability, of OAD over a full lactation is still uncertain because the decrease in milk yields has been a barrier to permanent adoption (Tong et al. 2002). The challenge, therefore, is to develop farming systems that capture the benefits of milking OAD but minimize the yield loss by identifying animals that show little change in production following transition from TAD to OAD system (Davis 2005).

The focus of this review is to:

1. Summarize production losses of full-lactation OAD compared to full-lactation TAD systems under pasture conditions;
2. To present the issues needed to test if sires would re-rank under OAD systems
3. To examine whether developing a separate selection program for the genetic improvement of dairy cattle milked OAD is required.

Milk production losses in once a day milking systems

Milk yield depends on the abundance of mammary secretory cells, their activity and apoptosis (programmed cell death; Knight 2000; Wall & McFadden 2012). Reduced MF will increase secretory cell loss as well as their activity, hence shorter lactations are expected. Consequently, lower milk yield and fewer days in milk contribute to production losses in cows milked OAD (Stelwagen et al. 2013).

The first study comparing OAD vs. TAD milking throughout the whole lactation was carried out by Claesson et al. (1959). They reported a production loss of 50% in the first lactation and 40% in the second lactation using Swedish red and white cows. After Claesson et al. (1959), only four studies reported milk yields from herds milked OAD compared to TAD systems during the entire lactation. Three of them were carried out in New Zealand (Holmes et al. 1992; Cooper 2000; Clark et al. 2006), and only one overseas (France; Rémond et al. 2004). In these studies, the decrease in milk yield in OAD relative to TAD systems ranged between relative 22% and 50% with and an average decrease of 34% (Stelwagen et al. 2013).

Full-lactation once a day milking studies in New Zealand

In New Zealand, there have been three controlled research studies which compared cows milked OAD and TAD during the entire lactation (Holmes et al. 1992; Cooper 2000; Clark et al. 2006). These studies are summarized in Table 2.1.

Table 2.1. Mean values for annual yields of milk yield traits over a full lactation from dairy cows milked once-a-day (OAD) or twice-a-day (TAD) in Holsteins Friesian (F), Jersey (J) and crossbred cows (F×J).

Study	Years of study	Breed	MF	Days in milk	Milk (kg/cow)	Fat (kg/cow)	Protein (kg/cow)	Lactose (kg/cow)	MS[1] (kg/cow)	MS (kg/ha)
Clark et al. (2006)	4	F	OAD	230	2,914	131	106	138	237	879
			TAD	244	4,234	187	149	205	336	1,051
		J	OAD	229	2,211	129	94	107	222	979
			TAD	242	2,839	162	116	141	278	1,045
			OAD vs. TAD	**	***	***	***	***	***	***
Cooper (2000)	1	F×J	OAD	255	2,427	122	93	115	215	753
			TAD	269	3,543	171	131	171	307	922
			OAD vs. TAD	NS	***	***	***	***	***	***
Holmes et al. (1992)[2]	1		OAD	251	2,810	144	110	136	254	
			TAD	253	4,320	208	162	217	370	
			OAD vs. TAD	NS	**	**	**	**	**	

*P<0.05, **P<0.01, ***P<0.001, NS = not significant.

[1] MS = milk solids (fat plus protein).

[2] Included F, J and F×J cows.

Compared to TAD, Holstein Friesian (F) crossbred cows milked OAD, yielded between 24.2% and 31.5% less milk per cow. In Jersey (J) cows, these yield reductions were 21.3% to 22.1%. Holstein-Friesian and F×J cows yielded between 19.3% and 30.0% less milk solids (MS; fat + protein) per cow milked OAD relative to their TAD counterparts, whereas in J, this difference was only 17.4% to 20.1%.

Reduced levels of milk production reported in J cows could be caused by this breed being capable of accumulating milk for longer periods (27-34 hours), while F cows, with a greater proportion of North American Holstein-Friesian (NAHF) genes, may have limited ability to do the same (Davis et al. 1998; 1999). L'Huillier et al. (1989) indicated that udder storage capacity longer than 30 hours can prevent reduction of milk production in J cows. NAHF cows may be less suited to OAD milking because, when fed with high amount of concentrate, they produce high volumes of less concentrated milk, but their udders can only accumulate milk for up to 19 hours before reaching capacity (Davis et al. 1998, 1999). Although considerable variation in milk yield reduction has been observed within both breeds, udder regression may be more pronounced in F than in J cows leading to impairment of lactation persistency (Davis et al. 1999; Phyn et al. 2010).

Breed differences for production efficiency under once a day milking

Production efficiency can be measured as biological efficiency (kg of MS yield per 100 kg of live weight [LW]), feed conversion efficiency (kg of MS yield per 1 tonne of dry matter intake [DMI]) and DMI capacity (kg of DMI per 100 kg of LW). Davis (2005) and Prendiville et al. (2009) indicated these efficiencies are critical to economic profitability in dairy systems. The current dairy cattle selection in New Zealand (breeding worth: [BW] index) implicitly increase production efficiency because BW includes metabolisable energy requirements calculated for milk production, pregnancy, maintenance, live weight loss and gain, and rearing replacements (Harris et al. 2007).

Potentially, the impact of production efficiency on profitability during the lactation period might be greater in OAD compared to TAD milking systems, due to the decrease in milk production. Studies in New Zealand (Mackle et al. 1996) and overseas

(Prendiville et al. 2009, 2010, 2011) have indicated that in general, J cows had greater production efficiencies than F×J and F cows under pasture-based systems milked TAD.

To date, no research has studied breed differences for production efficiency under OAD systems. Evaluating the breed performance of F, J and F×J cows under pasture-based conditions under OAD systems represents a challenge for the industry in order to elucidate the most appropriate breed to be used in OAD milking systems.

Crossbreeding under once a day milking

In New Zealand, crossbreeding between F and J has been adopted since the 1960s to upgrade J into F cows. However, since 1985, crossbreeding has been implemented as a mating strategy (Montgomerie 2005). This has brought favourable heterosis for production, fertility and survival traits, resulting in increased overall farm profitability (López-Villalobos et al. 2000). For New Zealand's dairy cattle, Harris (2005) summarized heterosis effects for economically important traits under TAD milking. Those values were: 139, 7.7 and 5.5 kg of milk, fat and protein, respectively, under TAD systems, but so far, no studies have calculated crossbreeding parameters (breed and heterosis effects) in cows milked OAD.

Therefore, estimating breed and heterosis effects is important because these can be used to evaluate whether crossbred cows under OAD systems are more profitable than F and J cows as has been undertaken with TAD milking systems New Zealand (López-Villalobos et al. 2000).

Effect of once-a-day milking on health and cow fitness

The overall benefits of reducing MF on health and fitness described by Davis et al. (1999) and Stelwagen et al. (2013) might be traduced in improvements of body condition score (BCS), increased reproduction performances and fewer lameness issues. Little research, however, is available in New Zealand comparing health and fitness performances under OAD and TAD during entire lactation.

Clark et al. (2006) found that cows milked OAD had 0.34 units BCS greater compared with their counterparts milked TAD. In herds milked OAD, the benefits of a reduced MF was greater in F compared with J cows.

There is evidence of greater pregnancy rate in herds milked OAD compared with TAD milking herds (89% vs. 57% at 102 days post calving; Rémond et al. 2004) In New Zealand, however, Clark et al. (2006) found that pregnancy rate was similar across MF. Nevertheless, Clark et al. (2006) indicated that F and J cows milked OAD were pregnant earlier than those milked TAD, indicating that cows milked OAD will have a desirable effect in reducing calving interval next season. In that study also was indicated that OAD herds had 11% fewer using of CIDER (controlled internal drug release insert) which implies fewer cows in anestrous at the start of mating.

Up to date no studies in New Zealand have evaluated the effect of OAD on animal health.

Milk composition and processing change during once a day milking

In general, OAD milking results in an increase in milk fat and protein content relative to milking TAD milking (Davis et al. 1999; Rémond & Pomiès 2005). In New Zealand, Clark et al. (2006) reported that increased milk fat and protein content in cows milked OAD relative to TAD was greater in J compared to F cows In contrast, lactose content decreased in both breeds. However, in a single-season full-lactation study carried out in France (Rémond et al. 2004), no differences in lactose content in F cows milked OAD and TAD were reported.

The increase in milk fat concentration is presumably caused by a concentrating effect due to reduced volume secretion (Stelwagen et al. 2013) possibly attributable to the fact that fat secretion is less affected by OAD compared to aqueous secretion. In contrast, the increase in milk protein content is likely due to an influx of serum protein and proteolysis (Stockdale 2006; Stelwagen et al. 2013). The reduction of lactose may be attributable to a decrease in gene expression of key enzymes (Grala et al. 2011), lower mammary uptake of glucose (Guinard-Flament et al. 2011) or an increased permeability of tight junctions among mammary epithelial cells, allowing diffusion of lactose from milk to extracellular fluid and blood (Stelwagen et al. 2001).

The studies referred to in Table 2.1 show increased somatic cell count (SCC) in cows milked OAD. The increase in SCC tends to be more evident after the peak of lactation (Lacy-Hulbert et al. 2005). Nevertheless, there was no increase in the incidence of clinical mastitis despite higher SCC in cows milked OAD. However, the study of Lacy-Hulbert et al. (2005), F cows developed more cases of clinical mastitis as well as subclinical mastitis than J cows when milked OAD. Kamote et al. (1994) suggested that part of the higher SCC could be caused by a “concentration effect” of lower yields rather than an actual higher SCC. Over the lactation period studied by Rémond et al. (2004) no differences in mean SCC between F cows milked OAD and TAD were reported, but SCC tended to be greater in late lactation, as observed in cows milked TAD. In New Zealand, there is evidence of lower SCC in OAD herds compared to TAD herds, after culling high SCC cows and other cows deemed unsuitable for OAD (Dalley et al. 2007). The latter attributed this occurrence to better management practices and possibly to less exposure to pathogens during the milking process because cows are only milked once daily.

Studies conducted to evaluate the effects of changes in composition of milk from OAD-milking farms on processing characteristics are limited. Nevertheless, OAD milking can potentially affect the processing characteristics of the milk (Stelwagen et al. 2013). O’Brien et al. (1996) and Pomiès et al. (2007) reported reduced levels of free fatty acids in milk from cows milked OAD in Ireland and France, respectively. The latter study found almost one third of the free fatty acid concentrations in milk from OAD-milked cows compared to TAD in F and Montbéliarde cows. This can be beneficial in manufacturing butter and cream due to a reduction of hydrolytic rancidity in dairy products (McDaniel et al. 1969; Connolly et al. 1979), assuming that the proportion of herds under OAD system increases.

The literature is inconclusive about possible negative effects of milk composition from OAD milking on cheese processing. For example, in Ireland, O’Brien et al. (2002) did not find major adverse effects on the cheese product made of milk from cows milked OAD and TAD in late lactation. In contrast, Pomiès et al. (2007) found that OAD milking increased rennet coagulation time and curd firmness, resulting in more difficult manufacturing of good quality cheese.

Although studies of O'Brien et al. (2002) and Pomiès et al. (2007) reported contradictory findings, milk produced through OAD milking may be less suitable for cheese-making. Cows under OAD-milking systems produce milk whit a composition (higher fat and protein level, and larger amounts of SCC and enzymes such as plasmin and plasminogen) that is similar to that produced by cows milked TAD during the late lactation period (Davis et al. 1999; Stockdale 2006). The plasmin-plasminogen system increases protease activity, increases coagulation time and moisture content of cheese. According to Lucey (1996), most cheese factories in Ireland stop operating during the late lactation period because milk quality is less suitable for making good quality cheese.

Interaction between milking frequency and parity

Previous studies reported that MS yield losses were greater in first-lactation than older cows milked OAD compared to cows milked TAD. This has been attributed to the relative immaturity of cisternal development in first-lactation cows during part (Carruthers et al. 1993) and entire lactations (Clark et al. 2006). The higher sensitivity of first-lactation cows may be because energy is used for growth instead of milk production (at least in F) (Clark et al. 2006).

Clark et al. (2006) found that two- and three-year-old F cows had a greater production drop under OAD milking than cows aged four and older (38.1 and 35.9% vs. 25% less total kg of MS yield per cow, respectively). In contrast, three and four+ year-old J cows had similar production losses under OAD milking (15.9 and 19.4%), while in first-lactation cows, milk yield decreased by 23.4%.

Lactation persistency comparison under once- and twice-a-day milking

Swalve & Gengler (1999) defined lactation persistency as the ability of the cow to produce milk yield constantly over the lactation period. This trait is positively associated with health and fertility (Dekkers et al. 1998), but has not been directly selected for in the dairy population in New Zealand (Morris et al. 2008), and is not currently included in international evaluations (Cole & Null 2009).

In New Zealand, cows milked OAD generally have lower lactation persistency and dry-off sooner than cows milked TAD (Hickson et al. 2006). Bernier-Dodier et al. (2010) indicated that MF modulates lactation persistency because reduced MF accelerates the rate of mammary secretory cell loss after peak lactation.

Hickson et al. (2006), using three seasons of data from the study of Clark et al. (2006), calculated three different measures of persistency (criteria based on ratios, variation of test-day yields, and application of random regression test-day models) in OAD and TAD systems. Cows from TAD-milking farms showed better persistency than cows from OAD farms. Meanwhile, in a French study over a single season with F cows (Rémond et al. 2004), it was found that although shorter lactations were reported in the group milked OAD relative to TAD cows, persistency between these two groups was similar after the lactation peak. However, the results reported by Hickson et al. 2006 and Rémond et al. (2004) are not directly comparable due to differences in the methodology for calculating lactation persistency (Grossman et al. 1999). Further, the management system in the study of Rémond et al. (2004) (restricted pasture plus mixed ration) and Hickson et al. (2006) (mostly pasture) were different.

Previously, Woolford et al. (1982) hypothesized that there may be an important genetic component to the decreased milk yield when cows went from TAD to OAD milking and therefore, some cows were more tolerant and adapt better to the OAD regime in successive lactations than other cows. Evaluating lactation persistency from data obtained in commercial farms represents an opportunity to investigate if those cows which are genetically prone to adapt to OAD systems, are those cows which show greater lactation persistency when they are milked OAD (Clark et al. 2006; Hickson et al. 2006).

Analysis of lactation traits curves in dairy cattle

The analysis of lactation persistency as well as lactation curves for milk traits and other important traits through the lactation period as somatic cell score (SCS=$\log_2$ [SCC]), LW and BCS may be achieved from test day records through random regression models (RRM; Schaeffer & Dekkers 1994). A detailed description of mathematical modelling of the lactation curves used in RRM can be found in Macciotta et al. (2011). The general purpose of RRM is to fit average lactation curves for a population (fixed) and cow specific curves (random) as a deviation from the average. Orthogonal polynomials (Kirkpatrick et al. 1990) are widely used in RRM since they are easy to fit and the correlation among parameters is low (Schaeffer 2004). The use of orthogonal polynomials to model lactation curves in genetic evaluations of dairy cattle has been implemented in New Zealand (Harris et al. 2007), Germany, Canada and the United Kingdom (Strabel et al. 2005).

Considering Y_t as the level of production of a trait i measured on day (t) of the lactation from calving. The polynomials of n order, which describe a single observation, is defined as: $Y_t = \sum_{i=0}^{n} \alpha_i P_i(x)$ where α_i are the regression coefficients to estimate, P_i are the functions normalized to x which is standardized to unit of time described by: $x = -1 + 2\frac{(t - t_{min})}{(t_{max} - t_{min})}$ where, t_{min} and t_{max} are the earliest and latest days in milk, respectively. These intervals are converted respectively to the interval -1 to +1 (Schaeffer 2004). According to Spiegel (1971) the normalized orthogonal polynomial's functions of standardised unit of time x and coefficients α_i can be calculated for the first five polynomials as: $P_0(t) = 1$, $P_1(t) = x$, $P_2(t) = \frac{1}{2}(3x^2 - 1)$, $P_3(t) = \frac{1}{2}(5x^3 - 3x)$, $P_4(t) = \frac{1}{8}(35x^4 - 30x^2 + 15)$, $P_5(t) = \frac{1}{8}(63x^5 - 70x^3 + 15x)$.

Using the polynomial equation described above, total lactation yields for milk production traits can be predicted as the sum from day 1 after calving to maximum lactation length. Average SCS, LW and BCS can be calculated as the mean of these traits using the polynomial equation. Knowing estimated daily and total milk yields, different measurements of lactation persistency and gross and feed efficiency can be estimated. Accurate description and predictions of lactation curves and breed efficiency for cows are important, as they allow a better understanding of the OAD production systems and comparison between OAD and TAD systems.

Interaction between milking frequency and genotype

The ability of animals to perform differently in diverse environments is defined as a genotype by environment (G×E) interaction (Falconer & Mackay 1996). A G×E interaction can be as a scaling effect (where the difference in production performances is smaller at a low feeding level compared to a high feeding level), or a re-ranking where genotypes rank differently for different production or feeding systems (Hammami et al. 2009). Clark et al. (2006) reported significant interactions for milk yield traits in F and J cows milked OAD or TAD. Holstein-Friesian and J cows milked OAD had 30% and 19% lower MS yields (kg/cow) than F and J cows milked TAD, with greater variability in OAD compared to TAD systems (Figure 2.1). Hickson et al. (2006), using data from three seasons from the study of Clark et al. (2006), reported that the best F cow milked OAD yielded almost as much milk and milk components as the best F cow milked TAD, but the worst F cow milked OAD yielded much less milk and milk components than the worst F cow milked TAD. Interestingly, in the J herd the best and worst animals milked OAD yielded less than the best and worst animal milked TAD. These results show that although F cows in general are more affected than J cows, some individuals are minimally affected by changes in MF.

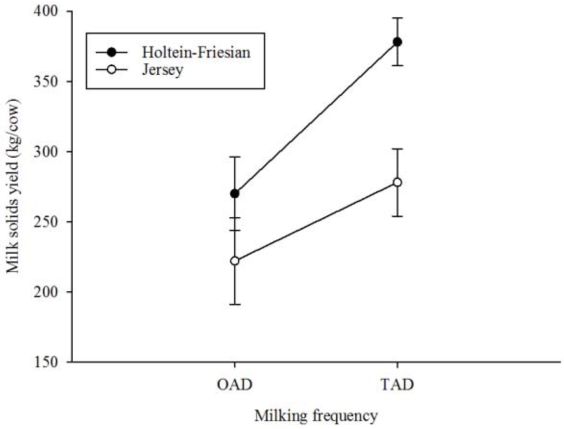

Figure 2.1. Milk solid yields per cow in Holstein-Friesian and Jersey cows milked once-a-day (OAD) and twice-a-day (TAD). Bars represent standard deviation expressed as a percentage of the mean.

Using results from the first two seasons of Clark et al. (2006), Tong et al. (2003) indicated that the differences between herds milked TAD and OAD tended to be smaller after a previous OAD lactation. Tong et al. (2003) reported that in the first season of study, F and J cows milked TAD yielded 31% and 22% more MS (kg/cow), respectively compared to their counterparts milked OAD. In the second season, however, these differences dropped to 28% and 14%, respectively.

Given the MF by breed interaction reported by Clark et al. (2006), there are two topics worthy of deeper investigation:

1. Genetic evaluation, since genetic parameters are population and environment specific and may have different magnitudes (López-Villalobos 2012).
2. Evidence of sire re-ranking between MF environments.

Sire re-ranking between MF would indicate that the true genetic correlation between milk yields on OAD and TAD is significantly less than 1.0 (Montaldo 2001). Nevertheless, Robertson (1959) suggested that only when the genetic correlation (r_G) became lower than 0.80 would it be economically important in agricultural systems. A $r_G < 0.80$ indicates that the interaction would have negative effects in the efficiency of selection programs by reducing the response in economically important traits in animals raised under environmental conditions different to those of the selected animals (Montaldo 2001).

Genetic parameters for milk production traits under once a day milking

The estimation of genetic parameters is an important issue in animal breeding. Accurate estimates of genetic parameters (phenotypic and genetic standard deviation, phenotypic and genetic correlations and heritability [h^2]) are required for the estimation of breeding values (EBVs) and for the prediction of the expected genetic response delivered by selection programs (López-Villalobos 2012). According to Hill (1981), expected responses to selection programs can be affected by errors in the estimation of genetic parameters, such as those coming from a different population or generation or further, that the estimates are subject to sampling errors due to the small number of animals recorded.

The estimation of genetic parameters for milk yields has been well documented in New Zealand (Ahlborn & Dempfle 1992; Johnson et al. 2000; Pryce & Harris 2006; Sneddon et al. 2015) and overseas (Berry et al. 2003; Rupp & Boichard 1999). In those studies, the genetic parameters were estimated with records from cows milked TAD. To date, no studies have been conducted to estimate genetic parameters in the population milked OAD.

The response to selection of a particular trait is affected by genetic correlations and phenotypic variance, and, in particular, by h^2 (López-Villalobos 2012). By definition, h^2 is the fraction of the total variation attributable to the genetic-additive difference between animals such as: $h^2 = \sigma_a^2/\sigma_y^2$ where σ_a^2 is the additive genetic variance and σ_y^2 is the phenotypic variance. In general, the studies cited in the previous paragraph reported estimates of h^2 for milk yield traits ranging between 0.20 and 0.45. When there are repeated measures of the same traits as is the case of milk yield traits, another source of variation is observed called permanent–environment variance (σ_p^2), that is partly non-additive genetic and partly environmental (Falconer & Mackay 1996). Therefore, this leads to $h^2 = \sigma_a^2/(\sigma_a^2 + \sigma_p^2 + \sigma_e^2)$ where σ_e^2 is the residual variance and $\sigma_a^2 + \sigma_p^2 + \sigma_e^2$ is equivalent to σ_y^2.

According to Ahlborn & Dempfle (1992), higher levels of production traits generally result in higher variances and h^2 estimates. This could lead to higher genetic parameters in the TAD compared to the OAD dairy population in New Zealand. The estimation of genetic parameters is of interest since its implication in the rate of genetic progress as is demonstrated in the following formula (Falconer & Mackay 1996):

$$\Delta G = \frac{ir\sigma_g}{L}$$

where ΔG is the response to selection, i is the intensity of selection, r is accuracy of selection, σ_g is the genetic standard deviation and L is the generation interval.

Correlation between sires estimating breeding values for milk yields in two milking frequencies

Sires that can produce high-ranking, profitable progeny in both TAD and OAD systems are desirable. There is some evidence of medium-high correlations for milk yields between EBVs of sires with progeny in OAD systems compared with the EBVs published in the official list, which are mostly derived from herd tests based on TAD milking (McPherson et al. 2007; Stachowicz et al. 2014). Those correlations are presented in Table 2.2.

Table 2.2. Correlation coefficients between once- and twice-a-day breeding values for milk yield and somatic cell score.

Breed	Study	Milk yield	Fat yield	Protein yield	SCS
Holstein-Friesian	McPherson et al. (2007)	0.82	0.77	0.78	0.77
	Stachowicz et al. (2014)	0.68	0.74	0.60	0.64
Crossbred (F×J)	McPherson et al. (2007)	0.82	0.81	0.76	0.82
	Stachowicz et al. (2014)	0.67	0.65	0.47	0.64
Jersey	McPherson et al. (2007)	0.80	0.84	0.75	0.76
	Stachowicz et al. (2014)	0.85	0.74	0.74	0.65

SCS= somatic cell score.

Both studies suggest that OAD and TAD milking traits are assumed to be genetically different (possible because the correlations between OAD systems and the New Zealand official EBVs were lower than 0.80 suggested by Robertson 1959), implying that sires would re-rank under OAD systems compared to TAD systems. However, this concept has not been robustly tested.

Notter & Díaz (1993) indicated that correlations between EBVs in different environments are sometimes difficult to interpret, thus observed correlations should be compared relative to their expected value. Accordingly, Charteris et al. (1997) and Garrick (2005) proposed methods to estimate expected correlations (r_E) in two separate environments.

Estimation of expected correlation between breeding values estimated in two environments

Charteris (1997) proposed a procedure to calculate r_E between EBVs of sires in two environments. This procedure is detailed as follow:

1. The BVs for each sire (*i*= 1, 2, …, n) result by the product of a lower triangular matrix $\mathbf{L}$ of the Cholesky decomposition of a co(variance) matrix $\mathbf{V}$, with a vector of independent of standardised random normal deviates (~N[0,1]) such as,

   $$\mathbf{T} = \mathbf{Lz},$$

   where $\mathbf{T}$ are the correlated BVs for the n sires and has the following elements,

   $$\mathbf{T}' = \begin{bmatrix} \mathrm{BV}_{1_i} & \mathrm{BV}_{2_i} \\ \mathrm{BV}_{1_j} & \mathrm{BV}_{2_j} \\ \vdots & \vdots \\ \mathrm{BV}_{1_n} & \mathrm{BV}_{2_n} \end{bmatrix};$$

   where $\mathrm{BV}_1$and BV_2 are the true breeding values for the same trait measured in environment 1 and 2, respectively; $\mathbf{L}$ is the lower triangular elements of the Cholesky decomposition of the (co)variance matrix $\mathbf{V}$ such as $\mathbf{LL}' = \mathbf{V}$; and $\mathbf{z}$ is a $2 \times \mathrm{n}$ vector of random independent normal deviates. Matrix $\mathbf{V}$ is constructed as follow:

   $$\mathbf{V} = \begin{bmatrix} \sigma^2_{g_1} & \sigma_{g_{1,2}} \\ \sigma_{g_{1,2}} & \sigma^2_{g_2} \end{bmatrix}$$

   where $\sigma^2_{g_1}$ and $\sigma^2_{g_2}$ are genetic variances in environment 1 or 2, respectively, $\sigma_{g_{1,2}}$ is the genetic covariance between environment 1 and 2, assuming a r_G = 1.

2. Then, EBVs for the same sires based in two environments 1 and 2 are estimated as:

   $$\mathrm{EBV}_{1i} = \mathrm{BV}_i \left[\frac{\mathrm{n}_i}{\mathrm{n}_i + \lambda}\right] + \left[\sqrt{\frac{\lambda}{\mathrm{n}_i + \lambda}}\right] \mathrm{Z}_i$$

   $$\mathrm{EBV}_{2i} = \mathrm{BV}_i \left[\frac{\mathrm{n}_i}{\mathrm{n}_i + \lambda}\right] + \left[\sqrt{\frac{\lambda}{\mathrm{n}_i + \lambda}}\right] \mathrm{Z}_{i'}$$

   where BV_i is the true breeding value, n_i= the number of daughters of sire i, λ corresponds to $(4 - \mathrm{h}^2)/\mathrm{h}^2$ and Z_i and $\mathrm{Z}_{i'}$ are two independent random number drawn from a normal distribution ~N(0,1).

3. Lastly, correlation between $\mathrm{EBV_1}$ and $\mathrm{EBV_2}$ is calculated for this one sample.

In contrast with Charteris et al. (1997), Garrick (2005) defined that a matrix $\mathbf{U}$ of correlated BVs and EBVs can be simultaneously simulated by the product of **L**, with the vector of independent of standardised random normal deviates generated ($\mathbf{z}$), such as $\mathbf{U} = \mathbf{Lz}$. In this methodology $\mathbf{z}$ is a $4 \times \mathrm{n}$ matrix (mean =0 and variance =1), and $\mathbf{U}'$ are one possible realization of the correlated BVs and EBVs. In that paper, the (co)variance matrix **V** is extended to the following structure:

$$\mathbf{V} = \begin{bmatrix} \sigma^2_{g_1} & \sigma_{g_{1,2}} & r_1^2\sigma^2_{g_1} & r_1^2\sigma_{g_{1,2}} \\ \sigma_{g_{1,2}} & \sigma^2_{g_2} & r_1^2\sigma_{g_{1,2}} & r_2^2\sigma^2_{g_2} \\ r_1^2\sigma^2_{g_1} & r_1^2\sigma_{g_{1,2}} & r_1^2\sigma^2_{g_1} & r_1^2 r_2^2\sigma_{g_{1,2}} \\ r_2^2\sigma_{g_{1,2}} & r_2^2\sigma^2_{g_2} & r_1^2 r_2^2\sigma_{g_{1,2}} & r_1^2\sigma^2_{g_2} \end{bmatrix}$$

where $\sigma^2_{g_1}$ and $\sigma^2_{g_2}$ are genetic variances in environment 1 or 2, respectively, $\sigma_{g_{1,2}}$ is the genetic covariance between environment 1 and 2, r_1^2 r_2^2 are the reliabilities of EBVs in environments 1 and 2.

In both methods, sampling is repeated *k* times (i.e. *k*=1000) to obtain a distribution of r_E between EBVs based on the given numbers of progeny records per sire. The threshold at the 5 percentile corresponds to the lower limit of r_E considered as the critical point to accept or reject the null hypothesis (H_0: $r_G = 1.0$). Calculating the r_E of milk production traits under OAD and TAD is suggested as the appropriate methodology to test for significant sire re-ranking in both MF environments.

Methodology to implement a breeding program for dairy cattle

The development of a separate OAD breeding program can only be realized when there is a large enough population of cows in this system. Currently, approximately 353 farmers (2.4% of New Zealand dairy herds) have adopted OAD for full lactations and are providing herd test data to the national data base. Therefore, because of the low proportion of herds milked OAD in New Zealand, it is unlikely that breeding companies will invest in a separate OAD selection scheme (Harris 2005; McPherson et al. 2007).

The main reason that a new breeding program would be required lies on previous evidence (McPherson et al. 2007; Stachowicz et al. 2014), where correlation between sires EBVs with progeny of both systems were in some cases < 0.80. Consequently, to investigate if there is sire re-ranking for milk traits in dairy cattle in New Zealand is important. The possibility of sire re-ranking plays an important role in order to identify the best bulls for each system because a bull's EBV can be different depending upon progeny testing of his daughters in TAD or OAD milking systems.

Breeding goal and selection objectives

The first step to develop a compressive genetic program is the definition of the breeding goal and the traits that are economically important that influence this breeding goal (Harris et al. 1984). The breeding goal indicates the direction of a genetic improvement program, and in New Zealand dairy cattle, this corresponds to conversion of feed into farm profit.

This breeding goal is expressed as a selection objective (H). The selection objective is calculated as weighting the true BVs with their respective economic values. Mathematically H can be expressed as follows:

$$\mathrm{Selection\ objective} = \mathrm{H} = \sum_{1}^{\mathrm{m}} \mathrm{v_i G_i} = \mathrm{v_1 G_1} + \mathrm{v_2 G_2} + \cdots + \mathrm{v_m G_m} = \mathbf{v}'\mathbf{g}$$

Where $\mathbf{g}$ = (G_1, G_2,…G_m) = a column vector of m unknown true breeding values.
$\mathbf{v}'$ = (v_1,v_2,…v_m) = a row vector of m known relative economic values**.**

In the New Zealand dairy industry, BW is the national selection objective (López-Villalobos & Garrick 2005). The BW index includes lactation yields of milk, fat, protein, SCS, LW, fertility, residual survival, and from 2016, BCS.

Selection index

The next step in designing a breeding program for the dairy cattle milked OAD is determination of the selection criteria. Those are the traits measured to predict the BVs of the animals. The measured traits are combined into an index (I) on which animals are selected. The selection index theory (Hazel 1943), therefore, is a method for estimating the BVs of an animal combining all the information available for the animal and its relatives. It is the basis on which animals are ranked for selection because it maximizes the correlation between the selection index (I) and selection objective (H), or where the square deviation $\sum(\mathrm{H}-\mathrm{I})^2$ is smallest.

Therefore, I is used as a predictor of H, which is focused on traits that influence the breeding goal. In New Zealand, the traits included in the H are lactation yield of milk, fat, protein, LW, SCS, fertility and residual survival (López-Villalobos & Garrick 2005).

Mathematically I can be expressed as follows:

$$\text{Selection index} = \mathrm{I} = \sum_{1}^{n} \mathrm{b_i X_i} = \mathrm{b_1 X_1} + \mathrm{b_2 X_2} + \cdots + \mathrm{b_n X_n} = \mathbf{b'x}$$

Where: $\mathbf{x}$ =(X_1, X_2,…X_n) = a column vector of m known phenotypic deviation values.

$\mathbf{b'}$ = (b_1, b_2,…b_n) = a row vector of n index weight coefficients to be computed.

Hazel (1943) proved that maximum $\mathrm{r_{IH}}$ is achieved with the following equation: $\mathbf{Pb} = \mathbf{Gv}$, hence the selection index coefficients ($\mathbf{b}$) are calculated as follows:

$$\mathbf{b} = \mathbf{P}^{-1}\mathbf{Gv}$$

Where $\mathbf{P}$ is an $\mathrm{n} \times \mathrm{n}$ phenotypic (co)variance matrix corresponding to the indicator traits (selection index); $\mathbf{G}$ is an $\mathrm{n} \times \mathrm{m}$ genetic (co)variance matrix between traits in the selection objective (m) and correlated indicator traits incorporates the selection index (n); $\mathbf{v}$ is and $\mathrm{m} \times 1$ vector of relative economic values. To derive weighting factors ($\mathbf{b}$) phenotypic variances, h^2, genetic and phenotypic correlations among the criteria and objective traits are needed (Cameron 1997).

Economic index based on estimated breeding values

The selection index was developed based on phenotypic records, and the main interest is to predict the individual true BVs for the aggregate genotype. Henderson (1963) suggested an alternative method of calculating index values in two steps, because in practice, the source of information that are available are EBVs for individual traits rather than phenotypic records (Dekkers et al. 2005). This method includes 1) the EBVs trough Best Linear Unbiased Predictor (BLUP; Henderson 1950) methodology for each trait included in the selection objective, and 2) the application of their economic values such that:

$$\mathrm{I} = \mathrm{v}_1\mathrm{EBV}_1 + \mathrm{v}_2\mathrm{EBV}_2 + \cdots \mathrm{v}_\mathrm{n}\mathrm{EBV}_\mathrm{n}$$

According to Hazel et al. (1994), the alternative addressed by Henderson (1963) allows the use of BLUP techniques to estimate individual breeding values for each trait including adjustments for difference source of information (relatives). Economic values can vary with different selection objectives, depending on how different breeds are used in a particular breeding or production and marketing systems, without recalculating the breeding values. In practice, this is the method used to calculate the BW index for cows and sires in the New Zealand dairy cattle evaluations.

Mixed models for genetic evaluation

According to Mrode (2014) the major disadvantage of the selection index theory for genetic evaluation is that records must have been pre-adjusted for the fixed or environmental factors, however, fixed factors are usually unknown in advance. Henderson (1950) developed the BLUP methodology, by which fixed effects and breeding values (random effects) are simultaneously estimated. The conventional selection index detailed above is thus a special case of BLUP with known fixed effects (Falconer & Mackay 1996).

The general form of the mixed model is written as (Mrode 2014): $\mathbf{y} = \mathbf{Xb} + \mathbf{Za} + \mathbf{e},$ where $\mathbf{y}$ is the vector of observations; $\mathbf{b}$ is the vector of fixed effects with design matrix $\mathbf{X}$, $\mathbf{a}$ is the vector with random effects with design matrix $\mathbf{Z}$ and $\mathbf{e}$ is the vector of random residual effects. The following expectation (E) of the variables are assumed: $\mathrm{E}(\mathbf{y}) = \mathbf{Xb}$; $\mathrm{E}(\mathbf{a}) = \mathrm{E}(\mathbf{e}) = \mathbf{0}$. The model assumes that residual effects, which included random environmental and non-additive genetic effects, are independently distributed. Therefore, $\mathrm{var}(\mathbf{a}) = \mathbf{A}\sigma_\mathrm{a}^2 = \mathbf{G}$; $\mathrm{var}(\mathbf{e}) = \mathbf{I}\sigma_\mathrm{e}^2 = \mathbf{R}$ and $\mathrm{var}(\mathbf{y}) = \mathbf{ZGZ}' + \mathbf{R}$, where σ_a^2 is the genetic-additive variance, σ_e^2 is the random residual variance and $\mathbf{A}$ is the numerator relationship matrix.

The mixed-model equations are represented as:

$$\begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{X} & \mathbf{X}'\mathbf{R}^{-1}\mathbf{Z} \\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{X} & \mathbf{Z}'\mathbf{R}^{-1}\mathbf{Z} + \mathbf{G}^{-1} \end{bmatrix} \begin{bmatrix} \hat{\mathbf{b}} \\ \hat{\mathbf{u}} \end{bmatrix} = \begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{y} \\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{y} \end{bmatrix}.$$

The vector $\mathbf{a}$ represent the random animal additive effect, however, there might be more than just one random effect, as is the case in dairy cattle when there are repeated measures of the same traits (permanent environmental). The effects in $\mathbf{a}$ determine the structure of $\mathbf{G}$. The single-trait animal model EBVs are fitted for each animal (cow) and refers to the fact that animals have observation of just one trait.

The multi trait model is an extension of the single trait case, in which the EBVs are estimated for each trait included. The results might be different compared to the single-trait analysis because each trait is used to give information to the other(s) trait(s), leading to more accurate evaluations (van del Werf 2002). An example of a multi trait model is the bivariate repeatability animal model, which is written as (Mrode 2014):

$$\begin{bmatrix}\mathbf{y_1}\\ \mathbf{y_2}\end{bmatrix}=\begin{bmatrix}\mathbf{X_1} & \mathbf{0}\\ \mathbf{0} & \mathbf{X_2}\end{bmatrix}\begin{bmatrix}\mathbf{b_1}\\ \mathbf{b_2}\end{bmatrix}+\begin{bmatrix}\mathbf{Z_1} & \mathbf{0}\\ \mathbf{0} & \mathbf{Z_2}\end{bmatrix}\begin{bmatrix}\mathbf{a_1}\\ \mathbf{a_2}\end{bmatrix}+\begin{bmatrix}\mathbf{e_1}\\ \mathbf{e_2}\end{bmatrix},$$

where $\mathbf{y_i}$ is the vector of observation for the *i*th trait, $\mathbf{b_i}$ is the vector of fixed effects for the *i*th trait, $\mathbf{a_i}$ is the vector of additive genetic effects for the *i*th trait, $\mathbf{e_i}$ is the vector of random residual effects for the *i*th trait; and $\mathbf{X_i}$ and $\mathbf{Z_i}$ are incidences matrices relating records of the *i*th trait to fixed and random (animal) effects, respectively. It is assumed that: $\mathrm{E}(\mathbf{y_i})=\mathbf{X_i}\mathbf{b_i}$; $\mathrm{E}(\mathbf{u})=\mathrm{E}(\mathbf{e})=\mathbf{0}$. The model assumes that random effects are normally distributed with zero mean and the following co(variance) structure:

$$\mathbf{V}\begin{bmatrix}\mathbf{a_1}\\ \mathbf{a_2}\\ \mathbf{e_1}\\ \mathbf{e_2}\end{bmatrix}=\begin{bmatrix}\mathbf{A}\sigma^2_{a_1} & \mathbf{A}\sigma_{a_{12}} & \mathbf{0} & \mathbf{0}\\ \mathbf{A}\sigma_{a_{12}} & \mathbf{A}\sigma^2_{a_2} & \mathbf{0} & \mathbf{0}\\ \mathbf{0} & \mathbf{0} & \mathbf{I}\sigma^2_{e_1} & \mathbf{I}\sigma_{e_{12}}\\ \mathbf{0} & \mathbf{0} & \mathbf{I}\sigma_{e_{12}} & \mathbf{I}\sigma^2_{e_2}\end{bmatrix}$$

where $\sigma^2_{a_1}$ is the additive genetic variance for trait 1, $\sigma^2_{a_2}$ is the additive genetic variance for trait 2 and $\sigma_{a_{12}}$ is the additive genetic covariance between both traits; $\mathbf{A}$ is the relationship matrix among animals; $\mathbf{I}$ is an identity matrix whose size corresponds to the number of records; $\sigma^2_{e_1}$ is the residual variance for trait 1, $\sigma^2_{e_1}$ is the residual variance for trait 2 and $\sigma_{e_{12}}$ is the residual covariance between both traits.

Selection scheme

The selection scheme dictates the potential rate of genetic progress that can be achieved in the breeding objective and has considerable influence on the cost-effectiveness of the breeding program (López-Villalobos & Garrick 2005). In this thesis, two alternative breeding schemes were investigated based on progeny testing (PT) and an alternative of genomic selection (GS).

Selection scheme based on progeny testing

Progeny testing (PT) corresponds to the use of several progeny records to evaluate males (bulls). Progeny testing increases the accuracy of selection, but also increases the generation interval (Falconer & Mackay 1996).

In dairy cattle, genetic improvement is achieved using assortative mating and selection (Holmes et al. 2002). That means that the best bulls are mated to the best cows to generate cow replacements. Thus there are four pathways of selection (Rendel & Robertson 1950). These pathways are: cows to breed cows (CC), cows to breed bulls (CB), bulls to bred cows (BC) and bulls to breed bulls (BB). The annual rate of genetic progress (ΔG) results from the following formula, proposed by Rendel & Robertson (1950):

$$\Delta \mathrm{G} = \frac{\sum_{j=1}^{4} (i_j r_j) \sigma_g}{\sum_{j=1}^{4} L_j}$$

where σ_g, r, L are the genetic standard deviation of the selection objectives, intensity of selection, accuracy of selection and generation interval, respectively in the *j*th selection pathways. In the design of a selection scheme, various combinations are possible. These combinations are determined by the number of cows and bulls in the selection pathways, and the generation interval, which is defined as the average age of the parents when the progeny is born. As an example, the four pathways of selection in the current selection scheme for the New Zealand dairy cattle are detailed in Table 2.3.

Table 2.3. Population size, population selected number of records and generation intervals in the New Zealand dairy cattle.

Pathway	Population	Population selected	Number of records	Generation interval
BB	440	12	85	6.5
BC	440	44	85	7.0
CB	1,800,000	3,000	2	4.2
CC	4,800,000	4,320,000	2	6.1

BB=bull to breed bull; BC=bull to bred cow; CB=cow to breed cow; CC=cow to breed cow.

So far, a selection scheme for the population milked OAD has not been implemented, but in case the New Zealand dairy cow population milked OAD increases to a level economically justifiable (20-30%; McPherson et al. 2007), the possible OAD selection scheme will modify the elements shown in Table 2.3, leading to a different rate of genetic gain and different costs of a selection program (López-Villalobos & Garrick 2005).

Selection scheme based on genomic selection

Since the implementation of artificial insemination, PT is the main method of evaluating bulls in a dairy selection schemes (Pryce & Daetwyler 2010), but genomic selection (GS) (Meuwissen et al. 2001) creates an opportunity to modify the conventional PT-selection scheme. In GS, genomic breeding values (GEBVs) are estimates from SNP (single nucleotide polymorphisms) markers. Schaeffer (2006) indicated that under this scheme, genetic gain can be doubled compared to PT.

In simulation studies for small dairy populations, such as the OAD herds in New Zealand, Lillehammer et al. (2011) (Norwegian Red) and Thomasen et al. (2014) (Danish Jersey) reported that the implementation of GS (Turbo scheme: bulls selected on the basis of parent average GEBVs and used for breeding purposes as soon as they are sexually mature) would achieve both greater genetic progress and economic profitability, compared to the conventional PT schemes. The greater genetic progress in the GS-scheme was mainly due to a shorter generation interval that compensated for the lower accuracy compared to the PT-scheme. A GS-scheme is cheaper because cost for housing and feeding bulls are reduced due bulls are slaughtered as soon as enough semen can be collected. The structure of the GS selection scheme simulated by Thomasen et al. (2014) is illustrated in Figure 2.2.

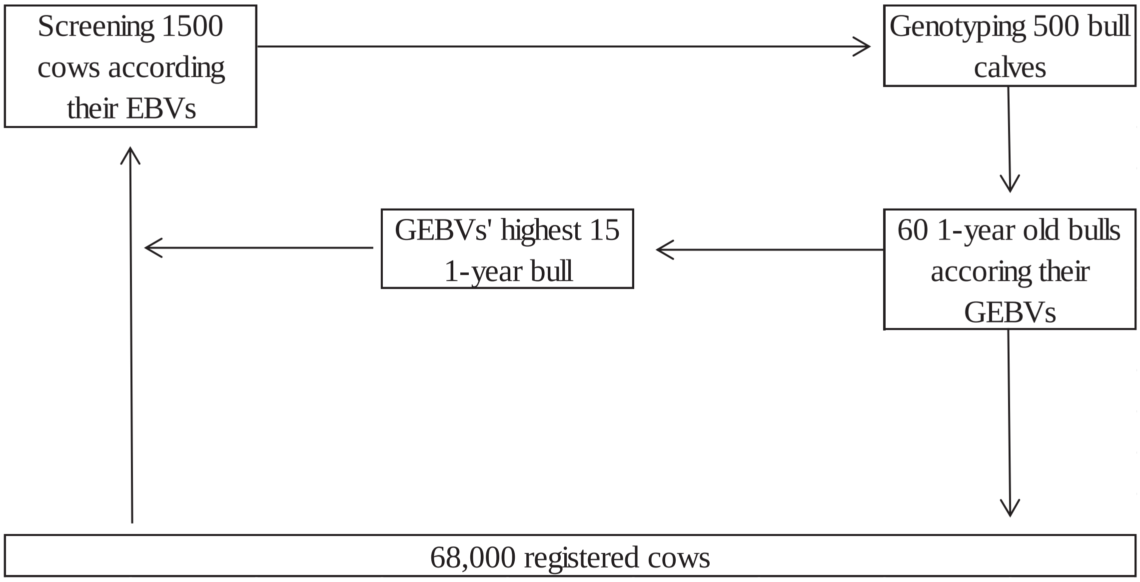

Figure 2.2. Illustration of selection scheme based on genomic selection (Thomasen et al. 2014).

The studies referred above proposed that GS-breeding program would be advised above conventional PT scheme for small dairy cattle populations, although the accuracy of GS-schemes is lower compared to the conventional scheme because of PT. Consequently, the advantage of GS methodology needs to be evaluated in the New Zealand OAD population.

Current situation for once a day milked population in New Zealand

Currently the only option for the New Zealand OAD dairy cattle is to select bulls tested in TAD and subsequently used in herds milked OAD. This option is to select bulls based either on BW or an OAD selection index developed by Livestock Improvement Corporation (LIC; Hamilton, New Zealand) (LIC 2004). The OAD index was developed using EBVs of bulls whose daughters were milked TAD to develop a predictive equation to estimate OAD EBVs, which are weighted by TAD economic values (Stelwagen et al. 2013). Therefore, correlated responses in the OAD dairy population, as a consequence of selecting bulls progeny-tested in TAD systems needs to be investigated.

Besides traits included in BW, other traits perceived desirable to improve from a genetic viewpoint in OAD systems are udder conformation traits and milking speed (McPherson et al. 2007). These traits are important because the OAD system requires faster milking speed, to facilitate removal of the increased milk volume and reduced electrical power cost and labour time. Also, udder support and front teat placement are also proposed to be included in the OAD selection index, because of the increased contained milk weight of the udder at the end of the 24h interval. These traits are also relevant in OAD selection index because they are moderate-correlated with milk yields and mastitis (Berry et al. 2004).

Conclusions

The literature reviewed showed that at least under experimental conditions, milk production losses relative to TAD per cow are the main barrier to adopt widely this management in order to capture the benefits of OAD in New Zealand.

Previews research has suggested that J cows are preferred under OAD systems, but have not necessarily established that this breed is more profitable than F and F×J after a long term change to OAD. Other topics worthy of deeper investigation is production efficiencies, and crossbreeding for milk production traits in cows milked OAD, may contribute to decide a preferred breed group for operating OAD.

In New Zealand, there have been studies conducted to estimate correlations between OAD and TAD EBVs of dairy sires for milk productions traits. Those studies suggest that dairy sires might re-rank across MF. However, this concept has not been robustly tested. If sire×MF is confirmed, the design of a specific OAD-selection scheme might be justified. The methodology to implement a separate scheme for the population milked OAD was presented in this review.

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CHAPTER 3

Comparative performance in Holstein-Friesian, Jersey, and crossbred cows milked once daily under a pasture-based system in New Zealand

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Abstract

Production and efficiency of Holstein-Friesian (F), Jersey (J) and crossbred F×J milked once-a-day (OAD) were studied at Massey University dairy farm No. 1. Herd test records of milk yields, somatic cell score (SCS), live weight (LW) and body condition score (BCS) were used to model the lactation curves using a third order orthogonal polynomial. Total lactation yields of milk (MY), fat (FY), protein (PY) and milk solids (MS = FY + PY) were calculated based on predicted daily yields. Predicted efficiencies were feed conversion efficiency (FCE; total lactation MS per kg of predicted total lactation dry matter intake [DMI]); biological efficiency (BE; total lactation MS per 100 kg of LW) and DMI capacity (DMIC; total lactation DMI per 100 kg of LW). Holstein-Friesian cows yielded 376 kg milk more than F×J cows and 1101 kg milk more than J cows per lactation. Holstein-Friesian and F×J produced similar total lactation MSY (366 and 369 kg, respectively). Jersey cows were more efficient than cows of the other breeds: FCE was 78.2, 82.3 and 86.3; BE was 69.7, 74.1 and 77.8; and DMIC was 887.9, 896.8 and 897.7 for F, F×J and J cows, respectively. There were significant differences in production and efficiency among the breeds, with J cows being more efficient per 100 kg of LW than F or F×J cows. Further research is required to compare breed profit per ha in order to conclude the best breed for OAD systems.

Keywords: once-a-day milking; milk yield traits; breed efficiency; stocking rate; Holstein-Friesian; Jersey

Introduction

Dairy cows under seasonal, pasture-based dairy farming in New Zealand traditionally have been milked twice-a-day (TAD). However, farmers have started to adopt once-a-day (OAD) milking for herd management and lifestyle benefits (Davis 2005). The economic viability of OAD systems, however, remains uncertain due to decreases in milk production (Clark et al. 2006; Lembeye et al. 2015).

Davis (2005) and Prendiville et al. (2009) indicated that traits related to efficiencies are critical to economic profitability in dairy systems. Potentially, the impact of efficiency on the profitability during the lactation period might be greater in OAD compared with TAD milking systems, due to the decrease in milk production. Production efficiency has previously been studied in dairy cattle (Mackle et al. 1996; González-Verdugo et al. 2005; López-Villalobos et al. 2008; Prendiville et al. 2009, 2010, 2011a, 2011b). Those studies, however, compared production and efficiency performances of Holstein-Friesian (F), Jersey (J) and their crosses (F×J) under pasture-based systems in cows milked TAD.

In July 2013, Massey University dairy farm No. 1 changed from a TAD split calving herd to a spring calving OAD herd with the feeding system based mainly on pasture of rye-grass and white clover. Stock numbers were reduced from 320 to 250 cows, resulting in a shift of stocking rate (SR) from 2.7 to 2.1 cows/ha. This was in line with farm policy to reduce nitrate leaching and achieve environmental guidelines. Switching from TAD to OAD milking was a strategy to reduce labour costs and remain profitable, while achieving good animal reproduction and health outcomes. This change represented an opportunity to evaluate the breed performance and production efficiencies of F, J and F×J cows milked OAD in a pasture-based system at Massey University’s dairy farm No. 1.

Different measurements of feed efficiency have been proposed in dairy cattle including feed conversion efficiency (Mackle et al. 1996), net efficiency (Schwager-Suter et al. 2001) and residual feed intake (López-Villalobos et al. 2008). In a comparative study among F, J and F×J grazing pasture, Prendiville et al. (2009) used alternative measurements of gross efficiencies defined as kg of milk solids (MS; fat + protein) per

100 kg of live weight (LW); MS per total dry matter intake (DMI) and total DMI per 100 kg of LW. These measurements can be referred to as biological efficiency, feed conversion efficiency and DMI capacity, respectively.

The objective of this study was to compare total lactation yields of milk production traits, somatic cell score (SCS), LW, body condition score (BCS), predicted total DMI, and efficiencies of three different breed groups milked OAD for the whole lactation.

Material and methods

The data analysis consisted of herd test records from 297 cows (77 F, 71 J and 149 F×J) that calved during spring of the dairy seasons 2013-2014 and 2014-2015 at dairy farm No. 1 of Massey University (40°22'S, 175°36'E). Those cows were daughters of 124 sires (39 F, 65 J and 20 F×J). The average breeding worth (BW) of F, J and F×J cows were 130 (range 17 to 221), 146 (range 30 to 229) and 123 (range 29 to 202), respectively. Reliabilities ranged from 25% to 56%. Average production worth (PW) was 164 (range 1 to 409), 155 (range -33 to 314) and 180 (range -10 to 412) for F, J and F×J respectively, with reliabilities ranging from 35%-93%. The farm has a total effective area of 119 ha, consisting of 10 ha of lucerne crop, 10 ha of mixed herb chicory and plantain pasture, and the remainder ryegrass-white clover pasture, with the whole area stocked at a SR of 2.1 cow/ha.

For supplementary feeding, during calving cows had access to a pasture comprised of plantain, chicory and red clover, lucerne and maize silage (an average of 3.5 kg DM supplement/cow/day). During October and November a mixed-herb pasture containing chicory and plantain (an average of 3.7 kg DM/cow/day) was rotationally grazed for a 2 weeks followed by a 2 week rest period. A brassica crop (6.3 kg DM/cow/day on average during summer) and lucerne (4.6 kg DM/cow/day) were grazed during late lactation.

Mean calving dates for seasons 2013-2014 and 2014-2015 were 11 August and 8 August, respectively. Breed groups were determined using pedigree information. Pure-bred F and J cows were defined as those animals where the breed composition was ≥93.75% (15/16) from a particular breed (F or J). Proportion of F and J genes in the F×J cows were on average 8/16 and 7/16 respectively, while 1/16 corresponded to unknown breed composition. In total, data from 427 lactating cows were analysed, 104 of them corresponded to first-lactation cows (22 F [19.8%], 33 J [33.6%] and 49 F×J [11.5%]).

Herd test records (2562) of daily milk yield (MY), percentage of fat and protein, days in milk (DIM) and somatic cell count (SCC) were used. Daily fat (FY) and protein (PY) yield were calculated from daily MY by multiplying by their respective percentages. Herd test SCC was transformed to SCS calculated as SCS=$\log_2$ (SCC). Lactation length was calculated as the difference between date at dry-off and date at calving. For cows that were culled before the end of the season, lactation length was calculated as the maximum DIM provided by the herd test records. Monthly (season 2013-2014) and bimonthly (season 2014-2015) average LW records (4945), along with individual BCS, on a 1-10 scale, (assessed six times during the lactation period in both seasons) were recorded (1916).

Model

Lactation curves were modelled using a third-order orthogonal polynomial (Kirkpatrick et al. 1990) for each cow-lactation combination. Considering y_t as the level of production of a trait 'i' measured on day (t) of the lactation from calving. The polynomial was defined as:

$$Y_t = \alpha_0 P_0 + \alpha_1 P_1 + \alpha_2 P_2 + \alpha_3 P_3$$

where α_i are the regression coefficients to be estimated for each trait.

The Legendre polynomial's functions of P_j were calculated as (Spiegel 1971):

$$P_0(t)=1, P_1(t)=x,\ P_2(t)=\frac{1}{2}(3x^2-1) \text{ and } P_3(t)=\frac{1}{2}(5x^3-3x)$$

where $x = -1+2\cdot\frac{(t-t_{min})}{(t_{max}-t_{min})}$ (Schaeffer 2004).

The polynomial equation presented includes the fixed regression coefficient for the population and random regression coefficients as deviation from the fixed population for each combination cow-lactation. For the cow-lactation 'i' in days in milk 't' the equation is re-written as follow:

$$Y_{ti} = (\beta_0 P_0 + \beta_1 P_1 + \beta_2 P_2 + \beta_3 P_3) + \alpha_{0_i} P_{0_i} + \alpha_{1_i} P_{1_i} + \alpha_{2_i} P_{2_i} + \alpha_{3_i} P_3 + e_{ti}$$

where β values are the fixed regression coefficients of the population, α values are the random regression coefficients for each combination cow-lactation and e_{ti} is the random error associated with each observation of day t and cow-lactation i.

Total lactation yields for milk production traits were estimated for each cow-lactation combination using the polynomial equation, as the sum from day 1 to maximum DIM. Average SCS, LW and BCS were calculated as the mean of these traits using the polynomial equation. Lactation persistency was calculated as total lactation MY divided by peak of daily MY multiplied by lactation length (modified from López-Villalobos et al. 2005).

Metabolisable energy requirements and dry matter intake

It was assumed that pasture contained 18.4 MJ gross energy (GE) and 10.5 MJ ME per kg^{-1} DM; where $q_m = ME/GE$, efficiencies of ME utilization, and energy requirements for maintenance, milk production and body weight change, were calculated as follows (AFRC 1993):

Maintenance: $k_m=0.35\ q_m+0.503$

Lactation: $k_l=0.35\ q_m+0.420$

Body weight gain: $k_g=0.95\ k_l$

Body weight loss: $k_t=0.84$

ME for maintenance (ME_m) was calculated from the following formula:

$$ME_m\left(MJd^{-1}\right)=\frac{F_m+A_c}{k_m}$$

where F_m is the energy requirement before feeding and A_c is the energy required for activity (cows walking 3 km under grazing conditions). F_m and A_c were calculated as follows:

$$F_m=0.53\ (W_t/1.08)^{0.67} \text{ and } A_c=0.016W_t$$

where W_t corresponds to LW on day t after calving.

ME for lactation (ME_l) was calculated with the following formula:

$$ME_l\left(MJd^{-1}\right)=\frac{MY\times EV_l}{k_l}$$

where MY is daily milk yield, EV_l is energy value of 1 kg of milk, $EV_l\,(\mathrm{MJ\ kg^{-1}}) = 0.0376\times F+0.0209\times P$, where F and P are fat and protein contents ($\mathrm{g\ kg^{-1}}$).

ME required for live weight change (ME_{lw}) was calculated as:

$ME_{loss}(\mathrm{MJ\ d^{-1}}) = \frac{EV_g\times 0.84}{k_l}\times\Delta W$ and $ME_{gain}(\mathrm{MJ\ d^{-1}}) = \frac{EV_g}{k_l}\times\Delta W$

where ΔW is change in LW and EV_g is the energy value of a unit of change LW of the cow, this value was assumed constant (19.3 MJ NE).

The total requirements for ME (ME_t) were adjusted for feeding level as:

$$ME_t = \{1 + 0.018(FL - 1)\} \times (ME_m + ME_l + ME_{lw})$$

where FL was calculated as:

$$FL = ([ME_m + ME_l + ME_{lw}]/ME_m).$$

Daily DMI per cow was estimated by dividing ME_t by the content of ME per kg pasture dry matter. It was assumed that cows could consume the pasture needed to achieve their specific energy demands (Brookes 2002). Total lactation of DMI (kg/cow) was calculated as the sum of daily DMI from day 1 to maximum DIM per cow per lactation.

Efficiency measurements

Estimates of efficiencies used in this study were described by Prendiville et al. (2009). Three measurements of efficiency were investigated: biological efficiency (BE), calculated as total lactation MS per 100 kg of LW; dry matter intake capacity (DMIC), calculated as total DMI per 100 kg of LW; and feed conversion efficiency (FCE), as total lactation MS per total DMI expressed as g of MS per kg DMI.

Statistical analysis

Estimates of regression coefficients of the third-order Legendre polynomial for each cow in each lactation, total lactation yields of milk, fat, protein, lactation persistency, mean of SCS, BCS and LW, BE, FCE and DMIC were analysed using the MIXED procedure of SAS version 9.3 (SAS Institute Inc). The mixed linear model included fixed effects of season, breed group, the interaction between season and breed group, the linear and quadratic effect of lactation number, and the linear effect of days from median calving date; and the random effect of the cow-lactation combination.

Results

Table 3.1 presents descriptive statistics for each trait considered in this study. Across the breeds, the predictive ability of the lactation curve methodology was high for the milk traits (r ≥0.93), meanwhile for LW and BCS linear correlations between actual and predicted values ranged between 0.82 and 0.91. Those correlations are presented in Table 3.2.

Table 3.1. Mean, standard deviation (SD), minimum and maximum values for the total lactation record of milk, fat and protein yield, and average somatic cell score, live weight and body condition score of all dairy cows at Massey University dairy farm No. 1 during the dairy seasons 2013-2014 and 2014-2015.

Trait	Mean	SD	Minimum	Maximum
Total milk yield (kg)	3991	1,117	684	7429
Total fat yield (kg)	204.7	48.3	34.4	324.0
Total protein yield (kg)	159.1	41.1	25.8	266.9
Average SCS	6.32	1.44	1.58	13.58
Lactation length (days)	261	37	52	333
Average live weight (kg)	495	67	272	700
Average BCS[1]	4.67	0.58	2.50	7.00

SCS=somatic cell score; BCS= body condition score.

[1] BCS on a 1-to-10 scale

Table 3.2. Estimated Pearson linear correlation and standard error for actual and predicted daily milk, fat and protein yield, somatic cell score, live weight and body condition score modelled with a third-order orthogonal polynomial fitted to Holstein-Friesian (F), Jersey (J) and F×J crossbred cows under once-a-day milking at Massey University dairy farm No. 1.

	Holstein-Friesian	Crossbred	Jersey
Milk yield (kg)	0.98±0.04	0.98±0.03	0.97±0.04
Fat yield (kg)	0.96±0.04	0.95±0.03	0.95±0.04
Protein yield (kg)	0.98±0.04	0.98±0.03	0.97±0.04
SCS	0.93±0.04	0.93±0.03	0.95±0.04
Live weight (kg)	0.91±0.03	0.88±0.02	0.72±0.03
BCS	0.87±0.04	0.89±0.03	0.87±0.05

SCS=somatic cell score; BCS= body condition score.

Table 3.3 details the estimates of regression coefficients describing the lactation curves of milk yield traits, SCS, LW and BCS of the different breed groups milked OAD. At the beginning of the lactation (intercept), F cows had greater values for MY and PY than J and F×J cows. However, FY, the intercept was greater in the crossbred cows. For SCS, the intercepts did not differ among the breeds studied

Table 3.3. Least squares means and standard errors of the estimates of regression coefficients of the lactation curves for milk (MY), fat (FY) and protein (PY) yields, somatic cell score (SCS), live weight (LW) and body condition score (BCS) modelled with a third-order orthogonal polynomial fitted to Holstein-Friesian (F), Jersey (J) and F×J crossbred cows under once-a-day milking at Massey University dairy farm No. 1

Trait	Breed	α_0	α_1	α_2	α_3
MY	F	$15.31^{a} \pm 0.201$	$-9.16^{c} \pm 0.193$	-0.96 ± 0.108	$1.50^{a} \pm 0.116$
	J	$11.61^{c} \pm 0.207$	$-6.66^{a} \pm 0.198$	-0.87 ± 0.111	$1.00^{b} \pm 0.119$
	F×J	$14.11^{b} \pm 0.138$	$-8.22^{b} \pm 0.132$	-1.18 ± 0.074	$1.27^{ab} \pm 0.079$
FY	F	$0.70^{b} \pm 0.010$	$-0.34^{ab} \pm 0.009$	-0.04 ± 0.004	0.04 ± 0.006
	J	$0.70^{b} \pm 0.011$	$-0.32^{a} \pm 0.009$	-0.05 ± 0.004	0.05 ± 0.006
	F×J	$0.74^{a} \pm 0.007$	$-0.35^{b} \pm 0.006$	-0.05 ± 0.003	0.05 ± 0.004
PY	F	$0.58^{a} \pm 0.008$	$-0.29^{b} \pm 0.008$	-0.02 ± 0.005	0.03 ± 0.004
	J	$0.51^{b} \pm 0.008$	$-0.23^{a} \pm 0.008$	-0.03 ± 0.005	0.03 ± 0.004
	F×J	$0.57^{a} \pm 0.005$	$-0.28^{b} \pm 0.006$	-0.04 ± 0.004	0.02 ± 0.003
SCS	F	6.44 ± 0.091	1.11 ± 0.082	$0.17^{b} \pm 0.046$	-0.05 ± 0.063
	J	6.44 ± 0.093	0.98 ± 0.085	$0.28^{ab} \pm 0.047$	-0.09 ± 0.064
	F×J	6.37 ± 0.062	0.98 ± 0.057	$0.29^{a} \pm 0.031$	-0.09 ± 0.043
LW	F	$524.16^{a} \pm 3.26$	$37.40^{a} \pm 1.436$	$-16.68^{c} \pm 0.947$	$19.80^{a} \pm 1.024$
	J	$438.46^{c} \pm 3.47$	$17.36^{c} \pm 1.530$	$-4.20^{a} \pm 1.009$	$5.17^{c} \pm 1.091$
	F×J	$497.59^{b} \pm 2.25$	$29.76^{b} \pm 0.993$	$-13.67^{b} \pm 0.655$	$15.81^{b} \pm 0.708$
BCS	F	$4.61^{b} \pm 0.034$	$0.03^{a} \pm 0.012$	-0.25 ± 0.014	$-0.41^{a} \pm 0.006$
	J	$4.55^{b} \pm 0.035$	$0.03^{a} \pm 0.013$	-0.23 ± 0.015	$-0.41^{a} \pm 0.006$
	F×J	$4.71^{a} \pm 0.023$	$-0.02^{b} \pm 0.008$	-0.25 ± 0.010	$-0.44^{b} \pm 0.004$

MY, milk yield; FY, fat yield; PY, protein yield; SCS, somatic cell score; LW, live weight; BCS, body condition score.

^{a,b,c} Means with different superscripts in the same column are significantly different ($P<0.05$).

Breed group had a significant effect on the traits studied except for SCS, peak day, and lactation persistency. Holstein-Friesian cows yielded 376 kg more milk than F×J cows and 1,101 kg more milk than J cows per lactation. There was no significant difference in total lactation MS between F and F×J cows (Table 3.4).

Table 3.4. Predicted means and standard errors of lactation length, total lactation yields of milk, fat and protein, average somatic cell score, live weight and body condition score, peak and persistency of milk yield of Holstein-Friesian, Jersey and crossbred cows under once-a-day milking at Massey University dairy farm No. 1.

	Holstein-Friesian	Crossbred	Jersey	P-value
Lactation length (days)	256±4	253±3	253±4	0.734
Total milk yield (kg)	4,437^{a} ± 76	4,061^{b} ± 53	3,336^{c} ± 79	<.0001
Total fat yield (kg)	199.7^{ab} ± 3.9	208.2^{a} ± 2.7	197.5^{b} ± 4.1	0.046
Total protein yield (kg)	165.8^{a} ± 3.1	160.3^{a} ± 2.1	142.4^{b} ± 3.2	<.0001
Average SCS	6.22 ± 0.10	6.15 ± 0.07	6.18 ± 0.11	0.834
Average live weight (kg)	518.2^{a} ± 3.2	492.5^{b} ± 2.2	435.0^{c} ± 3.4	<.0001
Average BCS[1]	4.63^{b} ± 0.04	4.74^{a} ± 0.02	4.56^{b} ± 0.04	0.001
Peak DIM (day)	27 ± 3	30 ± 2	31 ± 3	0.524
Peak milk yield (kg)	22.9^{a} ± 0.3	20.9^{b} ± 0.2	17.2^{c} ± 0.3	<.0001
Milk persistency[2] (%)	77.3 ± 0.7	78.9 ± 0.5	78.6 ± 0.8	0.186

SCS=somatic cell score; BCS=body condition score; DIM= days in milk.

[1] BCS on a 1-to-10 scale.

[2] Milk persistency calculated as total milk yield divided by peak daily milk multiplied by lactation length, expressed as percentage.

[a,b,c] Means with different superscripts in the same row are significantly different ($P<0.05$).

Lactation persistency (%) for MY was similar among the breed groups ($P>0.05$) (Table 3.4). Peak daily MY occurred at the end of the first month after calving (Figure 3.1) and was greater in F, followed by F×J and J cows ($P<0.05$). The typical milk lactation curve, with a rapid increase in MY up to about 30 days post-calving and then a gradual decline to the end of the lactation (Grossman et al. 1999) was found in all three breeds. A less well-defined peak, however, was also observed in lactation curves for MS of F and F×J cows (Figure 3.2).

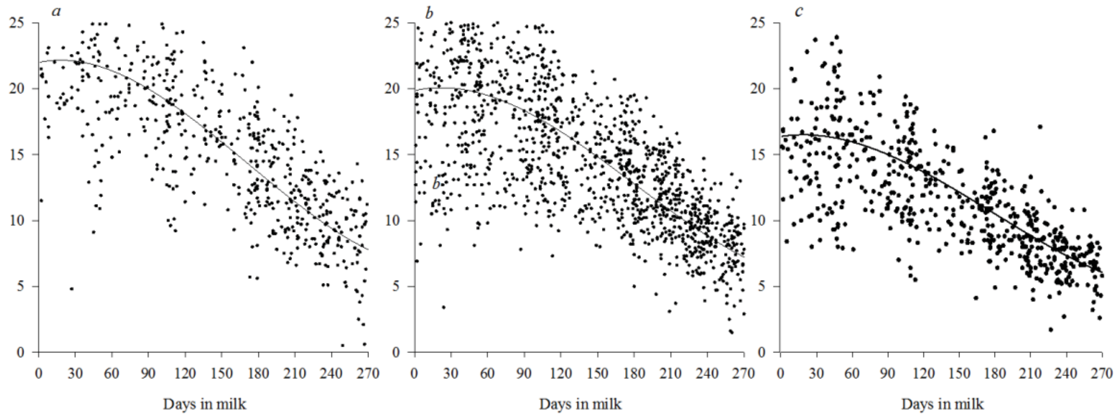

Figure 3.1. Actual herd test record and predicted lactation curves of milk yield (kg/day) of ***a,*** Holstein-Friesian; ***b,*** F×J crossbred; and ***c,*** Jersey cows milked once-a-day at Massey University dairy farm No. 1.

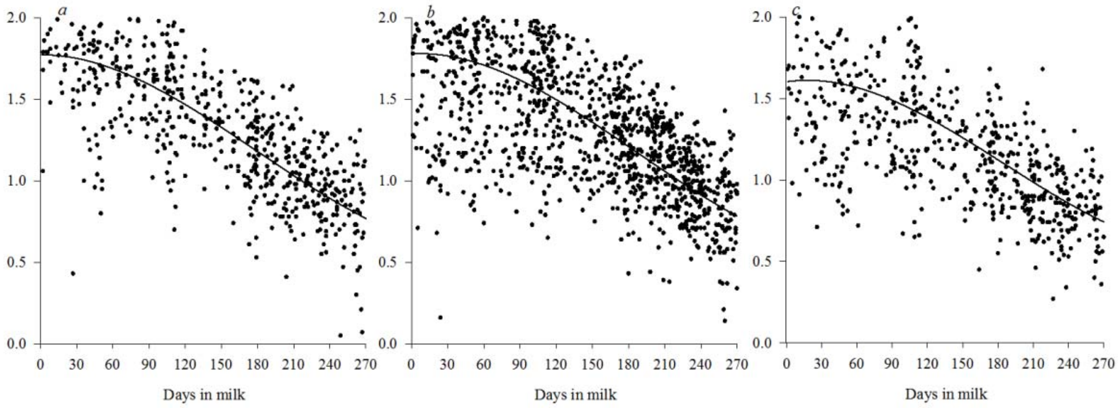

Figure 3.2. Actual herd test record and predicted lactation curves of milk solids yield (kg/day) of ***a,*** Holstein-Friesian; ***b,*** F×J crossbred; and ***c,*** Jersey cows milked once-a-day at Massey University dairy farm No. 1.

The three breed groups studied had similar average SCS. Holstein-Friesian cows were 25.7 kg and 83.2 kg heavier than F×J and J cows, respectively. Crossbred cows had a slightly greater BCS than F and J breeds ($P<0.05$), with no difference between the pure breeds ($P>0.05$).

On average, predicted total lactation DMI of F cows were 18% and 8.7% greater than J and F×J cows, respectively (Table 3.5). Jersey cows had greater FCE (g MS/kg DMI) and BE (kg/100 kg LW) than the other breed groups (10% and 12% greater for FCE and

BE, respectively, compared with F and 5% for both FCE and BE compared with F×J). In contrast, DMIC (kg/100 kg LW) was similar among the breeds studied (Table 3.5).

Table 3.5. Least squares means and standard errors of predicted total dry matter intake, feed conversion efficiency, biological efficiency, dry matter intake capacity of Holstein-Friesian, Jersey and crossbred cows under once-a-day milking at Massey University dairy farm No. 1.

	Holstein-Friesian	Crossbred	Jersey	P value
DMI (kg/cow)	$4599^a \pm 68.0$	$4229^b \pm 47.1$	$3894^c \pm 72.5$	<.0001
FCE (g MS/kg DMI)	$78.2^c \pm 0.56$	$82.3^b \pm 0.39$	$86.3^a \pm 0.60$	<.0001
BE (kg MS/100 kg LW)	$69.7^c \pm 1.38$	$74.1^b \pm 0.95$	$77.8^a \pm 1.47$	<.0001
DMIC (kg DMI/100 kg LW)	887.9 ± 13.9	896.8 ± 9.6	897.7 ± 14.8	0.85

DMI, total dry matter intake; FCE, feed conversion efficiency; BE, biological efficiency; DMIC, dry matter intake capacity; MS, milk solids (fat + protein).
^{a,b,c} Means with different superscripts in the same row are significantly different (*P* <0.05).

Discussion

Total lactation MY per cow estimated in the current study was greater than those reported under research conditions by Clark et al. (2006) with F cows (2914 kg) and J cows (2211 kg) and more recently in commercial herds milked OAD in New Zealand by Lembeye et al. (2015) in F (3198 kg), J (2637 kg) and in F×J cows (3014 kg).

Total lactation MS per cow was also greater than those reported for OAD cows in previous studies (Clark et al. 2006; Lembeye et al. 2015). Clark et al. (2006) and Lembeye et al. (2015) reported values ranging between 222-278 kg/cow, compared with the range of 340-369 kg/cow found in the current study. Production performances found in the current study are similar to the TAD production of cows reported by Clark et al. (2006) and Lembeye et al. (2015).

The three breed groups had similar average SCS, which is in agreement with the study of Prendiville et al. (2010) in Ireland. In New Zealand, Berry et al. (2007) reported a greater SCS for J cows milked TAD, compared with the SCS found for J cows milked OAD in this study (Table 3.4). The SCS results of this study were similar to previously reported values for cows milked TAD (Clark et al. 2006; Lembeye et al. 2015) and lower than those observed in previous OAD studies (Clark et al. 2006; Lembeye et al.

2015). During the transition from TAD to OAD, an increase in SCS is expected (Lacy-Hulbert et al. 2005; Clark et al. 2006). This study indicates that switching from TAD to OAD systems does not necessarily imply an increase in SCS. The latter is attributed to better management practices and possibly to lower exposure to pathogens during the milking process as cows are milked just OAD (Dalley et al. 2007).

Farmers milking their herds OAD generally increase their SR by an average of 17% (Cooper & Clark 2001); however, the 2.2 SR at dairy farm No. 1 of Massey University is lower than the New Zealand average (2.86 cows/ha; LIC & Dairy NZ 2015). A reduced SR generally results in an increase in total MS per cow, but a decrease in total lactation MS per ha (Penno 1999; Macdonald et al. 2001, 2008, 2011). In the current study, the reduced SR may have led to higher availability of dry matter per cow, and more time available for grazing plus supplementary feeding may have allowed the cows to express more of their genetic potential. This may partly explain the higher total lactation milk yield traits compared with those from typical OAD systems in New Zealand. For instance, the average BW and PW of the three breed groups were in the upper quartile of herds in New Zealand (124 and 142, for BW and PW, respectively; LIC & Dairy NZ 2015). Total lactation MS of the herd (kg/cow), on average over the two seasons was slightly lower than the average yield in New Zealand under TAD systems for the same period (371-377 kg; LIC & Dairy NZ 2015). The results of the current study, however, do not necessarily imply that the optimal economic margin in herds milked OAD can be achieved with the SR used in this study. There is a quadratic relationship between SR and net income, being optimal at 3.0-3.5 SR in a typical TAD system in New Zealand (Macdonald et al. 2001). To date, no study has been conducted to estimate the optimum SR in OAD systems. Although the common practice is to increase SR, there is evidence that a 17% higher SR in OAD does not fully compensate for the decrease in milk production in the herds milked OAD compared with herds milked TAD (Clark et al. 2006).

On this farm, total MS per cow from spring calving cows in the last season milked TAD were 427, 343 and 378 kg for F, J and F×J cows, respectively. Those values are 17%, 1% and 2.5% greater than the values presented in Table 3.4 for the same breed groups milked OAD. This suggests that the reduced SR applied when the farm switched to

OAD has been effective in compensating for the reduction in milk yields by providing more energy per cow.

The low SR mentioned previously might also explain the greater average LW in the current study compared with the national average in New Zealand (458, 430 and 376 kg for F, F×J and J cows, respectively; LIC & Dairy NZ 2015), These values are also greater than those reported by Prendiville et al. (2011b) for F×J and J breed groups in Ireland.

Prendiville et al. (2009) reported 15% and 4.3% greater DMI in F compared with J and F×J cows, respectively, which is in agreement with the differences presented in Table 3.5 between F and J, although in that study, DMI was calculated as daily DMI, instead of total lactation DMI as in the current study.

Feed conversion efficiency (g MS/total kg DMI) was consistently higher in J compared with F and F×J. The values presented in Table 3.5 are similar to the findings by Prendiville et al. (2009) (79-88 g of MS/kg DMI), but lower than those of Mackle et al. (1996) (114-132 g MS/kg DMI). Holstein-Friesian and F×J cows had greater milk trait production and predicted total lactation DMI than J cows. However, the utilization of ME and total lactation DMI per unit of LW was higher in J cows. For this reason, cows with higher total lactation DMI (such as F cows) tend to be less suitable for grazing pastures (Veerkamp et al. 1995). Several experiments have demonstrated that J cows are more efficient at converting dry matter into yields of fat and protein (Grainger & Goddard 2004).

Biological efficiency (kg MS/100 kg LW) was greater for J compared with F and F×J cows (Table 3.5), reflecting greater utilisation of the ME and lower heat increment from J cows (L'Huillier et al. 1988). More efficient cows generally have lower BCS (Prendiville 2011a), which is consistent with a reduced BCS found in the J cows compared with F, but BCS was greater in F×J cows compared to the pure breeds, suggesting that some degree of heterosis is possible (Prendiville et al. 2011a, 2011b; Table 3.4).

Dry matter intake capacity (kg DMI/100 kg LW) was similar among the three breeds groups (Table 3.5). This observation was unexpected given that J cows have a greater ability to consume more feed per unit of LW than F cows (2.4%-10.2% more) (Mackle et al. 1996; Prendiville et al. 2009, 2011a), due to a larger reticulo-rumen volume (Smith & Baldwin 1974) and greater digestive efficiency (Ferris et al. 2014).

In general, J cows were more efficient than F and F×J cows due to similar predicted DMIC and lower LW, while only producing slightly less MS per cow compared with the other groups. This implies that J cows required less energy than F cows to produce 1 kg of MS, which is consistent with previous studies (Prendiville et al. 2009, 2011a). However, differences in BE and FCE between J and F×J cows were only 5%, indicating that F×J cows can be effectively suited to OAD systems.

The results of this study indicate that J cows perform best under OAD systems, they have lower LW and DMI, greater FCE and BE, and slightly lower total lactation MS.

Conclusion

The results of this study indicate that there were differences in total MY traits, LW, BCS, total DMI, BE and FCE among F, J and F×J cows milked OAD. In general, J cows were more efficient per kilogram of LW that the other breed groups, which agrees with the higher ranking of this breed for OAD systems. However F×J cows can be suitable for OAD systems, with greater MS and an intermediate FCE and BE. Comparing breed profit and efficiency per ha would provide additional data that would indicate the best breed for pasture-based OAD systems.

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CHAPTER 4

Milk production of Holstein-Friesian, Jersey and crossbred cows milked once-a-day or twice-a-day in New Zealand

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Abstract

The objective of this study was to compare Holstein-Friesian (F), Jersey (J) and crossbred (F×J) cows milked once-a-day (OAD) or twice-a-day (TAD) in New Zealand for milk, fat and protein yield, lactation persistency and average somatic cell score (SCS). Data consisted of 223,149 herd-test records (89,297 and 133,852 OAD and TAD, respectively) from 11,848 F; 11,677 J and 27,720 F×J spring-calving cows between 2008 and 2012. Compared to TAD systems, cows milked OAD yielded 722, 28.0 and 22.2 kg less milk, fat and protein, respectively. Crossbred and J cows were less affected than F cows by OAD milking with a reduction in milk yield traits of ≤19.0%, while in F cows the reduction ranged between 19%-25%. Cows milked OAD had higher SCS than cows milked TAD (6.20 vs. 6.08). The greatest SCS difference in OAD and TAD systems was in first-lactation cows (6.40 vs. 6.02). Persistency of production traits was greater in F and F×J cows milked OAD than in F and F×J cows milked TAD, but J cows had similar milk and protein persistency in both systems. Overall, cows milked OAD had greater persistency than cows milked TAD (79%-90% vs. 76%-85%). These results show that, in commercial herds, the relative difference in production traits between OAD and TAD systems was smaller than those reported in experimental trials.

Keywords: milking frequency; dairy cattle; New Zealand; milk yield traits; lactation persistency

Introduction

Dairy production in New Zealand is typically a spring-calving, pasture-based system. This seasonal system is largely determined by the pattern of pasture growth, where calving of cows precedes a period of rapid pasture growth and cows are dried-off in late-autumn when the pasture growth is slowing (Holmes et al. 2002). In this context, dairy farming has been mostly undertaken using twice-a-day (TAD) milking. However, milking once-a-day (OAD) for the entire season has been adopted by some farmers for herd management and lifestyle benefits (Davis et al. 1999). The popularity of this system increased during the early 2000s (Bewsell et al. 2008), but the number of herds milked OAD has been stable in recent seasons. Currently, up to 5% of herds in New Zealand are milked OAD for the whole season (Stachowicz et al. 2014).

In New Zealand, three controlled research studies have compared cows milked OAD and TAD during the entire lactation (Holmes et al. 1992 [one season]; Cooper 2000 [one season]; Clark et al. 2006 [four seasons]). In these studies the breed groups were: Holstein-Friesian (F), Jersey (J) and their crosses Holstein-Friesian×Jersey (F×J) (Holmes et al. 1992), F×J (Cooper 2000) and purebred F and J (Clark et al. 2006). In general, F and F×J cows milked OAD were more affected than J cows because those breeds had decreased milk production (milk yield and milk solids yield) per cow and per hectare at a greater magnitude than J cows. Jersey cows may not have been affected as much because they can accumulate milk in their udders for longer periods than F cows (Davis et al. 1999).

In the literature, definitions of lactation persistency show a great inconsistency (Grossman et al. 1999). Swalve & Gengler (1999) defined persistency of lactation yield as the ability of the cow to produce milk yield constantly over the lactation period. This trait is positively associated with health and fertility (Dekkers et al. 1998), but has not been directly selected for in the dairy population in New Zealand (Morris et al. 2008), and is not currently included in international evaluations (Cole & Null 2009).

Although there are several definitions of lactation persistency (Grossman et al. 1999; Lopez-Villalobos et al. 2005; Togashi & Lin 2006), there is no general agreement about the most suitable function to calculate it (Swalve & Gengler 1999). Swalve and Gengler

(1999) indicated that an appropriate measure of persistency should be independent of total yields. They indicated that ratios of partial yields (splitting the lactation period in 90- or 100-day intervals) are more suitable and have been used widely since they are easy to compute and compare ascending and descending phases of lactation.

Under OAD systems, Harding et al. (2002) indicated that persistency is a major concern because generally cows dry off early in the season. For this reason selection for persistency is the main option to reduce production losses in OAD systems (Clark et al. 2006; Hickson et al. 2006). Hickson et al. (2006) is the only study comparing lactation persistency in OAD and TAD systems. They used data from the study of Clark et al. (2006) and calculated three different measures of persistency (criteria based on ratios, variation of test-day yields and applications of random regression test-day models). In general, cows from TAD farms had shown better persistency than cows from OAD farms.

Quantifying milk production, lactation persistency and SCS under both milking systems is desirable because breed comparison in both OAD and TAD systems has only been evaluated previously in research facilities. The objective of this study was to compare, using data from commercial farms, milk production traits (milk, fat and protein), lactation persistency and somatic cell score between spring calving F, J and F×J cows milked either OAD or TAD for an entire lactation in New Zealand.

Materials and methods

Data

A total of 16.8 million herd-test records of milk yield (MY), fat yield (FY), protein yield (PY) and somatic cell count (SCC) recorded from 2008 to 2012, and pedigree information were provided by Livestock Improvement Corporation (LIC), New Zealand. Only records from F, J and their crosses were considered, discarding animals missing breed identification.

Initial data were restricted as follows. Firstly, herd-test records were sorted based on milking frequency code provided by LIC (cows milked either OAD or TAD). In the present study, OAD herds are those in which 100% of the cows were milked OAD for the whole lactation. Using the GPS Visualizer (Schneider 2012), TAD herds were selected in a radius of 30 km from OAD herds. In some cases, in a given single map co-ordinate, an OAD herd was surrounded by several TAD herds. In such cases all TAD herds were selected. Also, in other cases, in a given single map co-ordinate, there were several OAD herds and only one TAD was found and selected. Secondly, herds with less than 40 cows were deleted from the analysis. Only records from spring calving cows in their first five lactations were considered. Lastly, lactations where the period from calving to the first herd-test record was longer than 45 days were removed from the analysis.

Cows were considered pure-bred when their breed composition was ≥93.75% (15/16) from a particular breed (F or J), and F×J cows were those cows not meeting the criteria of purebred cow (i.e ≥3/16 breed F or J and ≤14/16 breed J or F, respectively). Coefficient of heterosis in a cow (h_{FxJ}) was calculated using the following equation (Dickerson 1973): $h_{FxJ} = \alpha_F^s \alpha_J^d + \alpha_J^s \alpha_F^d$; where α_F^s and α_J^s are proportion of F or J in the sire and α_J^d and α_F^d are proportion of J and F in the dam, respectively. Somatic cell count was transformed to somatic cell score (SCS) calculated as SCS=$\log_2$ (SCC).

The final data set included 89,297 herd-test records from 278 herds milked OAD and 133,852 herd-test records from 248 herds milked TAD. A summary of the population studied is presented in Table 4.1 by breed and lactation number.

Table 4.1. Number of herd-test records, number of lactations and cows per milking frequency and breed group.

	Once-a-day				Twice-a-day			
	F	F×J	J	Total	F	F×J	J	Total
Herd-test records	11,525	44,005	33,767	89,297	38,081	72,531	23,240	133,852
Lactations	4,116	14,813	9,881	28,810	11,632	22,215	6,298	40,145
Cows	3,234	11,795	7,348	22,377	8,614	15,925	4,329	28,868

F=Holstein-Friesian; J=Jersey; F×J= crossbred Holstein-Friesian×Jersey.

Lactation curves

Lactation curves were modelled using a fifth order Legendre polynomial (Kirkpatrick et al. 1990). Considering Y_t as the level of production of a trait measured on day (t) of the lactation from calving. A polynomial of fifth order, which described a single observation, was defined as:

$$Y_t = \alpha_0 \times P_0 + \alpha_1 \times P_1 + \alpha_2 \times P_2 + \alpha_3 \times P_3 + \alpha_4 \times P_4 + \alpha_5 \times P_5$$

where α_i are the regression coefficients to estimate, P_i are the functions normalised to x which is standardised to unit of time described by: $x = -1 + 2\frac{(t - t_{min})}{(t_{max} - t_{min})}$

where t_{min}=5 d and t_{max}=270 d, which means that herd-test records between 5 to 270 days were converted respectively to the interval -1 to +1 (Schaeffer 2004).

According to Spiegel (1971), first fifth Legendre polynomial's functions of standardised unit of time x and coefficients α_i were calculated as: $P_0(t) = 1$, $P_1(t) = x$, $P_2(t) = \frac{1}{2}(3x^2 - 1)$, $P_3(t) = \frac{1}{2}(5x^3 - 3x)$, $P_4(t) = \frac{1}{8}(35x^4 - 30x^2 + 15)$, $P_5(t) = \frac{1}{8}(63x^5 - 70x^3 + 15x)$.

The polynomial equation presented, includes the fixed regression coefficient for the population and random regression coefficients as deviation from the fixed population for each combination cow-lactation. For the cow-lactation 'i' in days in milk 't' the equation is re-written as follow:

$$Y_{ti} = (\beta_0 P_0 + \beta_1 P_1 + \beta_2 P_2 + \cdots \beta_5 P_5) + \alpha_{0_i} P_{0_i} + \alpha_{1_i} P_{1_i} + \alpha_{2_i} P_{2_i} + \cdots \alpha_{5_i} P_5 + e_{ti}$$

where β values are the fixed regression coefficients of the population, α values are the random regression coefficients for each combination cow-lactation and e_{ti} is the random error associated with each observation of day t and cow-lactation i. The ASREML 3.0 software package (Gilmour et al. 2009) was used to model the lactation curves for MY, FY PY and SCS.

Pearson’s correlation (r) between actual and estimated daily yields and SCS was calculated as a measurement of goodness of fit. Correlation summarises the discrepancy between observed values and the values predicted under the model used.

In addition to the fifth-order Legendre polynomial, polynomials of order 2, 3 and 4 were also tested. The decision to use a fifth-order polynomial was based on the smallest “Akaike's Information Criterion" (AIC) value (Akaike 1973), which was achieved with polynomial of order 5. Therefore, this was selected to predict daily MY, FY, PY, lactation persistency and average SCS.

Persistency

In this study, lactation persistency of each combination cow-lactation was calculated as the area under the lactation curve from day 121 to 180 divided by the area under the curve from day 1 to 60, expressed as a percentage (Lopez-Villalobos et al. 2005). Compared to other measures of persistency, López-Villalobos et al. (2005) found that the selected measure in this study was less dependent of total yields, as recommended by Swalve and Gengler (1999).

Statistical analysis

Accumulated yields of milk, fat and protein for each cow were estimated using the polynomial equation as the sum from day 5 to actual lactation length through 270 days. With respect to average SCS, it was calculated as the mean of the estimated SCS using the orthogonal polynomial’s function. Then the following statistical linear model was used to obtain least square means and standard errors for each parameter of the lactation curve, lactation persistency, predicted accumulated milk, fat and protein yields and average SCS using PROC MIXED of SAS Version 9.3 (SAS Institute Inc.). The model was:

$$y_{ijk} = \mu + HS_i + M_j + L_k + ML_{jk} + \beta_1 f_{j=1} + \beta_2 f_{j=2} + \beta_3 h_{j=1} + \beta_4 h_{j=2} + \beta_5 d + e_{ijk}$$

where y_{ijk} is the MY, FY, PY or average SCS of herd-season i, milking frequency j and lactation number k; μ is population mean; HS_i is random effect of contemporary group i defined as cows calving in the same herd and production season (i=1,2…1568); M_j is the fixed effect of the milking frequency (j=1 and 2); L_k is fixed effect of the lactation number k (k=1,2…5); ML_{jk} is the interaction between milking frequency j and lactation number k; $\beta_1 f_{j=1}$ is the regression coefficient associated with the linear effect of proportion of F in milking frequency 1; $\beta_2 f_{j=2}$ is the regression coefficient associated with the linear effect of proportion of F in milking frequency 2; $\beta_3 h_{j=1}$ is the regression coefficient associated with the linear effect of coefficient of heterosis in milking frequency 1; $\beta_4 h_{j=2}$ is the regression coefficient associated with the linear effect of coefficient of heterosis in milking frequency 2; $\beta_5 d$ is the regression coefficient associated with linear effect of deviation days from the median calving date of the herd per a given season and e_{ijk} is the residual random error associated to the observation y_{ijk}.

Results

Tables 4.2-4.5 detail the estimate of regression coefficients describing the lactation curves of MY, FY, PY and SCS by lactation number for cows of the different breed groups under the two milking frequencies.

At the beginning of the lactation (intercept), cows milked TAD had higher values for yields of milk, fat and protein than cows milked OAD. For SCS, however, the intercept was only different in F, F×J and first-lactation cows, where SCS was higher in cows under OAD systems.

In general, the predictive ability of fifth order Legendre polynomial for the four traits studied was high for all the traits ($r \geq 0.98$) (data not shown), and it showed a more flexible lactation shape than the other Legendre polynomials tested.

Across milking frequency, typical milk lactation curves (rapid increase in milk yield up to about 30-45 days post calving, and then a gradual decline to the end of the lactation; Grossman et al. 1999) were found in mature cows (second to fifth lactation) (Figure 4.1) and in the three breeds (Figure 4.2), although a less well-defined peak, in particular in J cows, is observed for lactation curves in OAD systems.

Importantly, for each breed and milking frequency, the predicted peaks occurred before 30 days of lactation. However, in first-lactation cows, for both milking frequencies, the same lactation curve did not exist. The predicted lactation curve for first-lactation cows milked OAD had a predicted peak of production at the beginning of the lactation, which gradually declined to a period of stability between day 30 and day 100 of lactation followed by a constant decline to the last day modelled. In first-lactation cows milked TAD there was a predicted peak at the beginning, a gradual decline to day 240 of lactation with a clear increase in the last 30 days of lactation.

Table 4.2. Least square means and standard errors of regression coefficients of the lactation curve for milk yield modelled with a fifth-order Legendre polynomial fitted to Holstein-Friesian (F), Jersey (J) and first F×J crossbred cows of different lactation number and milking frequency (MF).

MF[1]	Breed	Lactation number	α_0	P-value	α_1	P-value	α_2	P-value	α_3	P-value	α_4	P-value	α_5	P-value
OAD			$11.16^{a} \pm 0.09$	<0.001	-5.08a ± 0.05	<0.001	$-0.55^{a} \pm 0.04$	<0.001	$0.57^{a} \pm 0.04$	0.138	$-0.24^{a} \pm 0.04$	<0.001	$-0.03^{a} \pm 0.04$	<0.001
TAD			$13.65^{b} \pm 0.08$		-6.32b ± 0.05		$-0.10^{b} \pm 0.04$		$0.50^{a} \pm 0.04$		$-0.58^{b} \pm 0.04$		$0.45^{b} \pm 0.04$	
OAD	F		$13.37^{a} \pm 0.16$	<0.001	-5.91a ± 0.09	<0.001	$-0.47^{a} \pm 0.08$	<0.001	$0.66^{a} \pm 0.06$	0.488	$-0.45^{a} \pm 0.06$	<0.001	$0.13^{a} \pm 0.06$	<0.001
TAD	F		$17.69^{b} \pm 0.11$		-8.17b ± 0.06		$0.03^{b} \pm 0.05$		$0.70^{a} \pm 0.04$		$-0.80^{b} \pm 0.04$		$0.83^{b} \pm 0.04$	
OAD	F×J		$12.61^{a} \pm 0.14$	<0.001	-5.61a ± 0.10	<0.001	$-0.62^{a} \pm 0.08$	<0.001	$0.57^{a} \pm 0.07$	0.267	$-0.26^{a} \pm 0.07$	<0.001	$0.22^{a} \pm 0.08$	<0.001
TAD	F×J		$15.65^{b} \pm 0.13$		-7.13b ± 0.10		$-0.22^{b} \pm 0.08$		$0.67^{a} \pm 0.07$		$-0.60^{b} \pm 0.07$		$0.56^{b} \pm 0.08$	
OAD	J		$11.13^{a} \pm 0.08$	<0.001	-5.10a ± 0.05	<0.001	$-0.55^{a} \pm 0.04$	<0.001	$0.55^{a} \pm 0.04$	0.639	$-0.21^{a} \pm 0.04$	<0.001	$-0.03^{a} \pm 0.04$	<0.001
TAD	J		$13.51^{b} \pm 0.09$		-6.14b ± 0.06		$-0.33^{b} \pm 0.05$		$0.51^{a} \pm 0.05$		$-0.48^{b} \pm 0.05$		$0.39^{b} \pm 0.05$	
OAD		1	$8.25^{a} \pm 0.09$	<0.001	-3.51a ± 0.06	<0.001	$-0.78^{a} \pm 0.05$	<0.001	$0.39^{a} \pm 0.04$	0.248	$0.01^{a} \pm 0.04$	<0.001	$-0.43^{a} \pm 0.04$	<0.001
TAD		1	$10.45^{b} \pm 0.09$		-4.72b ± 0.06		$-0.22^{b} \pm 0.05$		$0.33^{a} \pm 0.04$		$-0.43^{b} \pm 0.04$		$0.11^{b} \pm 0.04$	
OAD		2	$10.70^{a} \pm 0.09$	<0.001	-4.81a ± 0.06	<0.001	$-0.58^{a} \pm 0.04$	<0.001	$0.53^{a} \pm 0.04$	0.005	$-0.23^{a} \pm 0.04$	<0.001	$-0.05^{a} \pm 0.04$	<0.001
TAD		2	$12.96^{b} \pm 0.09$		-5.91b ± 0.05		$-0.11^{b} \pm 0.04$		$0.37^{b} \pm 0.04$		$-0.52^{b} \pm 0.04$		$0.44^{b} \pm 0.04$	
OAD		3	$11.83^{a} \pm 0.09$	<0.001	-5.47a ± 0.06	<0.001	$-0.47^{a} \pm 0.05$	<0.001	$0.60^{a} \pm 0.04$	0.160	$-0.29^{a} \pm 0.04$	<0.001	$0.08^{a} \pm 0.04$	<0.001
TAD		3	$14.44^{b} \pm 0.09$		-6.68b ± 0.06		$-0.03^{b} \pm 0.05$		$0.52^{a} \pm 0.04$		$-0.66^{b} \pm 0.04$		$0.49^{b} \pm 0.04$	
OAD		4	$12.39^{a} \pm 0.09$	<0.001	-5.73a ± 0.06	<0.001	$-0.45^{a} \pm 0.05$	<0.001	$0.64^{a} \pm 0.04$	0.927	$-0.33^{a} \pm 0.04$	<0.001	$0.13^{a} \pm 0.04$	<0.001
TAD		4	$15.08^{b} \pm 0.09$		-7.08b ± 0.06		$-0.06^{b} \pm 0.05$		$0.65^{a} \pm 0.04$		$-0.66^{b} \pm 0.04$		$0.59^{b} \pm 0.04$	
OAD		5	$12.63^{a} \pm 0.09$	<0.001	-5.87a ± 0.06	<0.001	$-0.48^{a} \pm 0.05$	<0.001	$0.71^{a} \pm 0.04$	0.096	$-0.33^{a} \pm 0.04$	<0.001	$0.14^{a} \pm 0.04$	<0.01
TAD		5	$15.29^{b} \pm 0.09$		-7.20b ± 0.06		$-0.07^{b} \pm 0.05$		$0.61^{a} \pm 0.04$		$-0.62^{a} \pm 0.04$		$0.64^{b} \pm 0.04$	

[1] MF OAD=once-a-day milking MF TAD=twice-a-day milking.

[a,b], Least squares means with different superscripts are significantly different between milking frequencies with breed-type or within lactation number.

Table 4.3. Least square means and standard errors (x10^2) of regression coefficients of the lactation curve for fat yield modelled with a fifth-order Legendre polynomial fitted to Holstein-Friesian (F), Jersey (J) and first F×J crossbred cows of different lactation number and milking frequency (MF).

MF[1]	Breed	Lactation number	α_0	P-value	α_1	P-value	α_2	P-value	α_3	P-value	α_4	P-value	α_5	P-value
OAD			$65.13^a \pm 0.40$	<0.001	$-16.83^a \pm 0.24$	<0.001	$-2.97^a \pm 0.19$	<0.001	$1.76^a \pm 0.17$	0.144	$-2.01^a \pm 0.15$	<0.001	$-0.47^a \pm 0.16$	<0.001
TAD			$76.76^b \pm 0.39$		$-22.09^b \pm 0.25$		$-1.24^b \pm 0.20$		$1.59^a \pm 0.17$		$-3.66^b \pm 0.16$		$1.23^b \pm 0.17$	
OAD	F		$65.16^a \pm 0.67$	<0.001	$-17.43^a \pm 0.40$	<0.001	$-1.87^a \pm 0.31$	<0.001	$1.57^a \pm 0.27$	0.005	$-2.26^a \pm 0.27$	<0.001	$-0.24^a \pm 0.23$	<0.001
TAD	F		$79.74^b \pm 0.45$		$-24.97^b \pm 0.26$		$0.82^b \pm 0.20$		$0.68^b \pm 0.17$		$-3.69^b \pm 0.17$		$3.63^b \pm 0.14$	
OAD	F×J		$67.34^a \pm 0.68$	<0.001	$-18.07^a \pm 0.48$	<0.001	$-2.55^a \pm 0.39$	0.003	$1.23^a \pm 0.34$	0.978	$-2.08^a \pm 0.33$	0.008	$0.36^a \pm 0.36$	0.216
TAD	F×J		$77.99^b \pm 0.68$		$-22.79^b \pm 0.48$		$-0.89^b \pm 0.40$		$1.21^a \pm 0.35$		$-3.20^b \pm 0.34$		$1.46^a \pm 0.37$	
OAD	J		$65.34^a \pm 0.43$	<0.001	$-17.06^a \pm 0.28$	<0.001	$-3.06^a \pm 0.23$	0.004	$1.74^a \pm 0.20$	0.597	$-1.96^a \pm 0.19$	<0.001	$-0.42^a \pm 0.19$	<0.001
TAD	J		$77.31^b \pm 0.50$		$-21.76^b \pm 0.34$		$-2.02^b \pm 0.27$		$1.58^a \pm 0.24$		$-3.44^b \pm 0.23$		$1.19^b \pm 0.23$	
OAD		1	$50.82^a \pm 0.42$	<0.001	$-11.26^a \pm 0.26$	<0.001	$-2.86^a \pm 0.21$	<0.001	$1.13^a \pm 0.18$	0.163	$-1.12^a \pm 0.17$	<0.001	$-1.98^a \pm 0.18$	<0.001
TAD		1	$62.08^b \pm 0.40$		$-16.69^b \pm 0.26$		$-0.60^b \pm 0.21$		$0.94^a \pm 0.19$		$-3.12^b \pm 0.18$		$0.27^b \pm 0.19$	
OAD		2	$62.97^a \pm 0.41$	<0.001	$-15.75^a \pm 0.25$	<0.001	$-3.02^a \pm 0.21$	<0.001	$1.60^a \pm 0.18$	0.078	$-2.02^a \pm 0.17$	<0.001	$-0.63^a \pm 0.18$	<0.001
TAD		2	$73.69^b \pm 0.40$		$-20.28^b \pm 0.26$		$-1.37^b \pm 0.21$		$1.15^a \pm 0.18$		$-3.45^b \pm 0.17$		$1.05^b \pm 0.18$	
OAD		3	$68.72^a \pm 0.42$	<0.001	$-18.40^a \pm 0.26$	<0.001	$-2.86^a \pm 0.21$	<0.001	$1.91^a \pm 0.18$	0.156	$-2.37^a \pm 0.17$	<0.001	$-0.04^a \pm 0.18$	<0.001
TAD		3	$80.55^b \pm 0.40$		$-23.31^b \pm 0.26$		$-1.23^b \pm 0.21$		$1.71^a \pm 0.18$		$-4.05^b \pm 0.17$		$1.32^b \pm 0.18$	
OAD		4	$71.01^a \pm 0.43$	<0.001	$-19.13^a \pm 0.27$	<0.001	$-3.05^a \pm 0.22$	<0.001	$2.03^a \pm 0.19$	0.344	$-2.47^a \pm 0.18$	<0.001	$0.08^a \pm 0.19$	<0.001
TAD		4	$83.32^b \pm 0.40$		$-24.98^b \pm 0.26$		$-1.38^b \pm 0.22$		$2.19^a \pm 0.10$		$-3.94^b \pm 0.18$		$1.57^b \pm 0.19$	
OAD		5	$72.12^a \pm 0.43$	<0.001	$-19.61^a \pm 0.28$	<0.001	$-3.09^a \pm 0.23$	<0.001	$2.11^a \pm 0.20$	0.235	$-2.52^a \pm 0.19$	<0.001	$0.26^a \pm 0.20$	<0.001
TAD		5	$84.18^b \pm 0.41$		$-25.22^b \pm 0.27$		$-1.62^b \pm 0.22$		$1.94^a \pm 0.19$		$-3.75^b \pm 0.18$		$1.95^b \pm 0.20$	

[1] MF OAD=once-a-day milking MF TAD=twice-a-day milking.

[a,b], Least squares means with different superscripts are significantly different between milking frequencies with breed-type or within lactation number.

Table 4.4. Least square means and standard error (x10^{2}) of regression coefficients of the lactation curve for protein yield modelled with a fifth-order Legendre polynomial fitted to Holstein-Friesian (F), Jersey (J) and first F×J crossbred cows of different lactation number and milking frequency (MF).

MF[1]	Breed	Lactation number	α_0	P-value	α_1	P-value	α_2	P-value	α_3	P-value	α_4	P-value	α_5	P-value
OAD			$47.71^{a} \pm 0.33$	<0.001	$-15.19^{a} \pm 0.19$	<0.001	$-1.03^{a} \pm 0.16$	<0.001	$0.57^{a} \pm 0.14$	0.165	$-0.77^{a} \pm 0.14$	<0.001	$-2.68^{a} \pm 0.14$	<0.001
TAD			$55.95^{b} \pm 0.31$		$-19.44^{b} \pm 0.19$		$0.91^{b} \pm 0.16$		$0.29^{a} \pm 0.15$		$-2.03^{b} \pm 0.14$		$-1.28^{b} \pm 0.14$	
OAD	F		$51.81^{a} \pm 0.58$	<0.001	-16.61a ± 0.33	<0.001	$-0.45^{a} \pm 0.29$	<0.001	$0.55^{a} \pm 0.25$	0.289	$-1.32^{a} \pm 0.22$	<0.001	$-2.51^{a} \pm 0.23$	<0.001
TAD	F		$64.50^{b} \pm 0.40$		$-24.01^{b} \pm 0.22$		$2.21^{b} \pm 0.17$		$0.23^{a} \pm 0.16$		$-2.57^{b} \pm 0.14$		$0.16^{b} \pm 0.15$	
OAD	F×J		$51.24^{a} \pm 0.52$	<0.001	$-16.34^{a} \pm 0.36$	<0.001	$-1.11^{a} \pm 0.32$	<0.001	$0.30^{a} \pm 0.27$	0.480	$-0.79^{a} \pm 0.29$	0.005	$-1.89^{a} \pm 0.31$	0.304
TAD	F×J		$60.54^{b} \pm 0.51$		$-21.56^{b} \pm 0.36$		$0.85^{b} \pm 0.32$		$0.53^{a} \pm 0.28$		$-1.94^{b} \pm 0.29$		$-0.90^{a} \pm 0.31$	
OAD	J		$47.88^{a} \pm 0.33$	<0.001	$-15.35^{a} \pm 0.21$	<0.001	$-1.09^{a} \pm 0.18$	<0.001	$0.53^{a} \pm 0.16$	0.478	$-0.66^{a} \pm 0.16$	<0.001	$-2.64^{a} \pm 0.16$	<0.001
TAD	J		$56.13^{b} \pm 0.38$		$-19.00^{b} \pm 0.25$		$-0.02^{b} \pm 0.21$		$0.40^{a} \pm 0.19$		$-1.73^{b} \pm 0.19$		$-1.46^{b} \pm 0.19$	
OAD		1	$36.02^{a} \pm 0.34$	<0.001	$-9.89^{a} \pm 0.21$	<0.001	$-1.58^{a} \pm 0.17$	<0.001	$0.09^{a} \pm 0.15$	0.437	$0.15^{a} \pm 0.15$	<0.001	$-3.97^{a} \pm 0.15$	<0.001
TAD		1	$43.83^{b} \pm 0.32$		$-13.79^{b} \pm 0.20$		$0.41^{b} \pm 0.17$		$-0.15^{a} \pm 0.15$		$-1.39^{b} \pm 0.15$		$-2.33^{b} \pm 0.15$	
OAD		2	$45.99^{a} \pm 0.33$	<0.001	$-14.27^{a} \pm 0.20$	<0.001	$-1.15^{a} \pm 0.17$	<0.001	$0.43^{a} \pm 0.15$	0.034	$-0.75^{a} \pm 0.15$	<0.001	$-2.72^{a} \pm 0.15$	<0.001
TAD		2	$53.66^{b} \pm 0.32$		$-18.08^{b} \pm 0.20$		$0.86^{b} \pm 0.17$		$-0.13^{b} \pm 0.15$		$-1.85^{b} \pm 0.15$		$-1.27^{b} \pm 0.15$	
OAD		3	$50.60^{a} \pm 0.34$	<0.001	$-16.60^{a} \pm 0.20$	<0.001	$-0.84^{a} \pm 0.18$	<0.001	$0.65^{a} \pm 0.15$	0.013	$-0.97^{a} \pm 0.15$	<0.001	$-2.31^{a} \pm 0.15$	<0.001
TAD		3	$59.09^{b} \pm 0.32$		$-20.81^{b} \pm 0.20$		$1.20^{b} \pm 0.17$		$0.36^{b} \pm 0.15$		$-2.36^{b} \pm 0.15$		$-1.16^{b} \pm 0.15$	
OAD		4	$52.57^{a} \pm 0.34$	<0.001	$-17.41^{a} \pm 0.21$	<0.001	$-0.73^{a} \pm 0.18$	<0.001	$0.77^{a} \pm 0.16$	0.992	$-1.14^{a} \pm 0.15$	<0.001	$-2.24^{a} \pm 0.16$	<0.001
TAD		4	$61.24^{b} \pm 0.32$		$-22.10^{b} \pm 0.20$		$1.06^{b} \pm 0.18$		$0.78^{a} \pm 0.16$		$-2.38^{b} \pm 0.15$		$-0.88^{b} \pm 0.16$	
OAD		5	$53.38^{a} \pm 0.35$	<0.001	$-17.81^{a} \pm 0.22$	<0.001	$-0.83^{a} \pm 0.19$	<0.001	$0.92^{a} \pm 0.17$	0.475	$-1.15^{a} \pm 0.16$	<0.001	$-2.15^{a} \pm 0.16$	<0.001
TAD		5	$61.90^{b} \pm 0.33$		$-22.41^{b} \pm 0.21$		1.03^{b} ±0 .19		$0.60^{a} \pm 0.16$		$-2.17^{b} \pm 0.16$		$-0.76^{b} \pm 0.16$	

[1] MF OAD=once-a-day milking MF TAD=twice-a-day milking.

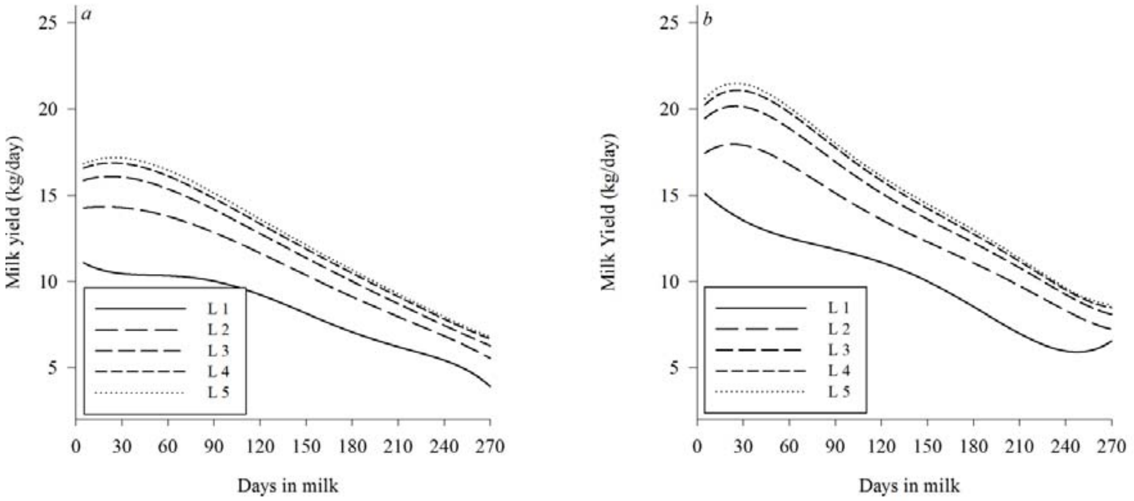
[a,b], Least square means with different superscripts are significantly different between milking frequencies with breed-type or within lactation number.

Table 4.5. Least squares means and standard error of regression coefficients of the somatic cell curve modelled with a fifth-order Legendre polynomial fitted to Holstein-Friesian (F), Jersey (J) and F×J crossbred cows of different lactation number and milking frequency (MF).

MF[1]	Breed	Lactation number	α_0	P-value	α_1	P-value	α_2	P-value	α_3	P-value	α_4	P-value	α_5	P-value
OAD			$6.29^{a} \pm 0.02$	0.301	$0.88^{a} \pm 0.01$	<0.001	$0.38^{a} \pm 0.01$	0.179	$-0.16^{a} \pm 0.01$	0.406	$0.08^{a} \pm 0.01$	0.347	$-0.16^{a} \pm 0.01$	0.034
TAD			$6.26^{a} \pm 0.02$		$0.82^{a} \pm 0.01$		$0.40^{a} \pm 0.01$		$-0.15^{a} \pm 0.01$		$0.09^{a} \pm 0.01$		$-0.13^{a} \pm 0.01$	
OAD	F		$6.48^{a} \pm 0.02$	<0.001	$0.97^{a} \pm 0.01$	<0.001	$0.26^{a} \pm 0.01$	<0.001	$-0.22^{a} \pm 0.01$	0.034	$0.10^{a} \pm 0.01$	0.157	$-0.13^{a} \pm 0.01$	0.480
TAD	F		$6.32^{b} \pm 0.02$		$0.87^{b} \pm 0.01$		$0.35^{b} \pm 0.01$		$-0.19^{b} \pm 0.01$		$0.12^{a} \pm 0.01$		$-0.12^{a} \pm 0.01$	
OAD	F×J		$6.47^{a} \pm 0.04$	0.001	$0.90^{a} \pm 0.03$	0.637	$0.36^{a} \pm 0.02$	1.000	$-0.23^{a} \pm 0.02$	0.013	$0.08^{a} \pm 0.02$	0.724	$-0.11^{a} \pm 0.02$	0.077
TAD	F×J		$6.28^{b} \pm 0.05$		$0.88^{a} \pm 0.03$		$0.36^{a} \pm 0.02$		$-0.16^{b} \pm 0.02$		$0.09^{a} \pm 0.02$		$-0.16^{a} \pm 0.02$	
OAD	J		$6.29^{a} \pm 0.02$	0.096	$0.87^{a} \pm 0.01$	<0.001	$0.39^{a} \pm 0.01$	0.005	$-0.15^{a} \pm 0.01$	0.480	$0.07^{a} \pm 0.01$	0.480	$-0.16^{a} \pm 0.01$	0.034
TAD	J		$6.23^{a} \pm 0.03$		$0.78^{b} \pm 0.02$		$0.43^{b} \pm 0.01$		$-0.14^{a} \pm 0.01$		$0.08^{a} \pm 0.01$		$-0.13^{b} \pm 0.01$	
OAD		1	$6.44^{a} \pm 0.02$	<0.001	$0.55^{a} \pm 0.01$	0.034	$0.46^{a} \pm 0.01$	<0.05	$-0.07^{a} \pm 0.01$	0.005	$0.05^{a} \pm 0.01$	0.480	$-0.13^{a} \pm 0.01$	0.034
TAD		1	$6.18^{b} \pm 0.02$		$0.58^{b} \pm 0.01$		$0.52^{b} \pm 0.01$		$-0.11^{b} \pm 0.01$		$0.06^{a} \pm 0.01$		$-0.10^{a} \pm 0.01$	
OAD		2	$6.08^{a} \pm 0.02$	0.480	$0.86^{a} \pm 0.01$	0.005	$0.43^{a} \pm 0.01$	0.480	$-0.13^{a} \pm 0.01$	0.480	$0.08^{a} \pm 0.01$	0.480	$-0.17^{a} \pm 0.01$	0.034
TAD		2	$6.06^{a} \pm 0.02$		$0.82^{b} \pm 0.01$		$0.44^{a} \pm 0.01$		$-0.14^{a} \pm 0.01$		$0.09^{a} \pm 0.01$		$-0.14^{b} \pm 0.01$	
OAD		3	$6.18^{a} \pm 0.02$	0.724	$0.97^{a} \pm 0.01$	<0.001	$0.36^{a} \pm 0.01$	0.480	$-0.18^{a} \pm 0.01$	0.157	$0.09^{a} \pm 0.01$	0.480	$-0.17^{a} \pm 0.01$	0.034
TAD		3	$6.19^{a} \pm 0.02$		$0.88^{b} \pm 0.01$		$0.37^{a} \pm 0.01$		$-0.16^{a} \pm 0.01$		$0.10^{a} \pm 0.01$		$-0.14^{b} \pm 0.01$	
OAD		4	$6.31^{a} \pm 0.02$	0.157	$0.99^{a} \pm 0.01$	<0.001	$0.33^{a} \pm 0.01$	0.480	$-0.19^{a} \pm 0.01$	0.157	$0.09^{a} \pm 0.01$	0.480	$-0.16^{a} \pm 0.01$	0.157
TAD		4	$6.35^{a} \pm 0.02$		$0.89^{b} \pm 0.01$		$0.34^{a} \pm 0.01$		$-0.17^{a} \pm 0.01$		$0.10^{a} \pm 0.01$		$-0.14^{b} \pm 0.01$	
OAD		5	$6.43^{a} \pm 0.02$	<0.001	$1.02^{a} \pm 0.02$	<0.001	$0.32^{a} \pm 0.01$	1.000	$-0.23^{a} \pm 0.01$	0.005	$0.08^{a} \pm 0.01$	0.480	$-0.15^{a} \pm 0.01$	0.157
TAD		5	$6.53^{b} \pm 0.02$		$0.90^{b} \pm 0.02$		$0.32^{a} \pm 0.01$		$-0.19^{b} \pm 0.01$		$0.09^{a} \pm 0.01$		$-0.13^{a} \pm 0.01$	

[1] MF OAD=once-a-day milking MF TAD=twice-a-day milking.

^{a,b}, Least square means with different superscripts are significantly different between milking frequencies with breed-type or within lactation number.



L_1=first-lactation, L_2= second-lactation, L_3= third-lactation, L_4=fourth-lactation, L_5=fifth-lactation

Figure 4.1. Predicted milk yield from calving to 270 d of lactation across lactation (L_1-L_5) in cows milked once-a-day (*a*) and twice-a-day (*b*).

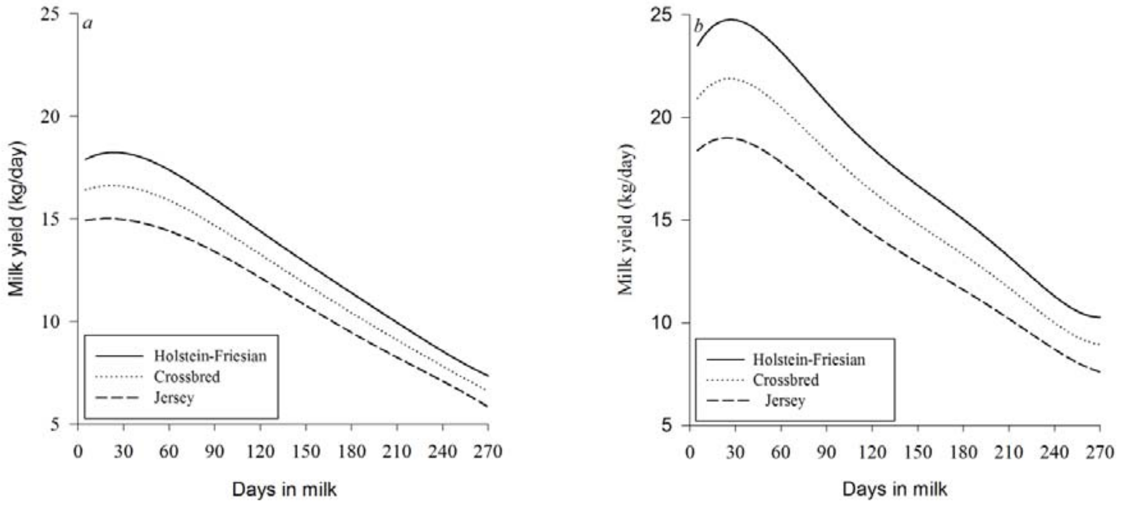


Figure 4.2. Predicted milk yield from calving to 270 d of lactation of Holstein-Friesian, Jersey and F×J crossbred cows milked once-a-day (*a*) and twice-a-day (*b*).

Least square means for predicted MY, FY, PY and average SCS and persistency for the lactation are presented in Tables 4.6-4.7. The results show that cows milked OAD yielded 722 kg less milk (21.1%), 28.0 kg less fat (16.9%), 22.2 kg less protein (17.2%) and had 0.12 greater SCS (1.9%) than their equivalent TAD cows.

Table 4.6. Predicted least square means with standard errors of total yields of milk, fat and protein, and average somatic cell score (SCS) in New Zealand dairy cattle, by milking frequency (MF), breed group and lactation number.

MF[1]	Breed[2]	Lactation number	Milk yield		Fat yield		Protein yield		Average SCS	
			Mean (kg/cow)	P-value	Mean (kg/cow)	P-value	Mean (kg/cow)	P-value	Mean (units)	P-value
OAD			2,698^{a} ± 30	<0.001	138.1^{a} ± 1.5	<0.001	106.7^{a} ± 1.2	<0.001	6.20^{a} ± 0.02	<0.001
TAD			3,420^{b} ± 27		166.1^{b} ± 1.4		128.9^{b} ± 1.1		6.08^{b} ± 0.02	
OAD	F		2,879^{a} ± 54	<0.001	135.5^{a} ± 2.4	<0.001	108.7^{a} ± 1.9	<0.001	6.30^{a} ± 0.04	<0.001
TAD	F		3,824^{b} ± 37		167.1^{b} ± 1.7		136.6^{b} ± 1.4		6.13^{b} ± 0.02	
OAD	F×J		2,787^{a} ± 40	<0.001	143.3^{a} ± 2.1	<0.001	110.4^{a} ± 1.6	<0.001	6.28^{a} ± 0.04	0.002
TAD	F×J		3,446^{b} ± 36		168.8^{b} ± 1.9		130.9^{b} ± 1.4		6.06^{b} ± 0.03	
OAD	J		2,427^{a} ± 30	<0.001	137.1^{a} ± 1.8	<0.001	101.4^{a} ± 1.3	<0.001	6.11^{a} ± 0.03	0.280
TAD	J		2,929^{b} ± 34		162.2^{b} ± 2.0		118.8^{b} ± 1.5		6.05^{a} ± 0.03	
OAD		1	2,006^{a} ± 30	<0.001	104.2^{a} ± 1.5	<0.001	79.0^{a} ± 1.9	<0.001	6.40^{a} ± 0.02	<0.001
TAD		1	2,675^{b} ± 27		131.9^{b} ± 1.4		100.5^{b} ± 1.1		6.02^{b} ± 0.02	
OAD		2	2,603^{a} ± 30	<0.001	133.8^{a} ± 1.5	<0.001	103.3^{a} ± 1.2	<0.001	5.97^{a} ± 0.02	<0.001
TAD		2	3,277^{b} ± 27		159.7^{b} ± 1.4		124.2^{b} ± 1.1		5.85^{b} ± 0.02	
OAD		3	2,868a ± 30	<0.001	147.1^{a} ± 1.5	<0.001	113.9^{a} ± 1.2	<0.001	6.06^{a} ± 0.02	0.035
TAD		3	3,611^{b} ± 27		175.3^{b} ± 1.4		136.5^{b} ± 1.1		5.99^{b} ± 0.02	
OAD		4	2,985^{a} ± 31	<0.001	151.7^{a} ± 1.5	<0.001	118.0^{a} ± 1.2	<0.001	6.21^{a} ± 0.02	0.083
TAD		4	3,750^{b} ± 28		181.3^{b} ± 1.4		141.2^{b} ± 1.1		6.15^{a} ± 0.02	
OAD		5	3,032^{a} ± 31	<0.001	153.9^{a} ± 1.5	<0.001	119.5^{a} ± 1.2	<0.001	6.34^{a} ± 0.03	0.605
TAD		5	3,785^{b} ± 28		182.3^{b} ± 1.4		142.2^{b} ± 1.1		6.36^{a} ± 0.02	

[1] MF OAD=once-a-day milking MF TAD=twice-a-day milking.

[2] F=Holstein-Friesian, J=Jersey and F×J crossbred cows.

[a,b], Least square means with different superscripts are significantly different between milking frequencies with breed-type or within lactation number.

Table 4.7. Predicted least square means with standard errors of lactation persistency of milk, fat and protein yield in New Zealand dairy cattle, by milking frequency (MF), breed group and lactation number.

MF[1]	Breed[2]	Lactation number	Milk yield		Fat yield		Protein yield	
			(%)	P-value	(%)	P-value	(%)	P-value
OAD			$78.7^{a} \pm 0.4$	<0.001	$89.8^{a} \pm 0.4$	<0.001	$84.6^{a} \pm 0.4$	<.0001
TAD			$75.9^{b} \pm 0.4$		$85.1^{b} \pm 0.4$		$79.4^{b} \pm 0.4$	
OAD	F		$79.4^{a} \pm 0.7$	<0.001	$88.8^{a} \pm 0.8$	<0.001	$84.3^{a} \pm 0.7$	<.0001
TAD	F		$75.8^{b} \pm 0.5$		$83.5^{b} \pm 0.5$		$78.1^{b} \pm 0.5$	
OAD	F×J		$80.5^{a} \pm 0.6$	<0.001	$90.5^{a} \pm 0.7$	<0.001	$86.0^{a} \pm 0.6$	<.0001
TAD	F×J		$76.9^{b} \pm 0.5$		$86.4^{b} \pm 0.6$		$80.6^{b} \pm 0.6$	
OAD	J		$78.3^{a} \pm 0.5$	0.238	$90.8^{a} \pm 0.6$	0.002	$84.7^{a} \pm 0.6$	0.2802
TAD	J		$77.4^{a} \pm 0.6$		$88.1^{b} \pm 0.7$		$82.4^{a} \pm 0.6$	
OAD		1	$82.8^{a} \pm 0.4$	<0.001	$92.4^{a} \pm 0.5$	<0.001	$88.4^{a} \pm 0.5$	<.0001
TAD		1	$77.2^{b} \pm 0.4$		$85.1^{b} \pm 0.4$		$81.2^{b} \pm 0.4$	
OAD		2	$78.8^{a} \pm 0.4$	<0.001	$90.1^{a} \pm 0.5$	<0.001	$84.9^{a} \pm 0.4$	<.0001
TAD		2	$76.3^{b} \pm 0.4$		$85.8^{b} \pm 0.4$		$79.9^{b} \pm 0.4$	
OAD		3	$77.4^{a} \pm 0.4$	<0.001	$88.6^{a} \pm 0.5$	<0.001	$83.3^{a} \pm 0.5$	<.0001
TAD		3	$75.3^{b} \pm 0.4$		$84.9^{b} \pm 0.4$		$78.7^{b} \pm 0.4$	
OAD		4	$77.5^{a} \pm 0.4$	<0.001	$89.0^{a} \pm 0.5$	<0.001	$83.2^{a} \pm 0.5$	<.0001
TAD		4	$75.2^{b} \pm 0.4$		$84.7^{b} \pm 0.4$		$78.5^{b} \pm 0.4$	
OAD		5	$77.2^{a} \pm 0.5$	0.004	$88.8^{a} \pm 0.5$	<0.001	$83.0^{a} \pm 0.5$	<.0001
TAD		5	$75.4^{b} \pm 0.4$		$85.0^{b} \pm 0.4$		$78.9^{b} \pm 0.4$	

[1] MF OAD=once-a-day milking MF TAD=twice-a-day milking.

[2] F=Holstein-Friesian, J=Jersey and F×J crossbred cows.

[a,b], Least square means with different superscripts are significantly different between milking frequencies with breed-type or within lactation number.

Comparison across breed groups showed that F cows were more affected than the other breed groups by OAD milking. Holstein-Friesian cows milked OAD yielded 24.7%, 18.9% and 20.4% less milk, fat and protein, respectively, than F cows milked TAD. Compared to J cows under TAD systems, J cows milked OAD yielded 17.1%, 15.5% and 14.6% less milk, fat and protein, respectively.

The reduction in milk production traits from TAD to OAD was not constant across lactation numbers. First-lactation cows milked OAD had 21%-25% less milk, fat and protein yield compared to their counterpart cows milked TAD. In mature cows, this difference was 16%-21%, reflecting an interaction between milking frequency and lactation number.

The difference of SCS across milking frequency was greatest in first-lactation cows (6.3%) and decreased in successive lactations, indicating a significant interaction between milking frequency and lactation number. In fourth and fifth-lactations, no difference was found across milking frequency. The results also indicate an interaction between breed groups and milking frequency, since F and F×J cows milked OAD had higher values of SCS than their counterpart cows milked TAD, meanwhile no difference in the average SCS was observed in J cows milked either OAD or TAD.

The results presented in Table 4.7 indicate that, in general, cows milked OAD had higher persistency of milk, fat and protein yield (79%-90% vs. 76%-85% in OAD and TAD, respectively). Within breeds, J cows milked OAD and TAD had similar milk and protein persistency; in contrast, F and F×J cows milked OAD had slightly greater lactation persistency for the three production traits than their counterparts milked TAD.

Discussion

The three breed groups milked OAD yielded 15%-25% less milk, fat and protein than the respective breed groups milked TAD. However the reduction in milk yield was, in relative values, greater in F cows than in F×J and J cows, which is in agreement with Cooper (2000) and Clark et al. (2006) and confirms that a breed × milking frequency interaction exists.

The reduction in milk yields in J cows milked OAD (15-17%) was smaller than the reduction of 20%-25% estimated in a farmlet study carried out in New Zealand (Clark et al. 2006). For the other breed groups, the relative differences were considerably smaller than the studies of Cooper (2000) in F×J, and Clark et al. (2006) in F cows. Both studies noted a difference ranging between 29%-32% in milk, fat and protein yield. Similar to the present study, the latter authors also observed that, compared to F cows, J cows were less affected by OAD milking.

The results of this study are important as the data came from commercial herds instead of experimental herds, and the reductions in milk and milk solids yield were not as large on commercial farms as has been reported in experiments. The latter suggest that commercial farms milking OAD have increased their stocking rate (SR) as a way to compensate the decrease in milk production (Stockdale 2006), and it appears that the increased SR may have been lower than the 17% suggested by Cooper & Clark (2001), because cows under OAD systems have similar (or slightly less) dry matter intake to cows under TAD (Stelwagen et al. 2013).

The reduction in the milk yield traits found in this study compared to experiments may be due to low input farms operating TAD, because the average yield of milk solids presented in Table 4.6 (295 kg/cow) is lower than the national milk solids average for the period 2008-2012 (330 kg/cow; LIC & Dairy NZ 2014), although this cannot be confirmed.

No data were available showing how long each farm had been operating under OAD milking systems; however, it is assumed that farmers have systematically selected and culled cows unsuited to less frequent milking, as theorized by Woolford et al. (1982). Tong et al. (2003), using the first two seasons of the study from Clark et al. (2006), reported a reduction between lactation length in TAD and OAD (from 26 to 8 days) and in milk solids (kg/cow) among J cows (from 55 to 42 kg), supporting the possibility of selection for OAD milking.

The greater reduction in first-lactation cows milked OAD compared to the same group milked TAD has been found in previous studies (Clark et al. 2006). In contrast, Cooper (2000) found that reduction in the milk, fat and protein yield was not affected by lactation number, and they observed that mature cows milked OAD tended to have greater losses than first-lactation cows milked OAD. The greater reduction in first-lactation cows found in this study could be attributed to cows in their first lactation having a relatively immature cisternal development in comparison to later lactations (Knight & Wilde 1993). Clark et al. (2006) theorised that those cows might not be capable of accommodating the storage of high amounts of milk. In this study, the reduction of milk solids between OAD and TAD in first-lactation cows was 17%. A reduction of 24% and 38% in J and F cows respectively, was reported in the pastoral study of Clark et al. (2006). The findings might indicate that first-lactation cows of this study are daughters of cows more adapted to OAD; consequently the reduction observed is lower than the reduction reported in experiments.

The results showed increased SCS in cows milked OAD compared with cows milked TAD, which is consistent with experimental studies (Holmes et al. 1992; Cooper 2000; Clark et al. 2006). Kamote et al. (1994) had suggested that higher levels of SCS could be caused by a “concentration effect” rather than higher SCC. However, several famers milking OAD have reported lower SCC (and therefore SCS), after culling high SCC cows and other cows deemed unsuitable for OAD. Dalley et al. (2007) attributed this occurrence to better management practices and possibly to less exposure to pathogens during the milking process because cows are only milked OAD. The variation in SCS observed in the initial three lactations may be the result of high SCS cows being culled prior to fourth and fifth lactations in OAD milking systems.

The lactation persistencies observed in the present study for the milk yield traits were slightly greater in OAD compared with to TAD (79%-90% vs. 76%-85%). These results were unexpected because there is evidence of an accelerated mammary involution with lower milking frequency (Knight & Dewhurst 1994; Capuco et al. 2003; Bernier-Dodier et al. 2010). Further, Hickson et al. (2006) had shown that F and J cows milked OAD had lower persistency than cows milked TAD. Those results were obtained in two of the three calculations of persistency, and neither of these calculations were used in this study. In a third measure of persistency (based on accumulated yields from quadratic polynomial curves; Kamidi (2005), Hickson et al (2006) found that J cows milked OAD and TAD had better lactation persistency of milk, protein and lactose than F cows milked OAD and TAD. Comparison of the results presented in this study with those in the study of Hickson et al. (2006) should be viewed with caution due to criteria differences in the measures of lactation persistency (Grossman et al. 1999).

The findings of this study might also support the conclusions from the study of Woolford et al. (1982). They indicated that there may be an important genetic component to the decrease of milk yield when cows went from TAD to OAD and therefore, some cows are more tolerant and adapt better to the OAD regime in successive lactations than other cows. Those cows which are genetically predisposed to adapt to OAD systems show greater lactation persistency when they are milked OAD (Clark et al. 2006; Hickson et al. 2006).

Conclusion

The three main breed groups in New Zealand produced significantly greater milk, fat and protein yield when milked TAD; however, the relative difference to OAD found in this study is smaller than reported in studies on research farms. In addition, greater lactation persistency under OAD systems in F and F×J may be an indication that cows have adapted to OAD systems. With the exception of J cows, cows milked OAD tend to show higher SCS, although these values varied with increasing lactation number.

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CHAPTER 5

Breed and heterosis effects for milk yield traits at different production levels, lactation number and milking frequencies

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Abstract

The objective of this study was to evaluate the effects of production level (PL) and lactation number (LN) on the expression of breed, and heterosis for yield traits in cows milked once (OAD) or twice-a-day (TAD) in New Zealand. Records were used from 35,192 Friesian (F), 31,118 Jersey (J) and 88,606 crossbred (F×J) cows that calved in spring between 2008 and 2012. With an average LN of five, F cows had a higher milk yield (592 kg in OAD and 909 kg in TAD), fat yield (2.1 kg in OAD and 6.3 kg in TAD) and protein yield (11.9 kg in OAD and 19.5 kg in TAD) compared with J cows. Expressed as a percentage, heterosis effects ranged from 4.1%-7.6% for production traits and were similar across milking frequencies. In absolute values, however, heterosis was different for fat and protein yield only in first-lactation cows, and no differences were found in milk yield. In a second analysis, breed effects, defined as F-J, increased as PL of the herd increased in both OAD and TAD systems. The highest heterosis (%) were found at medium (5.9%-6.4%) and low (5.2%-6.8%) PL in cows milked OAD and TAD, respectively. However, in absolute values, the greatest heterosis was observed at high PL in the population milked TAD. The estimates of breed and heterosis obtained can be used for simulation studies to evaluate the profitability of crossbreeding systems under OAD and TAD milking systems in New Zealand dairy farms, at different PL.

Keywords: milking frequency; dairy cattle; New Zealand; breed effects; heterosis effects; production level

Introduction

Traditionally, cows in milk production systems in New Zealand have been milked twice-a-day (TAD). However, milking once-a-day has been increasing in popularity due to herd management and lifestyle benefits (Davis et al. 1999; Clark et al. 2006).

Crossbreeding between New Zealand Holstein-Friesian (F) and Jersey (J) has been adopted since the 1960s to upgrade J into F cows. However, since 1985, crossbreeding has been implemented as a mating strategy (Montgomerie 2005). This has brought favourable heterosis for production, fertility and survival traits, resulting in increased overall farm profitability (López-Villalobos et al. 2000). For New Zealand’s dairy cattle, Harris (2005) summarized heterosis effects for economically important traits under TAD milking, but so far, no studies have quantified breed and heterosis effects in cows milked OAD.

Several studies (Bryant et al. 2007; Penasa et al. 2010a; Kargo et al. 2012) have evaluated dairy cattle performance and expression of heterosis effects at different production levels (PL). In those studies, breed and heterosis effects have varied across PL.

Crossbreeding in animal production systems has been considered beneficial when management (environmental─nutritional) conditions are poor (Kargo et al. 2012). In an extensive review, Barlow (1981) concluded that heterosis is better expressed when the environmental conditions are suboptimal. Nonetheless, Bryant et al. (2007) found low or no heterosis in restricted environments, under TAD systems, in New Zealand dairy cattle.

The objective of this study was to evaluate the effects of PL and lactation number (LN) on the expression of breed and heterosis effects for milk yield traits in cows milked OAD or TAD in New Zealand.

Materials and methods

Data

Lactation records for milk yield (MY), fat yield (FY) and protein yield (PY) recorded from 2008 to 2012, and pedigree information, were provided by Livestock Improvement Corporation (Hamilton, New Zealand). Data were edited as follows:

1. Lactation records were sorted based on codes indicating whether the cow was milked OAD or TAD. Herds milked OAD were those in which 100% of the cows were milked OAD. Using GPS Visualizer (Schneider 2012), TAD herds were selected within a radius of 20 km of OAD herds. In some cases, in a given single map coordinate, an OAD farm was surrounded by several TAD herds; in such cases, all TAD herds were selected.
2. Herds with fewer than 50 cows were removed from the dataset.
3. Only records from spring calving cows in their first five lactations with lactation lengths between150 and 305 days were considered.
4. Only records from F, J and their crosses (F×J) were included, discarding cows of unknown breed and pedigree.

The breed composition of each cow was calculated using the following equation:

$$\alpha_i^P = \frac{\alpha_i^s + \alpha_i^d}{2}$$

where α_i^P is the proportions of genes from breeds F or J in the progeny, and α_i^s and α_i^d are the proportions of breeds F or J in the sire and dam, respectively. Pure breed cows were considered when their breed composition was ≥93.75% from a particular breed.

Coefficient of heterosis in a cow (h_{FxJ}) was calculated using the following equation (Dickerson 1973):

$$h_{FxJ} = \alpha_F^s \alpha_J^d + \alpha_J^s \alpha_F^d$$

where α_F^s and α_J^s are the proportions of F or J in the sire and α_J^d and α_F^d are the proportions of J and F in the dam, respectively.

The final dataset used in this analysis contained 124,620 lactation records from 298 herds milked OAD and 194,631 records from 350 herds milked TAD. The population studied included 9122 (5.8%) and 26,239 (16.8%) pure F cows milked OAD and TAD, respectively. The pure J cows were: 18,417 (11.8%) and 13,129 (8.4%) milked OAD and TAD, respectively. Finally, F×J cows milked OAD were 38,180 (24.5%) and 50,956 (32.7%) milked TAD.

Three groups per milking frequency (MF) were constructed based on herd PL (low, medium or high) for milk solids (fat + protein) per cow using the FASTCLUS procedure of SAS version 9.3 (SAS Institute Inc). The procedure uses Euclidean distances, guaranteeing that the distances between all the observations in the same cluster are less than the distances between observations in different clusters. Number of herds and average milk solids per PL are presented in Table 5.1.

Statistical Analysis

A univariate linear model was used to obtain breed and heterosis effects for total lactation yield of milk, fat and protein using the ASREML 3.0 software package (Gilmour et al. 2009). The model included the fixed effects of MF, LN, interaction between MF and LN; linear regression of MY, FY or PY on mean calving date deviation from median calving date of the herd for a given season; linear regression of MY, FY or PY on mean days in milk deviation from median days in milk of the herd for a given season; linear regressions of MY, FY or PY on gene proportion of F per MF; linear regressions of MY, FY or PY on coefficient of expected heterosis per MF; and the random effects of herd-season, additive genetic effect of cow, permanent environmental effect of cow and residual error.

For each MF, the estimate of the regression coefficient of the proportion of F and linear effect of heterosis, gives, respectively, the estimation of the breed effect between F and J and heterosis in the first cross cow (Back & López-Villalobos 2007).

A second univariate linear model was implemented to evaluate the effect of PL. The model was similar to the model described above, but included the fixed effect of PL and the interaction between MF and PL.

Results

Number of herds and average milk solids per PL are presented in Table 5.1. Table 5.2 and Table 5.3 present predicted performances of pure F and J and first crosses (F_1) F×J, and breed and heterosis effects for MY, FY and PY for each MF by LN and PL, respectively.

Table 5.1. Number of herds and lactations, and mean of milk solids (kg/cow) by production level and milking frequency.

Milking frequency	Production level	Number of herds	Number of lactations	Milk solids[a] (kg/cow)
OAD	Low	110	30,126	203.6
	Medium	141	60,165	269.2
	High	47	34,329	339.9
TAD	Low	168	62,960	272.7
	Medium	150	86,761	353.8
	High	32	44,910	434.1

[a] Defined as the sum of fat and protein yields. OAD= once-a-day milking; TAD= twice-a-day milking.

Breed effects, defined as the difference between production performances of F and J, indicate that, overall, F cows were superior for the production traits compared with J cows in both OAD and TAD systems. However, the superiority of F cows was higher in TAD. The breed effect increased in successive lactations in all of the three traits studied, with the exception of FY under OAD systems, where the highest breed effect was found in fifth-lactation cows followed by first-lactation cows. Estimated yields (average of the five LN) of F compared with J cows were 317 kg of milk, 4.2 kg of fat and 7.5 kg of protein greater in TAD compared with OAD (Table 5.2).

In mature cows, heterosis effects across MF were 5.4%-7.6% in OAD and 4.1%-7.1% in TAD systems. In first-lactation cows milked OAD, however, the relative values of heterosis ranged from 4.7%-5.0%; different from the 4.6%-7.2% found in first-lactation cows milked TAD (Table 5.2).

Table 5.2. Predicted means and standard errors of production traits for Holstein-Friesian (F), Jersey (J) and first cross (F_1) F×J cows and estimates of breed and heterosis effects by milking frequency and lactation number.

Lactation number	MF^{1}	F	F_1F×J	J	Breed effect	Heterosis effect	
					F-J (kg)	kg†	%‡
Milk yield (kg/cow)							
1	OAD	2402±26	2343±25	2075±26	327^{a}±14	105^{a}±11	4.7
1	TAD	3345±21	3224±21	2822±22	523^{b}±12	141^{a}±9	4.6
2	OAD	3105±26	3024±25	2610±26	495^{a}±13	167^{a}±11	5.8
2	TAD	4063±21	3827±21	3267±22	796^{b}±12	162^{a}±9	4.4
3	OAD	3486±26	3349±25	2868±26	618^{a}±13	172^{a}±11	5.4
3	TAD	4520±21	4203±21	3547±22	973^{b}±12	170^{a}±9	4.2
4	OAD	3689±26	3552±25	2978±26	711^{a}±14	219^{a}±12	6.6
4	TAD	4741±21	4360±21	3637±22	1104^{b}±12	171^{b}±10	4.1
5	OAD	3813±27	3605±25	3004±26	809^{a}±15	197^{a}±14	5.8
5	TAD	4821±22	4441±21	3670±22	1151^{b}±13	196^{a}±11	4.6
Fat yield (kg/cow)							
1	OAD	117.7±1.3	122.5±1.2	115.6±1.3	2.1^{a}±0.7	5.8^{a}±0.6	5.0
1	TAD	152.0±1.0	162.4±1.0	151.1±1.1	0.9^{a}±0.6	10.9^{b}±0.5	7.2
2	OAD	147.9±1.3	156.4±1.2	147.3±1.3	0.6^{a}±0.7	8.8^{a}±0.6	6.0
2	TAD	182.9±1.0	193.4±1.0	179.5±1.1	3.4^{b}±0.6	12.2^{b}±0.5	6.7
3	OAD	163.8±1.3	173.6±1.2	163.0±1.3	0.8^{a}±0.7	10.2^{a}±0.6	6.2
3	TAD	202.7±1.0	211.7±1.0	196.5±1.1	6.2^{b}±0.6	12.1^{a}±0.5	6.1
4	OAD	171.5±1.3	183.5±1.2	169.5±1.3	2.0^{a}±0.7	13.0^{a}±0.7	7.6
4	TAD	212.2±1.0	220.7±1.0	202.4±1.1	9.8^{b}±0.6	13.4^{a}±0.5	6.5
5	OAD	176.2±1.3	185.5±1.2	171.2±1.3	5.0^{a}±0.8	11.8^{a}±0.8	6.8
5	TAD	215.8±1.1	225.0±1.0	204.4±1.1	11.4^{b}±0.7	14.9^{b}±0.6	7.1
Protein yield (kg/cow)							
1	OAD	91.7±1.0	92.4±1.0	84.4±1.0	7.3^{a}±0.5	4.3^{a}±0.4	4.9
1	TAD	121.4±0.8	122.4±0.8	110.2±0.8	11.2^{b}±0.5	6.6^{b}±0.3	5.7
2	OAD	118.6±1.0	121.0±1.0	108.9±1.0	9.7^{a}±0.5	7.3^{a}±0.4	6.4
2	TAD	148.6±0.8	148.0±0.8	131.7±0.8	16.9^{b}±0.4	7.9^{a}±0.4	5.6
3	OAD	132.6±1.0	134.4±1.0	120.6±1.0	12.0^{a}±0.5	7.8^{a}±0.4	6.2
3	TAD	164.5±0.8	162.3±0.8	144.0±0.8	20.5^{b}±0.4	8.1^{a}±0.4	5.2
4	OAD	139.2±1.0	142.0±1.0	125.4±1.0	13.8^{a}±0.5	9.7^{a}±0.5	7.3
4	TAD	171.8±0.8	168.3±0.8	148.0±0.9	23.8^{b}±0.5	8.4^{a}±0.4	5.3
5	OAD	143.2±1.0	143.4±1.0	126.3±1.0	16.9^{a}±0.5	8.7^{a}±0.5	6.4
5	TAD	174.2±0.8	171.1±0.8	149.3±0.9	24.9^{b}±0.5	9.3^{a}±0.4	5.8

[1] MF = milking frequency, OAD = once-a-day milking and TAD = twice-a-day milking.

† Expressed as F_1 F×J – ((F + J)/2).

‡ Expressed as a percentage of heterosis effects relative to the phenotypic average of the parental breeds under milking frequency andlactation number, as appropriate.

[a,b] Within traits and production level, breed and heterosis effects with different superscripts were significantly different between milking frequencies (P<0.05).

Table 5.3. Predicted means and standard errors of production traits for Holstein-Friesian (F), Jersey (J) and first cross (F_1) F×J cows and estimates of breed and heterosis effects at different production levels.

Production level[1]	MF[2]	F	F_1 F×J	J	Breed effect	Heterosis effect	
					F-J (kg)	kg†	%‡
Milk yield (kg/cow)							
L	OAD	2554±25	2499±23	2178±25	376^{a}±18	133^{a}±14	5.6
	TAD	3529±17	3351±16	2843±18	686^{b}±13	165^{a}±10	5.2
M	OAD	3313±20	3221±19	2770±20	543^{a}±13	179^{a}±10	5.9
	TAD	4471±17	4174±16	3577±18	894^{b}±12	150^{a}±9	3.7
H	OAD	4184±28	3903±27	3369±17	815^{a}±16	126^{a}±13	3.3
	TAD	5548±26	5139±26	4247±28	1301^{b}±16	241^{b}±13	4.9
Fat yield (kg/cow)							
L	OAD	121.3±1.2	128.7±1.1	120.2±1.2	1.1^{a}±0.9	7.9^{a}±0.7	6.5
	TAD	158.8±0.8	167.3±0.8	154.6±0.9	4.2^{b}±0.6	10.6^{b}±0.5	6.8
M	OAD	157.7±1.0	167.1±0.9	156.5±0.9	1.2^{a}±0.6	10.0^{a}±0.5	6.4
	TAD	202.8±0.8	212.4±0.8	198.1±0.8	4.7^{b}±0.6	11.9^{a}±0.4	5.9
H	OAD	195.5±1.3	203.1±1.3	192.0±1.3	3.5^{a}±0.8	9.3^{a}±0.6	4.8
	TAD	246.8±1.2	258.4±1.2	238.1±1.3	8.7^{b}±0.8	15.9^{b}±0.6	6.6
Protein yield (kg/cow)							
L	OAD	97.3±1.0	99.0±0.9	88.9±0.9	8.4^{a}±0.6	5.9^{a}±0.5	6.3
	TAD	127.7±0.7	127.6±0.6	113.1±0.7	14.6^{b}±0.5	7.2^{a}±0.3	6.0
M	OAD	126.4±0.8	128.6±0.7	115.3±0.7	11.1^{a}±0.5	7.7^{a}±0.4	6.4
	TAD	163.2±0.6	161.4±0.6	144.1±0.7	19.1^{b}±0.4	7.7^{a}±0.3	5.0
H	OAD	158.9±1.1	156.8±1.0	141.5±1.1	17.4^{a}±0.5	6.6^{a}±0.4	4.4
	TAD	203.2±1.0	199.0±1.0	173.9±1.0	29.3^{b}±0.6	10.4^{b}±0.4	5.5

[1] L= low milk solids (fat + protein) yield, M = medium milk solids yield, H = high milk solids yield.

[2] MF = milking frequency, OAD = once-a-day milking and TAD = twice-a-day milking. † Expressed as F_1 F×J – ((F + J)/2).

‡ Expressed as a percentage of heterosis effects relative to the phenotypic average of the parental breeds under milking frequency and production levels, as appropriate.

[a,b] Within traits and production level, breed and heterosis effects with different superscripts were significantly different between milking frequencies (P<0.05).

The findings show that estimates of heterosis effects were not consistently greater in TAD compared with OAD. Compared with OAD systems, estimates of heterosis were similar in MY, except in fourth-lactation cows. For FY and PY, estimates of heterosis effects were greater in first-lactation cows; further second- and fifth-lactation cows milked TAD had significantly greater heterosis for FY (Table 5.2).

In general, breed effects increased in favour of F as the PL of the herds increased in both OAD and TAD systems. The smaller breed difference at low and medium PL compared with high PL suggest that J cows might have an advantage over F cows in those environments, in particular in OAD systems (Table 5.3).

Heterosis effects, expressed in relative values at low PL, were slightly greater compared with high PL in TAD systems, and the lowest percentage of heterosis effects was observed at medium PL. In absolute values, however, heterosis estimates were greatest at high PL in the population milked TAD. In OAD systems, the relative heterosis effects for MY, FY and PY were greater at low and medium compared with high PL. Percentage of heterosis at low and medium PL ranged between 5.6%-6.5%, and at high PL ranged between 3.3%-4.8% (Table 5.3).

Discussion

The results presented in Table 5.2 show greater breed effects in TAD than in OAD, suggesting, in agreement with Clark et al. (2006), a breed × MF interaction.

Generally, cows under OAD systems have reduced availability of dry matter due to higher stocking rates (Cooper & Clark 2001). The smaller breed differences for the production traits in OAD milking suggest, in consequence, that J cows are better adapted than F cows to OAD systems.

Similar to the results of the present study, several researchers (Macmillan et al. 1981; Ahlborn-Breier & Hohenboken 1991; Bryant et al. 2007; Penasa et al. 2010b) have observed that F cows have superior production traits compared with J in grazing conditions. The results confirm the superiority of F cows regarding milk traits. However, in dairy systems where the payment scheme gives greater emphasis to milk solids, as is the case of New Zealand, the J breed has an important role in the industry. For instance, in New Zealand, F and J cows have similar milk value per lactation when milk processing is 100% whole milk powder and skim milk powder; and J cows have greater milk value per litre in a payment scheme that favours the production of fat and protein, and penalizes volume (Sneddon et al. 2015). In addition, smaller sized cows are often preferred under grazing conditions (Prendiville et al. 2009, 2011).

In this study, the percentage of heterosis found for productive traits is similar to the 5.5% reported by Prendiville et al. (2010) in F and J cows using TAD milking under Irish grazing conditions. In New Zealand, Ahlborn-Breier & Hohenboken (1991) had reported for first-lactation first-cross cows milked TAD, a heterosis of 6.1% and 7.1% for MY and FY, respectively. These percentages agree with the results presented in Table 5.2 for FY, but are greater for MY in cows milked TAD.

In absolute values, however, Harris (2005) reported heterosis lower than our findings (in both MF) (139, 7.7 and 5.5 kg of MY, FY and PY, respectively) in New Zealand under TAD systems. Comparing that study with values presented in Table 5.3, heterosis effects is similar only for the milk traits at low PL herds milked OAD. Differences between production performances of the dairy cattle populations might explain this discrepancy.

The heterosis effects found in TAD systems in this study are in agreement with research carried out in Europe using North American Holstein-Friesian crossbred with Dutch-Friesian (Van der Werf & de Boer (1989), Black and White cattle (Boichard et al. 1993) and European Friesian (Akbas et al. 1993), but lower than the results found by Penasa et al. (2010b) in Ireland, where crosses of North American Holstein-Friesian with F, J and Montbéliarde were used.

Across MF, the estimates of heterosis were similar in mature cows milked OAD and TAD. It is possible that the greater reduction in first-lactation cows milked OAD, compared with the group milked TAD, is in part due to limitations in their milk storage capabilities (Clark et al. 2006) and might indicate this interaction. Consequently, both breeds F and J might not only express their additive genetic effects for milk production under OAD systems, but also the favourable dominance and epistatic effects of their crosses. The interaction between MF and LN could also be due to first-lactation cows being less capable of competing for forage, consequently, the low dry matter availability under OAD milking may have reduced the expression of heterosis in first-lactation cows milked OAD compared with the corresponding group milked TAD.

Estimates of heterosis were lower in first-lactation cows than in mature cows under both milking systems. McAllister (1986) suggested that this might be due to different gene expression, either intra-locus or inter-locus, affecting LN. McAllister reported lower heterosis for MY and FY in third-lactation cows (0.7%-0.8%), compared to first- (3.7%-3.9%), second- (1.5%-3.4%) and fourth-lactation cows (1.6%-2.6%) in Holstein-Friesian and Ayrshire hybrids (F_1). These findings differ from the results presented in Table 2; however, comparison of purebreds and crossbreds must consider records over several LN in order to evaluate profitability of crossbreeding in the production system.

The superiority of F for use in TAD systems and in high PL indicates a genotype × environment interaction. The genotype by environment interaction found in this study can be referred to as a scaling effect, which is when phenotypic performance between breeds increases with more favourable environments (Bryant et al. 2005). Studies by Bryant et al. (2007), Penasa et al. (2010a) and Kargo et al. (2012) indicate that in general, more productive cows (with large proportion of North American genes) increased their superiority in higher input systems compared with F, J and Dutch-Friesian. In more intensive systems, the nutritional requirements of highly productive cows are better met (Penasa et al. 2010a) allowing high producing cows to more fully express their genetic merit for milk production.

The amount of FY and PY of F cows milked OAD in low and medium PL was considerably smaller compared with high PL, suggesting that J cows might have an advantage over F cows in those environments. The nutritional status of cows in grazing conditions varies considerably across the seasons; hence, F cows cannot express their potential when intake is restricted (Ahlborn-Breier & Hohenboken 1991).

According to Barlow (1981), estimates of heterosis tend to be smaller in less favourable environments, which are supported by the results obtained by Panesa et al. (2010a). However, the latter study refers to a crossbred population upgrading from Dutch-Friesian into North American Holstein-Friesian, which might have generated a bias.

Studies by Bryant et al. (2007) and Kargo et al. (2012) reported heterosis × environment interaction for milk traits ranging from 2.7% to 9.5%. The results presented in this study are into that range. In absolute values, greater heterosis was found in high PL milked TAD, indicating a scaling effect on the expression of heterosis. The average PL in the present study, and in Bryant et al. (2007) (with crosses of F and J with overseas Holstein-Friesian) and in Kargo et al. (2012) between two strains of J (Danish and North American) were considerably lower than in the study of Penasa et al. (2010a), indicating that the evaluation of heterosis expression must consider the environment and the breeds involved.

The results presented in this study are important because farmers generally cull the less productive cows on the basis on their production worth (PW) index, which represents the genetic superiority or inferiority of a cow to convert 5 t of feed dry matter into farm profit (Dairy NZ 2015). This index allows farmers to compare cows of different breeds and ages over a typical lifetime (Montgomerie 2005). Production worth considers the production values for MY, PY, FY and live weight, each weighted by their respective economic values (Holmes et al. 2002). Production values are calculated as the sum of estimated breeding values plus heterosis effects and permanent environmental effects (Holmes et al. 2002). Therefore, PW is higher in crossbred F×J (and their backcrosses) than in pure breeds (Montgomerie 2005). For instance, Lopez-Villalobos et al. (2000) with a deterministic model under pastoral conditions in New Zealand showed that rotational crossbreeding systems were more profitable (net income per hectare) than milk production with pure breeds. Under OAD conditions, PW of crossbred cows might be relatively higher than their counterparts milked TAD, because the benefits of crossing animals are generally achieved when the genetic differences between purebreds are low (Falconer & Mackay 1996). The smaller breed differences between F and J suggest that relative to pure breeds, crossbreeding in OAD systems could increase farm profitability by a greater magnitude than in TAD.

Conclusions

Breed effects for production traits between F and J cows in New Zealand differed across LN and MF. Breed performance is strongly influenced by PL. The results suggest that F cows are better suited to high PL environments milked TAD, in contrast with J cows which are more adapted to low—medium PL environments milked OAD.

Lactation number and PL are factors that affect the expression of heterosis. The estimates of breed and heterosis reported in this study can be used for simulation studies to evaluate if crossbred cows under OAD systems are more profitable than F and J cows as found in TAD milking systems under New Zealand grazing conditions at different PL.

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CHAPTER 6

Estimation of genetic parameters for milk traits in cows milked once- or twice-daily in New Zealand

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Abstract

The objective of the present study was to estimate genetic parameters for milk yields, average somatic cell score (SCS) and milk composition traits in dairy cows milked either once-a-day (OAD) or twice-a-day (TAD) in New Zealand. The data set comprised 124,620 and 194,631 lactation records from OAD and TAD populations, respectively, during the period 2008 to 2012. Overall, estimates of parameters were similar between milking frequencies (MF), although heritabilities of production traits tended to be greater in the TAD cows. Estimates of heritability in OAD and TAD were: 0.33 and 0.36 for milk yield; 0.21 and 0.26 for fat yield; 0.22 and 0.25 for protein yield; and 0.12 and 0.12 for SCS, respectively. Estimates of correlations were similar across MF, in particular the genetic correlation between milk yield and protein yield (0.84 for TAD and 0.85 for OAD). Estimates of genetic correlations between SCS and other traits tended to be close to zero in both populations. The results indicate that genetic progress can be lower in the OAD population due to lower phenotypic and genetic variances compared to the TAD population. However, a potential disadvantage is that evaluating both dairy populations together could lead to systematic inaccuracies and biases in the estimation of breeding values for the population milked OAD as future dams.

Keywords: heritability; genetic correlation; milking frequency; dairy cattle

Introduction

The estimation of genetic parameters for milk yield and milk composition traits has been well documented in New Zealand (Ahlborn & Dempfle 1992; Johnson et al. 2000; Pryce & Harris 2006; Sneddon et al. 2015) and overseas (Berry et al. 2003; Rupp & Boichard 1999). In those studies, the genetic parameters were estimated with records from cows milked twice-a-day (TAD), which is the standard milking frequency (MF) for dairy cattle in New Zealand. However, since the late 1990s, milking once-a-day (OAD) has been adopted by some farmers for herd management and lifestyle benefits (Clark et al. 2006; Davis et al. 1999).

In New Zealand, the prevalent breeds used in the dairy industry are Holstein-Friesian (F), Jersey (J) and their crosses (F×J), which represent 37.0%, 11.7% and 42.6% of the national herd, respectively (LIC and Dairy NZ, 2014). In an experimental study, Clark et al. (2006) reported a significant MF by breed interaction for the milk production traits. This interaction corresponds to a scaling effect, in which the breed groups perform differently with differing MF but without changing the ranking among them (Hammami et al. 2009). However, from the study of Clark et al. (2006), a large variability in production has been observed in cows milked OAD compared to TAD, in particular in F cows, where some OAD F cows yielded as much as the highest F milked TAD (Hickson et al. 2006). This large variability might suggest that the apparent genetic merit of cows for production can change depending upon the MF environment.

In the New Zealand dairy industry, the genetic merit of an animal is evaluated according to the breeding worth index (BW) (López-Villalobos & Garrick, 2005). The BW index is calculated as weighting the estimated breeding values (EBVs) for lactation yields of milk (MY), fat (FY) and protein (PY), somatic cell score (SCS), live weight, fertility and residual survival, with their respective economic values. In this index, bulls and cows are ranked according to their expected ability to produce more profitable replacements, which represents the genetic superiority or inferiority of an animal to convert 5 tonnes of dry matter into farm profit. Given the MF by breed interaction reported by Clark et al. (2006), OAD farmers might be concerned if genetic evaluation is affected by this interaction since phenotypic and genetic parameters are population and environment specific, and may have different magnitudes. The response to selection of a particular trait is affected by genetic correlations and phenotypic variance and in particular heritability (López-Villalobos 2012). Therefore, accurate estimates of genetic parameters are required to develop an effective and comprehensive selection program for the OAD population.

The aim of this study was to estimate genetic parameters for milk yields, average SCS and milk composition traits in dairy populations milked either OAD or TAD in New Zealand.

Materials and methods

Data

Lactation records of MY, FY and PY recorded from 2008 to 2012, and pedigree information were provided by Livestock Improvement Corporation (LIC, Hamilton, New Zealand). Fat percentage (FP) and protein percentage (PP) were calculated as the ratio between FY or PY and MY. Protein to fat ratio (P:F) was calculated from these estimates. Another data set provided by LIC containing herd-test records of somatic cell count (SCC) was used to calculate average somatic cell score (SCS) during the same period. Somatic cell score was calculated as SCS= $\log_2$ (SCC) (Harris & Winkelman, 2004).

Total lactation records were sorted based on a code to determine if the cow was milked OAD or TAD. Once-a-day herds were identified as those where 100% of the cows were milked OAD all season. Using the GPS Visualizer (Schneider 2012), TAD herds were selected within a radius of 20 km of the OAD herds. In some cases, in a given single map co-ordinate a OAD herd was surrounded by several TAD herds; in such cases, all TAD herds were selected. Any herds with less than 50 cows were removed from the dataset. Only records from spring calving cows in their first five lactations with lactation lengths comprised between 150 and 305 days were considered. Lastly, only records from F, J and their crosses were considered, discarding data from animals without information on breed composition.

The breed composition for each cow was determined with the following equation:

$\alpha_i^p = (\alpha_i^s + \alpha_i^d)/2$, where α_i^P is the proportions of genes from breed i in the cow, α_i^s and α_i^d are proportion of breed i in the sire and dam, respectively, and i is breed F or J. Pure breed cows were defined as having a breed composition of ≥93.75% from a single breed.

Coefficients of expected heterosis for individual cows (h_{FxJ}) was calculated using the following equation (Dickerson 1973):

$h_{FxJ} = \alpha_F^s\alpha_J^d + \alpha_J^s\alpha_F^d$, where α_F^s and α_J^s are proportion of breeds F and J in the sire, and α_J^d and α_F^d are proportion of breeds J and F in the dam, respectively.

The final dataset used for statistical analysis contained 124,620 lactations from 298 OAD herds and 194,631 lactations from 350 TAD herds. The population included 9,122 and 26,239 purebred F cows in OAD and TAD herds, respectively. The purebred J cows were 18,417 and 13,129 in OAD and TAD herds, respectively. Finally, crossbred F×J cows were 38,180 and 50,956 in OAD and TAD herds, respectively. The breed proportions were: 13.9 and 29.1% F cows, 28.0 and 14.5% J cows, and 58.1 and 56.4% F×J cows in OAD and TAD herds, respectively. Jersey cows were more represented in the OAD population compared to F and F×J cows likely because farmers choose Jersey cows when they change to OAD milking. Experimental results show that reduction in milk production per cow and per hectare caused by OAD in Jersey cows is less than the reduction in F and F×J cows (Cooper 2000; Clark et al. 2006). Number of lactation records, yield averages and coefficients of variation for each trait considered in the analysis are presented by breed group and MF in Table 6.1.

Table 6.1. Mean (coefficient of variation, %) for milk production traits by breed group and milking frequency (MF).

Breed	MF[1]	N	MY, kg	FY, kg	PY, kg	SCS, units	FP, %	PP, %	P:F
Holstein-Friesian	OAD	16,936	3,275	149.2	122.2	6.56	4.61	3.75	0.82
			(33.3)	(32.4)	(32.6)	(21.4)	(14.3)	(7.4)	(12.4)
	TAD	57,018	4,503	195.9	162.1	6.12	4.39	3.61	0.83
			(27.8)	(27.6)	(27.6)	(21.0)	(14.0)	(7.2)	(12.4)
Crossbred F×J	OAD	71,066	3,009	156.9	121.8	6.37	5.28	4.07	0.78
			(31.2)	(30.3)	(30.5)	(20.7)	(13.7)	(7.7)	(12.1)
	TAD	109,339	3,973	194.6	152.1	6.06	4.96	3.85	0.79
			(29.2)	(28.0)	(28.4)	(20.7)	(14.3)	(7.7)	(12.4)
Jersey	OAD	36,618	2,575	151.5	110.6	6.27	5.91	4.30	0.73
			(27.6)	(28.1)	(27.7)	(20.0)	(11.0)	(6.6)	(9.9)
	TAD	28,274	3,234	186.0	133.7	6.09	5.77	4.14	0.72
			(26.0)	(26.6)	(26.0)	(20.0)	(11.4)	(7.1)	(10.3)

[1] MF= milking frequency, OAD= once-a-day milking and TAD= twice-a-day milking.
N= Number of observations; MY= milk yield; FY= fat yield; PY=protein yield; SCS=somatic cell score; FP=fat percentage; PF=protein percentage; P:F=protein to fat ratio.

Estimation of variance and covariance components

Heritability, repeatability, correlations and their standard errors were calculated with restricted maximum likelihood (REML) procedures using the ASReml 3.0 software package (Gilmour et al. 2009). Estimates of variance components required for the calculation of heritabilities and repeatabilities for each trait were assessed using a single-trait repeatability animal model. A bivariate repeatability animal model was used to assess the estimates of covariance components required for the calculation of phenotypic and genetic correlations.

Single-trait animal model

A single-trait repeatability animal model was represented as follows (Mrode 2014):

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Za} + \mathbf{Wp} + \mathbf{e},$$

Where $\mathbf{y}$ is the vector of observations for each of the traits MY, FY, PY, SCS, FP, PP and P:F; $\mathbf{b}$ is the vector of fixed effects, $\mathbf{a}$ is the vector additive genetic effects; $\mathbf{p}$ is the vector of random permanent environmental effects; and $\mathbf{e}$ is the vector of random residual effects. $\mathbf{X}$, $\mathbf{Z}$ and $\mathbf{W}$ are incidence matrices relating records to fixed animal, additive genetic and permanent environmental effects, respectively.

The effects included in $\mathbf{b}$ were contemporary group (CG) defined as the combination of herd-season-lactation number; the regression coefficient associated with the linear effect of proportion of F; the regression coefficient associated with the linear effect of coefficient of heterosis; and the regression coefficient associated with linear effect of deviation days from median calving date of the herd in a given season.

The following expectation (E) of the variables was assumed: $\mathrm{E}(\mathbf{y}) = \mathbf{Xb}$; $\mathrm{E}(\mathbf{a}) = \mathbf{0}$; $\mathrm{E}(\mathbf{p}) = \mathbf{0}$ and $\mathrm{E}(\mathbf{e}) = \mathbf{0}$. It was also assumed that the residual and permanent environmental effects were independently distributed, therefore $\mathrm{var}(\mathbf{a}) = \mathbf{A}\,\sigma^2_{\mathrm{a}}$; $\mathrm{var}(\mathbf{p}) = \mathbf{I}\,\sigma^2_{\mathrm{p}}$; $\mathrm{var}(\mathbf{e}) = \mathbf{I}\,\sigma^2_{\mathrm{e}} = \mathbf{R}$ and $\mathrm{var}(\mathbf{y}) = \mathbf{ZAZ'A}\sigma^2_{\mathrm{a}} + \mathbf{WI}\sigma^2_{\mathrm{p}}\mathbf{W'} + \mathbf{R}$,

where σ^2_{a} is the animal variance, σ^2_{p} is the permanent environmental variance, σ^2_{e} is the random residual variance, and $\mathbf{A}$ is the numerator relationship matrix between all cows considered in the data set. The size of the matrix $\mathbf{A}$ was 110,671 animals in the OAD population and 149,593 animals in the TAD population. Identity matrix ($\mathbf{I}$) corresponds to the number of cows with records, whose sizes were 65,719 and 90,324 in the OAD and TAD populations, respectively. In the same order, the numbers of sires were 2,713 and 3,309, respectively.

The mixed model equations used for the estimation of fixed, additive and permanent environmental effects in matrix notation are presented as:

$$\begin{bmatrix} \hat{\mathbf{b}} \\ \hat{\mathbf{a}} \\ \hat{\mathbf{p}} \end{bmatrix} = \begin{bmatrix} \mathbf{X'X} & \mathbf{X'Z} & \mathbf{X'W} \\ \mathbf{Z'X} & \mathbf{Z'Z} + \mathbf{A}^{-1}\alpha_1 & \mathbf{Z'W} \\ \mathbf{W'X} & \mathbf{W'Z} & \mathbf{W'W} + \mathbf{I}\,\alpha_2 \end{bmatrix}^{-1} \begin{bmatrix} \mathbf{X'y} \\ \mathbf{Z'y} \\ \mathbf{W'y} \end{bmatrix},$$

where $\alpha_1 = \sigma^2_{\mathrm{e}}/\sigma^2_{\mathrm{a}}$ and $\alpha_2 = \sigma^2_{\mathrm{e}}/\sigma^2_{\mathrm{p}}$.

Bivariate-trait analysis:

The bivariate repeatability animal model was written as (Mrode 2014):

$$\begin{bmatrix} \mathbf{y_1} \\ \mathbf{y_2} \end{bmatrix} = \begin{bmatrix} \mathbf{X_1} & \mathbf{0} \\ \mathbf{0} & \mathbf{X_2} \end{bmatrix} \begin{bmatrix} \mathbf{b_1} \\ \mathbf{b_2} \end{bmatrix} + \begin{bmatrix} \mathbf{Z_1} & \mathbf{0} \\ \mathbf{0} & \mathbf{Z_2} \end{bmatrix} \begin{bmatrix} \mathbf{a_1} \\ \mathbf{a_2} \end{bmatrix} + \begin{bmatrix} \mathbf{W_1} & \mathbf{0} \\ \mathbf{0} & \mathbf{W_2} \end{bmatrix} \begin{bmatrix} \mathbf{p_1} \\ \mathbf{p_2} \end{bmatrix} + \begin{bmatrix} \mathbf{e_1} \\ \mathbf{e_2} \end{bmatrix},$$

Where $\mathbf{y_1}$ is the vector of observation for trait 1, $\mathbf{b_1}$ is the vector of fixed effects for trait 1, $\mathbf{a_1}$ is the vector of additive genetic effects for trait 1, $\mathbf{p_1}$ is the vector of random permanent effects and non-additive genetic effects for trait 1, $\mathbf{e_1}$ is the vector of random residual effects for trait 1; and $\mathbf{X_1}$ $\mathbf{Z_1}$ and $\mathbf{W_1}$ are incidences matrices relating records of trait 1 to fixed, random animal effects and random permanent effects and non-additive effects, respectively. Meanwhile, $\mathbf{y_2}$ is the vector of observation for trait 2, $\mathbf{b_2}$ is the vector of fixed effects for trait 2, $\mathbf{a_2}$ is the vector of additive genetic effects for trait 2, $\mathbf{p_2}$ is the vector of random permanent effects and non-additive genetic effects for trait 2, $\mathbf{e_2}$ is the vector of random residual effects for trait 2; and $\mathbf{X_2}$ $\mathbf{Z_2}$ and $\mathbf{W_2}$ are incidences matrices relating records of trait 2 to fixed, random animal effects and random permanent effects and non-additive effects, respectively.

The following assumptions were considered: $\mathrm{E}(\mathrm{y}_1) = \mathbf{X_1 b_1;}$ $\mathrm{E}(\mathrm{y}_2) = \mathbf{X_2 b_2}$; $\mathrm{E}(\mathrm{a}) = \mathbf{0}$; $\mathrm{E}(\mathrm{p}) = \mathbf{0;}$ and $\mathrm{E}(\mathrm{e}) = \mathbf{0}$. The random effects were assumed to be normally distributed with zero mean and the following co(variance) structure:

$$\mathrm{var}\begin{bmatrix}\mathbf{a_1}\\ \mathbf{a_2}\\ \mathbf{p_1}\\ \mathbf{p_2}\\ \mathbf{e_1}\\ \mathbf{e_2}\end{bmatrix} = \begin{bmatrix}\mathbf{A}\sigma^2_{\mathrm{a}_1} & \mathbf{A}\sigma_{\mathrm{a}_{12}} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0}\\ \mathbf{A}\sigma_{\mathrm{a}_{12}} & \mathbf{A}\sigma^2_{\mathrm{a}_2} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0}\\ \mathbf{0} & \mathbf{0} & \mathbf{I_1}\sigma^2_{\mathrm{p}_1} & \mathbf{I_1}\sigma_{\mathrm{p}_{12}} & \mathbf{0} & \mathbf{0}\\ \mathbf{0} & \mathbf{0} & \mathbf{I_1}\sigma_{\mathrm{p}_{12}} & \mathbf{I_1}\sigma^2_{\mathrm{p}_2} & \mathbf{0} & \mathbf{0}\\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{I_2}\sigma^2_{\mathrm{e}_1} & \mathbf{I_2}\sigma_{\mathrm{e}_{12}}\\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{I_2}\sigma_{\mathrm{e}_{12}} & \mathbf{I_2}\sigma^2_{\mathrm{e}_2}\end{bmatrix},$$

Where $\sigma^2_{\mathrm{a}_1}$ is the additive genetic variance for trait 1, $\sigma^2_{\mathrm{a}_2}$ is the additive genetic variance for trait 2 and $\sigma_{\mathrm{a}_{12}}$ is the additive genetic covariance between both traits;

$\mathbf{I_1}$ is an identity matrix which corresponds to the number of cows with records, $\sigma^2_{\mathrm{p}_1}$ is the permanent environmental variance for trait 1, $\sigma^2_{\mathrm{p}_2}$ is the permanent environmental variance for trait 2 and $\sigma_{\mathrm{p}_{12}}$ is the permanent environmental covariance between both traits;

$\mathbf{I_2}$ is an identity matrix of size 124,620 and 194,631 for OAD and TAD milking populations respectively (number of lactation records), $\sigma^2_{\mathrm{e}_1}$ is the residual variance for trait 1, $\sigma^2_{\mathrm{e}_2}$ is the residual variance for trait 2 and $\sigma_{\mathrm{e}_{12}}$ is the residual covariance between both traits.

Estimation of genetic parameters

Heritability (h^2) and repeatability (rep) for each trait were respectively calculated with the following ratios (Falconer & Mackay 1996):

$h^2 = \sigma_a^2/(\sigma_a^2 + \sigma_p^2 + \sigma_e^2)$ and

$\mathrm{rep} = (\sigma_a^2 + \sigma_p^2)/(\sigma_a^2 + \sigma_p^2 + \sigma_e^2)$.

Genetic (r_a) and phenotypic (r_y) correlations were calculated as Falconer & Mackay (1996):

$r_a = \sigma_{g_{12}}/(\sigma_{g_1} \times \sigma_{g_2})$ and

$r_y = \sigma_{y_{12}}/(\sigma_{y_1} \times \sigma_{y_2})$,

Where $\sigma_{y_{12}}$ is the phenotypic covariance between traits 1 and 2; σ_{g_1} and $\sigma_{y_1}$are the additive genetic and phenotypic standard deviations for trait 1, respectively; and $\sigma_{g_2}^2$ and $\sigma_{y_2}^2$ are the additive genetic and phenotypic standard deviation for trait 2, respectively.

Results

Descriptive statistics for milk yields, average SCS and milk composition traits for total lactation are presented in Table 6.1. The values presented for the population milked TAD are similar to the average national herd in New Zealand (LIC & Dairy NZ 2014).

Currently, up to 5% of dairy herds in New Zealand are milked OAD for the whole season (Stachowicz et al. 2014). Therefore, the number of OAD herds included in this study corresponded to at least 50% of the OAD population in the country. Comparison across MF indicates that cows in the OAD population produced between 19 and 25% less milk and milk solids (fat + protein) than cows in the TAD population. Milk composition traits were consistent across MF, although cows milked OAD tended to have a slightly more concentrated milk, and J cows had the lowest P:F. Coefficients of variation for milk traits in the TAD population were lower than in the OAD population.

Variance components, heritability and repeatability

Estimates of variance components, heritability and repeatability are presented in Tables 6.2 and 6.3 for OAD and TAD populations, respectively. It is highlighted that additive, permanent and residual variances were considerably lower in the OAD compared to the TAD population.

In general, in both populations the traits analysed had similar heritabilities, although they tended to be slightly greater in the TAD population. In both populations, estimates of heritability were greatest for the milk composition traits (>0.45). Heritabilities for FP and PP were greater than twice the estimates for their respective yield traits. In the traits included in BW (MY, FY, PY and SCS), the greatest heritability was estimated for MY (>0.30) and least in SCS (0.12 in both populations), while for FY and PY estimates of heritability were 0.21 and 0.22 in the OAD and 0.26 and 0.25 in the TAD populations, respectively.

Estimates of repeatabilities were greater in the TAD population with the exception of SCS and PP, which were slightly greater in the OAD population. Similar to heritability, repeatability estimates were greatest in the milk composition traits, but in this case, repeatabilities values of composition traits were not much higher than their respective yield traits as was observed for heritability. The values of repeatability ranged between 0.40 and 0.48 (OAD), 0.43 and 0.52 (TAD) for milk yield traits, and 0.55 and 0.81 (OAD), and 0.65 and 0.80 (TAD) for milk composition traits.

Table 6.2. Estimates of variance components, heritabilities and repeatabilities with their respective standard errors of the mean for milk production traits in the once-a-day milking population.

Trait	σ_a^2	σ_p^2	σ_e^2	σ_{total}^2	h^2	Rep
MY	90,445	42,493.9	145,391	278,330	$0.33\pm0.012^{**}$	$0.48\pm0.004^{***}$
FY	153.107	145.305	440.125	738.537	$0.21\pm0.012^{*}$	$0.40\pm0.004^{***}$
PY	82.3157	78.557	221.754	382.627	$0.22\pm0.012^{*}$	$0.42\pm0.004^{***}$
SCS	0.17007	0.30757	0.90184	1.37948	0.12 ± 0.010	$0.35\pm0.004^{***}$
FP	0.25005	0.03399	0.12017	0.40422	$0.62\pm0.011^{***}$	$0.70\pm0.003^{***}$
PP	0.04494	0.00937	0.01270	0.06700	$0.67\pm0.012^{***}$	$0.81\pm0.002^{***}$
P:F	0.00340	0.00047	0.00317	0.00705	$0.48\pm0.012^{***}$	$0.55\pm0.003^{***}$

MY= milk yield; FY= fat yield; PY=protein yield; SCS=somatic cell score; FP=fat percentage; PF=protein percentage; P:F=protein to fat ratio; σ_a^2=animal additive variance; σ_p^2=cow permanent environmental variance; σ_e^2= residual variance; σ_{total}^2=sum of the variances; h^2 = heritability; rep = repeatability.

$^{*, **, ***}$ Different from 0 at $p < 0.05$, $p < 0.01$ and $p < 0.001$, respectively, based on a two-tailed z-test.

Table 6.3. Estimates of variance components, heritabilities and repeatabilities with their respective standard errors of the mean for milk production traits in the twice-a-day milking population.

Trait	σ_a^2	σ_p^2	σ_e^2	σ_{total}^2	h^2	rep
MY	163,396	71,054.3	216,332	450,782	0.36±0.010**	0.52±0.003***
FY	264.786	172.784	579.195	1016.77	0.26±0.010**	0.43±0.003***
PY	127.362	101.819	289.874	519.055	0.25±0.010**	0.44±0.003***
SCS	0.15341	0.25578	0.85613	1.26532	0.12±0.008	0.32±0.003***
FP	0.24951	0.04147	0.08566	0.37665	0.66±0.009***	0.77±0.002***
PP	0.04245	0.00846	0.01257	0.06348	0.67±0.009***	0.80±0.001***
P:F	0.00457	0.0007	0.00282	0.00809	0.56±0.009***	0.65±0.002***

MY= milk yield; FY= fat yield; PY=protein yield; SCS=somatic cell score; FP=fat percentage; PF=protein percentage; P:F=protein to fat ratio; σ_a^2=animal additive variance; σ_p^2=cow permanent environmental variance; σ_e^2= residual variance; σ_{total}^2=sum of the variances; h^2 = heritability; rep = repeatability.

$^{*, **, ***}$ Different from 0 at $p < 0.05$, $p < 0.01$ and $p < 0.001$, respectively, based on a two-tailed z-test.

Correlations

Estimates of phenotypic and genetic correlations are presented in Tables 6.4 and 6.5 for OAD and TAD populations, respectively. There was a high phenotypic correlation among the milk yield traits (≥0.68) and high genetic correlation between MY and PY (OAD: 0.85; TAD: 0.84). Genetic correlations, however, were moderate when the estimation involved FY. For instance, the genetic correlation between MY and FY was 0.40 and 0.35 in OAD and TAD populations, respectively.

For both MF, phenotypic and genetic correlations between FP and PP were moderate to high (OAD: 0.57 and 0.72, respectively; TAD: 0.60 and 0.72, respectively), and high and negative between FP and P:F (OAD: -0.82 and -0.83, respectively; TAD: -0.81 and -0.81, respectively). The phenotypic and genetic correlations between PP and P:F were negative and low (OAD: -0.06 and -0.25, respectively; TAD: -0.09 and -0.24, respectively).

Estimates of phenotypic and genetic correlations between milk yields and composition traits were moderate to low (OAD: -0.60 to 0.46; TAD: -0.65 to 0.48). It is worth nothing that correlations of MY and PY with the composition traits had the opposite sign compared to the correlation of FY with the composition traits.

The lowest phenotypic and genetic correlations were found when one of the traits was SCS in both populations (OAD: -0.14 to 0.11; TAD: -0.09 to 0.16). Further, in some cases the genetic correlations were not different from zero (SCS with PP, and SCS with P:F in OAD and TAD populations, respectively).

Table 6.4. Estimates of genetic (below the diagonal) and phenotypic (above the diagonal) correlations, with their standard errors of the mean, for the milk production traits in the once-a-day milking population.

	MY	FY	PY	SCS	FP	PP	P:F
MY		0.74±0.002	0.93±0.001	-0.13±0.004	-0.33±0.004	-0.37±0.004	0.16±0.004
FY	0.40±0.038		0.82±0.001	-0.14±0.003	0.34±0.004	0.02±0.004	-0.42±0.003
PY	0.85±0.008	0.60±0.024		-0.13±0.005	-0.14±0.004	-0.02±0.004	0.14±0.004
SCS	0.07±0.044	0.02±0.052	0.10±0.051		0.01±0.004	0.05±0.004	0.03±0.004
FP	-0.60±0.019	0.46±0.023	-0.27±0.026	-0.08±0.033		0.57±0.003	-0.82±0.001
PP	-0.58±0.018	0.17±0.027	-0.07±0.026	-0.01±0.033 ^{ns}	0.72±0.009		-0.06±0.004
P:F	0.39±0.024	-0.55±0.023	0.33±0.029	0.11±0.037	-0.83±0.006	-0.25±0.018	

MY= milk yield; FY= fat yield; PY=protein yield; SCS=somatic cell score; FP=fat percentage; PF=protein percentage; P:F = protein to fat ratio.
ns, non-significantly different from 0.

Table 6.5. Estimates of genetic (below the diagonal) and phenotypic (above the diagonal) correlations, with their standard errors of the mean for the milk production traits in the twice-a-day milking population.

	MY	FY	PY	SCS	FP	PP	P:F
MY		0.68±0.002	0.91±0.001	-0.09±0.003	-0.37±0.003	-0.43±0.003	0.16±0.004
FY	0.35±0.021		0.78±0.001	-0.06±0.003	0.38±0.003	0.02±0.003	-0.48±0.002
PY	0.84±0.006	0.54±0.019		-0.06±0.003	-0.15±0.003	-0.05±0.004	0.13±0.003
SCS	-0.04±0.033	0.10±0.038	0.07±0.039		0.04±0.003	0.09±0.003	0.01±0.003 ^{ns}
FP	-0.63±0.013	0.48±0.016	-0.32±0.019	0.08±0.026		0.60±0.003	-0.81±0.001
PP	-0.65±0.012	0.12±0.019	-0.15±0.020	0.16±0.026	0.72±0.007		-0.09±0.003
P:F	0.33±0.017	-0.64±0.015	0.27±0.021	0.01±0.028 ^{ns}	-0.81±0.005	-0.24±0.013	

MY= milk yield; FY= fat yield; PY=protein yield; SCS=somatic cell score; FP=fat percentage; PF=protein percentage; P:F = protein to fat ratio.
ns, non-significantly different from 0.

Discussion

Coefficients of variation for milk traits in the OAD population were greater than in the TAD population. Davis et al. (1999) indicated that there is considerable variation among individual cows in the degree of milk yields reduction from TAD to OAD (3 to 47%), even animals on some occasions show close to zero change. In the experimental study of Clark et al. (2006), a large variability in milk yield traits was observed in cows milked OAD compared to TAD, particularly in F cows, where some OAD F cows yielded as much as the highest F milked TAD (Hickson et al. 2006).

Variance components, heritability and repeatability

Generally, heritability estimates for FY and PY are within the range reported in the literature for these traits (0.20 to 0.29) in TAD populations (Ahlborn & Dempfle 1992; Johnson et al., 2000; Pryce & Harris 2006; Rupp & Boichard 1999; Visscher & Goddard 1995), but lower than the range reported by Berry et al. (2003) and Miglior et al. (2007) (0.36 to 0.45 and 0.32 to 0.40 for FY and PY, respectively). In this study, the estimates of heritability for MY (0.33 and 0.36 in OAD and TAD, respectively) were greater than the range 0.24 to 0.28 reported by the authors previously cited, with the exception of the study from Pryce & Harris (2006), who found a heritability of 0.36 for 270 day-cumulative yield of milk in first-lactation cows in New Zealand, with the same breed groups used in this study.

The greater heritability observed for MY compared to FY and PY in both populations might be a consequence of the breeding objective being focused on production of milk solids instead of volume (López-Villalobos 2012) which could have resulted in a decreased additive variance in the MS traits compared to milk volume.

According to Ahlborn & Dempfle (1992), higher yield traits generally result in higher variances and heritability estimates. Tables 6.2 and 6.3 show greater phenotypic and genetic variances in milk yield traits in TAD-milked cows compared to those milked OAD. This could lead to expected higher heritability estimates in the TAD population. However, the heritabilities in cows milked TAD were very similar to those found in the population milked OAD. This similarity is unexpected in view of the large difference for milk yields in cows milked OAD and TAD shown in Table 6.1.

The values of repeatability found in this study for both OAD and TAD populations are in agreement with previous studies in first-lactation cows in New Zealand (Sneddon et al. 2015) and in J cows (Roman et al. 2000) using test-day records. The values reveal that cows express similar levels of milk production across seasons in both systems, although in the OAD population, yields of milk traits within cows vary in a slightly higher magnitude compared to the TAD population.

The results of this study suggest under the two MF systems, first-lactation records provide similar indication about their successive lactation yields (Falconer & Mackay 1996). Consequently, farmers in both systems could cull unsuitable cows using first lactation milk yields with similar reliability.

Correlations

The values presented in Tables 6.4 and 6.5 indicate that in both OAD and TAD populations, correlations tended to have similar direction and magnitudes, possibly because of similarities between management systems. In practical terms, the correlations were similar and likely the differences across MF are attributable to the data set, being a large one compared to other studies. For instance, the size of the data set used in this study was larger compared to the studies of Berry et al. (2003) (8,591 multiparous cows), Rupp & Boichard (1999) (29,284 multiparous cows) and Sneddon et al. (2015) (4,378 first-lactating cows), but smaller than the study of Pryce & Harris (2006) (169,661 in first-lactating cows).

The genetic correlations found in this study suggest that an increase in MY results a slight, unfavourable SCS increase in the OAD population while in the TAD population, the increase in MY results in a low (favourable) SCS decrease. These results suggest that an increased selection pressure against SCS might be applied by the farmers on the cow population milked OAD due to greater SCS in this population compared to the TAD population (Clark et al. 2006).

The correlations for milk yield traits and SCS are within the range of those reported by López-Villalobos & Spelman (2010) for a TAD population in New Zealand. In this study, however, some genetic and phenotypic correlations were found to differ from those presented elsewhere. The most relevant discrepancy involves the genetic correlation of FY with either MY or PY. Analysing first-lactation cows, Ahlborn & Dempfle (1992) (two seasons using F and J records), Pryce & Harris (2006) (four seasons using the same breed groups considered in this study), and Sneddon et al. (2015) (one season using records from F, F×J, J and other breeds) found greater genetic correlations between FY and MY (0.55-0.87) and PY (0.69-0.90) than the values presented in Tables 4 and 5 (OAD: 040-0.60; TAD: 0.35-0.54).

Implications

The annual rate of genetic progress (ΔG) can be described by the following formula (Rendel & Roberston 1950):

$$\Delta \mathrm{G} = \frac{\mathrm{i} \times \mathrm{r}_{\mathrm{A},\hat{\mathrm{A}}} \times \sigma_{\mathrm{g}}}{\mathrm{L}}$$

where σ_{g}, i, $\mathrm{r}_{\mathrm{A},\hat{\mathrm{A}}}$ and L are the genetic standard deviation, intensity of selection, accuracy of selection and generation interval, respectively. Based on this equation, the results of the current study are important because they indicate that if selection is applied separately in each of the populations, expected genetic progress in the production traits in the OAD population would be lower than the expected genetic progress in the TAD population, because lower genetic variances were found in the OAD population (see Tables 6.2 and 6.3).

Due to the size of OAD population (3%-5%), it is unlikely that it is economically viable to produce a genetic evaluation specifically for OAD dairy cattle (McPherson et al. 2007). Hence, dairy cattle milked OAD are currently evaluated along with cattle milked TAD. The latter would lead to genetic evaluation with heterogeneous variances across MF populations.

The best linear unbiased prediction procedure (Henderson 1973) used in breeding programs of dairy cattle assumes that variances are homogeneous (Visscher & Hill 1992). Vinson (1987) simulated potential bias due to heterogeneous variances across herds, indicating that most of the individuals selected are from high yield herds, which usually show higher heritability compared to lower yielding herds.

The heterogeneity of variance could lead to systematic biases in the estimation of breeding values of the individuals. This bias is cumulative over time, since cows remain constantly under the same conditions (Vinson 1987). The problem of heterogeneity of variance has been identified in the animal evaluation system in New Zealand (Harris et al. 1996). For instance, incomplete lactation records have lower variances (genetic and phenotypic) than total lactation records; thus, methods for correction for heterogeneous variances are implemented in the national evaluation of New Zealand dairy cattle (Harris et al. 1996). The issue is whether the model used in the animal evaluation system is robust enough to account for differences in variances due to MF. If the model assumes homogenous variances in the population milked OAD and TAD, cows milked OAD will be assigned greater variances than the actual variances, which would, hypothetically overestimate their EBVs.

Conclusions

The estimates of genetic parameters obtained in this study are within the ranges previously reported in dairy cattle populations. The results obtained indicate that heritability showed great consistency across MF, but estimates of genetic and residual variances were larger in the TAD than in the OAD population. The practice of evaluating both dairy populations together could lead to systematic biases in the EBVs if heterogenous variances are not accounted for.

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CHAPTER 7

Comparison of sire breeding values for milk yields traits based on daughters milked once- or twice-daily in New Zealand

Abstract

In New Zealand cows are usually milked twice-a-day (TAD), but it has become increasing popular to milk once-a-day (OAD) for the entire lactation. It is argued that a genetic correlation (r_G) for the same trait expressed in two environments, such as between TAD and OAD, that is substantially less than 1.0, would imply that genetic merit assessed from TAD herds may not be reliable for predicting genetic merit in OAD herds. This study aims to test if sire re-rankings occur in New Zealand at different milking frequencies (MF). Regression coefficients and observed rank correlations (r_S) between estimated breeding values (EBVs) of 242 sires (86 Holstein-Friesian, 60 Holstein-Friesian×Jersey and 96 Jersey with progeny in both MF) for yields of milk (MY), fat (FY) and protein (PY), and somatic cell score (SCS) were calculated. These sires had progeny distributed over 298 OAD and 350 TAD herds. Within and across-breed, regression coefficients were lower than unity and r_S between TAD and OAD EBVs of the same sires were high (> 0.75) for MY, medium-high for FY and PY (0.55-0.77), and medium for SCS (0.41-0.65). Rank correlations were contrasted with expected rank correlations (r_E) between TAD and OAD EBVs assuming a r_G=1 between true breeding values expressed at the two MF. Estimates of r_S were generally higher than their expected critical r_E value (5th percentile), indicating no significant sire re-ranking across MF. In conclusion, no evidence of sire re-ranking for milk yield traits due to MF was found. Therefore, a selection program using adjustment factors for each MF environment can be recommended.

Keywords: once-a-day milking; breeding values; rank correlation; expected correlation; genotype × environment interaction.

Introduction

The milking frequency (MF) for dairy cattle in New Zealand is typically twice-a-day (TAD), although for many years some farmers have strategically used once-a-day (OAD) milking, particularly during periods of feed shortage. However, since the late 1980s, milking OAD over the entire lactation has been adopted by some farmers for herd management and lifestyle benefits (Davis et al. 1999; Clark et al. 2006).

In an experimental study, Clark et al. (2006) reported significant interactions between Holstein-Friesian (F) and Jersey (J) breeds for milk yield traits when milked TAD compared to OAD. Holstein-Friesian and J cows milked OAD yielded 30% and 19% less milk solids (MS, kg/cow) than cows of the same breeds milked TAD. Over the four seasons of that trial, the top 25% of F cows milked OAD averaged 350 kg MS/cow compared with only 150 kg MS/cow for the bottom 25%. This represents a larger inter-quartile range than is typically observed in cows milked TAD. Despite these larger variations in production that have been observed, some cows milked OAD have yielded as much as cows milked TAD (Hickson et al. 2006). This variability in milk yield makes it difficult to predict the extent of lost productivity when changing from TAD to OAD milking, and to identify the most suitable cows for OAD milking systems (Guinard-Flament et al. 2011). Nevertheless, it suggests there may be the potential to identify and select cows (or sires) whose yields will be more comparable between TAD and OAD milking frequencies (Stelwagen et al. 2013). There is some evidence of medium-high correlations between estimated breeding values (EBVs) for milk yields (0.47-0.85) of sires with progeny in OAD systems compared with the EBVs published in the official list, which are mostly derived from herd tests based on TAD milking (McPherson et al. 2007; Stachowicz et al. 2014).

In the New Zealand dairy industry, the genetic merit of an animal is evaluated according to the breeding worth index (BW) (López-Villalobos & Garrick 2005). BW is calculated by weighting EBVs for lactation yields of milk (MY), fat (FY) and protein (PY), somatic cell score (SCS), live weight, fertility, and residual survival, with their respective economic values. BW ranks sires and cows according to their expected ability to produce more profitable replacements, quantified in terms of marginal changes to profit per five tonnes of consumed dry matter. Given the MF by breed interaction reported by Clark et al. (2006), it was of interest to investigate if the interaction is a consequence of a scaling effect between breeds or if extends to re-rank sires between MF environments (Hammami et al. 2009).

Sire re-ranking between MF would indicate that the true genetic correlation between milk production traits is less than unity. The results of McPherson et al. (2007) and Stachowicz et al. (2014) suggest that OAD and TAD milking traits are genetically different. However, this concept has not been robustly tested, because usually observed correlations between EBVs of the same trait across environments are < 1.0; therefore, observed correlations should be interpreted relative to their expected value (Notter & Díaz 1993).

The aim of this study was to determine the effect of MF environments on the genetic evaluation of dairy sires with progeny milked either TAD or OAD in grazing systems. This was achieved by estimating rank correlations between EBVs of the same sires in the two MF systems, and to formally test for evidence of sire re-ranking for milk production traits.

Materials and methods

Data

Livestock Improvement Corporation (LIC, Hamilton, New Zealand) provided pedigree information and MY, FY and PY records from cows calving from 2008 to 2012, along with herd-test records of somatic cell count (SCC) which were used to calculate average SCS during each lactation for each cow. Somatic cell score was calculated as SCS = $\log_2$ (SCC) (Harris & Winkelman 2004).

Milking herds defined as OAD were identified as those where 100% of cows were milked OAD during the whole production season. Using the GPS (Global Position System) Visualizer (Schneider 2012), all TAD herds within a radius of 20 km of each OAD herd were selected for comparison. Only records from spring-calving cows in their first five lactations with lactation lengths between 150 and 305 days and from herds with more than 50 cows were considered. Records from F, J and their crosses were retained. Records were discarded from animals representing other breeds and those without information on breed composition.

After these data filters, 1550 sires (511 F, 301 F×J and 738 J sires) were identified with progeny in both MF systems. A further filter was applied to only select sires with at least 20 (different) daughters in both MF systems. The dataset was reduced to 242 sires (86 F, 60 F×J and 96 J sires) which had progeny distributed in 350 and 298 herds milked TAD and OAD, respectively.

Estimation of breeding values

Best Linear Unbiased Prediction (BLUP) (Henderson 1973) breeding values were obtained for the sires with at least 20 daughters in each MF. EBVs were obtained for each MF (subset) environment separately using the ASReml 3.0 software package (Gilmour et al. 2009). The BLUP procedure was a single repeatability animal model across breeds. In matrix notation, the model is represented (e.g. Mrode 2014) as,

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Za} + \mathbf{Wp} + \mathbf{e}$$

where $\mathbf{y}$ is the vector of observations for one of the traits MY, FY, PY or SCS; $\mathbf{b}$ is the vector of fixed effects, $\mathbf{a}$ is the vector of random additive genetic effects, $\mathbf{p}$ is the vector of random permanent environmental effects and $\mathbf{e}$ is the vector of random residual effects. The incidence matrices $\mathbf{X}$, $\mathbf{Z}$ and $\mathbf{W}$ relate records to fixed, additive genetic and permanent environmental effects, respectively.

The effects included in $\mathbf{b}$ were: contemporary group (CG) defined by the group of cows of the same lactation number calving in the same herd and production season; the regression coefficient associated with the linear effect of proportion of breed F; the regression coefficient associated with the linear effect of coefficient of heterosis; the regression coefficient associated with the linear effect of deviation in lactation length from median lactation length of the herd in a given season; and the regression coefficient associated with linear effect of deviation in days from median calving date of the herd in a given season. Heterosis was calculated for every cow following

Dickerson (1973) as $h_{FxJ} = \alpha_F^s \alpha_J^d + \alpha_J^s \alpha_F^d$; where α_F^s or α_J^s are proportions of F or J in the sire and α_F^d and α_J^d are proportions of F and J in the dam.

Across-breed EBVs were calculated by adding to the vector of individual animal additive genetic effects the vector of relative proportions of the F breed in product with the scalar estimate of the F breed effect.

Correlation between breeding values for bulls evaluated separately at each milking frequency

The EBVs obtained were used to calculate product-moment Spearman's rank (r_S) correlations between EBVs of sires for each trait using the CORR procedure of SAS version 9.3 (SAS Institute Inc., Cary, NC., USA). Those EBVs were the result of separate genetic evaluation of sires with progeny in both MF. Rank correlations between EBVs were compared to the expected distribution of correlations (r_E) between EBVs as suggested by Notter & Díaz (1993).

Simulation of expected correlation between breeding values estimated in two milking frequency environments

Notter & Díaz (1993) indicated that some assumptions are required for calculating r_E. The assumptions are: a) no environmental correlation between performance in the different environments; b) no relationship among parents of measured animals; c) no other (co)variances among EBV within either environment and d) sires are chosen at random. Those assumptions are usually met if sires are measured in different environments, such as two different MF (a), through choice of sires (b and d). Assumption c will not normally hold for BLUP.

The procedure to simulate r_E between EBVs of sires calculated separately in the two MF systems was derived as in Garrick (2005) using the IML procedure of SAS version 9.3 (SAS Institute Inc., Cary, NC., USA). The procedure described in that paper uses Monte Carlo simulation assuming a genetic correlation (r_G) between MF environments equal to a unity ($r_G = 1$). The observed r_S was compared to a test statistic corresponding to the fifth percentile (α=0.05) for r_E. The distributions of the r_E between EBVs of sires estimated in two MF were as follows:

1. A column vector $(\mathbf{u}_i)$ containing the true (g_{tad}, g_{oad}) and estimated breeding ($\hat{g}_{tad}$, $\hat{g}_{oad}$) values for each sire (i= 1, 2, …, n) was simultaneously obtained for the four traits in the two MF as,

$$\mathbf{u}_i = \mathbf{L}_i\mathbf{z}_i,$$

where $\mathbf{u}_i$ had the following elements,

$$\mathbf{u}'_i = [g_{TAD_{MY}} \quad g_{OAD_{MY}} \quad \hat{g}_{TAD_{MY}} \quad \hat{g}_{OAD_{MY}} \quad \cdots \quad g_{TAD_{SCS}} \quad g_{OAD_{SCS}} \quad \hat{g}_{TAD_{SCS}} \quad \hat{g}_{OAD_{SCS}}];$$

$\mathbf{L}_i$ is the lower triangular elements of the Cholesky decomposition of the 16×16 (co)variance matrix $\mathbf{V}_i$ such as $\mathbf{L}_i\mathbf{L}'_i = \mathbf{V}_i$; and $\mathbf{z}_i$ is a 16×1 column vector of random independent normal deviates. There were as many matrix $\mathbf{V}_i$ as sires generated. Derivation of matrix $\mathbf{V}_i$ is shown in the appendix 7.1.

2. The set of column vectors $\mathbf{u}_i$ for each sire formed a matrix $\mathbf{U}$, that contained one possible realisation of the correlated true BVs and EBVs of unrelated sires. Therefore, matrix $\mathbf{U}'$ had as many columns as traits simulated and as many rows as the number of sires generated such as,

$$\mathbf{U}' = \begin{bmatrix} \mathbf{u}'_1 \\ \mathbf{u}'_2 \\ \vdots \\ \mathbf{u}'_n \end{bmatrix}$$

3. Product-moment correlation between EBVs for each trait in the two MF was calculated for this one sample.
4. Steps 1-3 were repeated 1000 times to obtain a distribution of r_E between EBVs based on the given numbers of progeny records per sire.

The threshold at the fifth percentile corresponds to the lower limit of r_E considered as the critical point to accept or reject the null hypothesis (H_0: $r_G = 1.0$) (Garrick 2005). The analyses were performed separately for F, F×J and J sires, and across breeds. Across-breed and F×J analysis, simulated EBVs were calculated by adding to the vector of $\hat{g}_{oad}$, $\hat{g}_{tad}$ resulting in $\mathbf{u}'_i$, the vector of relative proportions of the F breed in product with the breed effect resulted in the BLUP analysis.

The simulation of the expected distribution of correlations required knowledge of the reliability of the EBV for each sire (see appendix). Sire reliability for each trait in each

MF environment was calculated according to Cameron (1997) as: $(\mathrm{n_i}/\mathrm{n_i} + \lambda)$, where $\mathrm{n_i}$ is the number of daughters of sire i in each MF system and λ corresponds to $(4 - \mathrm{h}^2)/\mathrm{h}^2$.

Garrick (2005) assumed that sires to be compared for EBVs from two different progeny tests are unselected. This was not the case in our field data because r_S were calculated within a selected sample of 242 TAD proven sires. Accordingly, in the simulation of data for this study, in the across-breed analysis, the same numbers of sires of the original data set (1550) were simulated and the best 242 were selected according to an economic index (EI) of their EBVs for TAD systems. The EI was calculated as: $\mathrm{EI} = \mathrm{EBV_{MY}} \times \mathrm{EV_{MY}} + \mathrm{EBV_{FY}} \times \mathrm{EV_{FY}} + \mathrm{EBV_{PY}} \times \mathrm{EV_{PY}} + \mathrm{EBV_{SCS}} \times \mathrm{EV_{SCS}}$, where $\mathrm{EBV_{MY}}$, $\mathrm{EBV_{FY}}$ $\mathrm{EBV_{PY}}$, $\mathrm{EBV_{SCS}}$ are EBV for MY, FY, PY and SCS, respectively and $\mathrm{EV_{MY}}$, $\mathrm{EV_{FY}}$, $\mathrm{EV_{PY}}$ $\mathrm{EV_{SCS}}$ are the official economic values reported by New Zealand Animal Evaluation Limited (NZAEL) as -0.097/L milk, 1.81/ kg fat, 8.18/kg protein and -38.61/score of SCS (LIC and Dairy NZ, 2015). A similar procedure was carried out in the within-breed analyses. In that case, 511 F sires, 301 F×J sires and 738 J sires (corresponding to the number of sires of each breed group of the original data) were simulated and the best 86, 60 and 96 sires, respectively were selected according the EI.

Genetic parameters used to calculate r_E were genetic variances, heritability and r_G between productions traits. Those values were published by Lembeye et al. (2016) and are presented in Table 7.1.

Table 7.1. Genetic parameters of total lactation yields of milk, fat, protein and average somatic cell score used to calculate expected correlations.

Trait	MF[1]	σ^2_G	h^2	Genetic correlation[1]		
				MY	FY	PY
MY	OAD	90,445	0.33			
	TAD	163,396	0.36			
FY	OAD	153.1	0.21	0.37		
	TAD	264.8	0.26			
PY	OAD	82.3	0.22	0.84	0.57	
	TAD	127.4	0.25			
SCS	OAD	0.17	0.12	0.02	0.09	0.09
	TAD	0.15	0.12			

MF= milking frequency, OAD= once-a-day milking, TAD= twice-a-day milking, MY= milk yield, FY= fat yield, PY= protein yield, SCS= somatic cell score, σ^2_G= genetic variance, h^2= heritability.

[1] These values correspond to the mean r_G across MF calculated by the inverse of their squared standard error Koots et al. (1994).

Results

Descriptive statistics for total days in milk, milk yield traits and SCS are presented in Table 7.2. Yields of milk, fat and protein were greater in progeny milked TAD compared to OAD, while SCS were slightly lower for TAD milking.

Table 7.3 presents EBVs and reliabilities of the same sires with progeny in both OAD and TAD systems. Sires had relatively high reliabilities (>0.69) in both MF systems, and the EBVs of sires in OAD were lower than their EBVs in TAD milking systems. There was, however, a larger difference in reliability across MF in F sires (0.69-0.84 vs. 0.84-0.94 of the EBVs in OAD and TAD, respectively), while for the other breeds; reliabilities were more similar across MF.

Table 7.2. Mean and standard deviation (SD) of total days in milk, total lactation yields of milk, fat, protein (kg/cow) and average somatic cell score by lactation number of the progeny of 242 sires with at least 20 daughter progeny per milking frequency system.

Trait	Lactation number	Milking frequency					
		Once-a-day			Twice-a-day		
		N	Mean	SD	N	Mean	SD
DIM	1	28,402	225	34	43,808	233	33
MY			2,315	698		3,376	925
FY			124.4	35.4		163.6	41.6
PY			94.2	27.1		127.6	33.4
SCS			6.41	1.12		5.95	1.10
DIM	2	24,752	223	34	38,256	228	34
MY			2,898	803		3,952	1,089
FY			154.1	39.5		191.2	47.6
PY			118.6	31.2		150.6	38.9
SCS			6.11	1.23		5.88	1.17
DIM	3	19,769	222	34	31,852	227	34
MY			3,203	874		4,335	1,190
FY			170.5	43.4		209.4	51.6
PY			131.2	33.4		164.8	41.9
SCS			6.3	1.34		6.07	1.27
DIM	4	15,555	223	33	25,017	229	34
MY			3,367	930		4,511	1,250
FY			178	45.1		218	54.4
PY			137.4	34.8		171.2	44.0
SCS			6.49	1.45		6.27	1.37
DIM	5	11,198	223	33	18,391	229	34
MY			3,434	955		4,553	1,266
FY			180.7	46.0		219.9	55.5
PY			139.3	35.5		172.6	44.6
SCS			6.66	1.56		6.49	1.46

DIM= days in milk, MY= milk yield, FY= fat yield, PY= protein yield; SCS= somatic cell score.

Table 7.3. Estimated breeding values and reliabilities for production traits of sires evaluated with progeny in either once- or twice-daily milking systems.

	Milking frequency							
	Twice-a-day				Once-a-day			
	MY	FY	PY	SCS	MY	FY	PY	SCS
	Holstein-Friesian (n= 86)							
Mean	961.1	9.1	22.6	0.09	668	4.5	15.1	0.25
SE	28	1.0	0.7	0.03	21.9	0.8	0.6	0.03
Reliability	0.94	0.91	0.91	0.84	0.85	0.78	0.79	0.69
	Crossbred F×J (n= 60)							
Mean	398.5	4.6	10.2	-0.02	216.1	0.9	5.3	0.11
SE	33.6	1.0	0.9	0.03	27.5	1.1	0.8	0.04
Reliability	0.90	0.86	0.85	0.74	0.89	0.83	0.84	0.75
	Jersey (n= 96)							
Mean	-12.4	2.7	1.5	0.02	13.2	2.3	1.9	-0.03
SE	25.3	0.8	0.7	0.03	19.9	0.8	0.6	0.03
Reliability	0.90	0.86	0.86	0.75	0.90	0.85	0.85	0.77

MY= milk yield, FY= fat yield, PY= protein yield, SCS= somatic cell score, SE= Standard error.

Rank correlations and regression statistics between EBVs for milk yield traits, SCS and the EI are presented in Table 7.4 for F sires, Table 7.5 for F×J sires, Table 7.6 for J sires and Table 7.7 across breeds. Within breed, regression coefficients less than 1.0 indicated a scaling effect across MF. Rank correlations presented in Tables 7.4-7.6 ranged from 0.41 (SCS, F×J sires) to 0.84 (MY, J sires). Assuming an r_G=1.0, in general, r_S correlations were below the mean r_E only for FY (F sires) and for PY and SCS (F×J sires). The observed values, however, were higher than the critical values of the r_E, indicating that sire re-ranking was not significant for the traits studied.

Across breeds, r_S of EI were lower than for their yield components traits (0.59 vs. 0.65-0.93). The simulated expected values were higher than the observed r_S only for SCS. The regression coefficients indicated that for each NZ$1.00 of EI in TAD systems, there is only a NZ$0.47 increase expected in OAD systems.

Table 7.4. Estimates of regression coefficients (intercept and slope) of estimated breeding values (EBVs) for milk traits from once-a-day (OAD) milking herds on EBV for the same traits from twice-a-day (TAD) milking herds for 86 Holstein-Friesian sires. Spearman's rank (r_S) correlations between OAD and TAD EBVs and the corresponding mean and critical values of the expected correlations (r_E) at different true genetic correlations (r_G) of the same trait expressed in two environments are also shown.

	Intercept	Slope	r_S	r_E (critical value)	r_E (mean)
Milk yield	88.3±53.9^{ns}	0.60±0.05	0.75	0.51	0.64
Fat yield	0.30±0.95^{ns}	0.46±0.07	0.55	0.42	0.57
Protein yield	3.54±1.72	0.51±0.07	0.61	0.39	0.55
Somatic cell score	0.19±0.03	0.67±0.09	0.63	0.38	0.56
Economic index	20.5±10.0	0.35±0.09	0.42	0.20	0.40

^{ns} non-significant different from 0.

Rank correlations are significantly different to the 0.05 percentile of expected correlation if r_S are lower than the critical value of r_E.

Table 7.5. Estimates of regression coefficients (intercept and slope) of estimated breeding values (EBVs) for milk traits from once-a-day (OAD) milking herds on EBV for the same traits from twice-a-day (TAD) milking herds for 60 crossbred Holstein-Friesian × Jersey sires. Spearman's rank (r_S) correlations between OAD and TAD EBVs and the corresponding mean and critical values of the expected correlations (r_E) at different true genetic correlations (r_G) of the same trait expressed in two environments are also shown.

	Intercept	Slope	r_S	r_E (critical value)	r_E (mean)
Milk yield	-37.9±32.1^{ns}	0.64±0.07	0.77	0.63	0.74
Fat yield	-2.72±0.98^{ns}	0.78±0.11	0.68	0.42	0.61
Protein yield	-0.62±1.20	0.58±0.10	0.57	0.47	0.64
Somatic cell score	0.12±0.04	0.67±0.14	0.41	0.38	0.59
Economic index	-9.7±9.3	0.54±0.14	0.46	0.20	0.45

^{ns} values not different from zero ($p > 0.05$).

Rank correlations are significantly different to the 0.05 percentile of expected correlation if r_S are lower than the critical value of r_E.

Table 7.6. Estimates of regression coefficients (intercept and slope) of estimated breeding values (EBVs) for milk traits from once-a-day (OAD) milking herds on EBV for the same traits from twice-a-day (TAD) milking herds for 96 Jersey sires. Spearman’s rank (r_S) correlations between OAD and TAD EBVs and the corresponding mean and critical values of the expected correlations (r_E) at different true genetic correlations (r_G) of the same trait expressed in two environments are also shown.

	Intercept	Slope	r_S	r_E (critical value)	r_E (mean)
Milk yield	21.2±11.5^{ns}	0.64±0.05	0.84	0.52	0.65
Fat yield	0.31±0.56^{ns}	0.72±0.07	0.74	0.41	0.57
Protein yield	0.91±0.41	0.64±0.06	0.77	0.40	0.56
Somatic cell score	-0.04±0.02^{ns}	0.68±0.09	0.58	0.37	0.55
Economic index	8.5±3.63	0.62±0.08	0.68	0.21	0.40

^{ns} values not different from zero ($p > 0.05$).

Rank correlations are significantly different to the 0.05 percentile of expected correlation if r_S are lower than the critical value of r_E.

Table 7.7. Estimates of regression coefficients (intercept and slope) of estimated breeding values (EBVs) for milk traits from once-a-day (OAD) milking herds on EBV for the same traits from twice-a-day (TAD) milking herds for 242 sires. Spearman’s rank (r_S) correlations between OAD and TAD EBVs and the corresponding mean and critical values of the expected correlations (r_E) at different true genetic correlations (r_G) of the same trait expressed in two environments are also shown.

	Intercept	Slope	r_S	r_E (critical value)	r_E (mean)
Milk yield	7.38±10.98^{ns}	0.66±0.02	0.93	0.72	0.78
Fat yield	-0.57±0.46^{ns}	0.60±0.04	0.65	0.46	0.56
Protein yield	-0.56±0.41^{ns}	0.61±0.03	0.85	0.55	0.64
Somatic cell score	0.08±0.02	0.70±0.06	0.54	0.44	0.55
Economic index	5.33±3.34^{ns}	0.47±0.04	0.59	0.26	0.39

^{ns} values not different from zero ($p > 0.05$).

Rank correlations are significantly different to the 0.05 percentile of expected correlation if r_S are lower than the critical value of r_E.

Discussion

The values presented in Table 7.2 for the population milked TAD are consistent with the average national herd in New Zealand (LIC & Dairy NZ 2015). The average milk yield in the OAD compared to TAD herds shows that the breed effect (difference between F and J) is greater in TAD milking (Lembeye et al. 2015).

When only the elite and widely-used sires are considered, the mean EBVs of the same sires were greater in TAD compared to OAD systems. That difference is explained by greater genetic variance in TAD-herds compared to OAD-herds (Lembeye et al. 2016).

Previously, McPherson et al. (2007) and Stachowicz et al. (2014) had reported estimated correlations between OAD and TAD EBVs in New Zealand. Both studies used the New Zealand official EBVs (provided by NZAEL, Hamilton, New Zealand) compared to the EBVs of OAD-milked herds. The estimates of correlations for the same breed groups of sires presented in Tables 7.4-7.6 are slightly lower than those reported by McPherson et al. (2007) for the milk yield traits. The correlations for SCS found in that study (0.76-0.82) were higher than the values presented in Tables 7.4-7.6. For MY, FY and PY, the correlation estimates ranged from 0.75 to 0.84 in EBVs estimated in OAD and TAD milking systems using data from LIC from two seasons (2005/06 and 2006/07).

More recently, Stachowicz et al. (2014) using data for the period 2007-2011 found correlations for milk production traits ranged between 0.47 and 0.85 (0.60-0.74 for F sires, 0.47-0.65 for F×J sires and 0.65-0.85 for J sires). Those values are in agreement with the correlations presented in Tables 7.4-7.6, although higher correlations were found in this study for MY in F and F×J sires, while a lower correlation was found for FY in F sires. Nevertheless, neither in McPherson et al. (2007) nor Stachowicz et al. (2014) were those observed correlations tested for significance by comparison with their $r_{E,}$ as in the present study.

From the data of Stachowicz et al. (2014), a S×MF interaction for milk production traits was inferred, considering that the correlations between OAD systems and the New Zealand official EBVs were lower than 0.80 (except for MY in J breed). Robertson

(1959) proposed an r_G of 0.80 as a critical value to interpret if an interaction is economically important. Instead of using a unique critical value of 0.80 as proposed by Robertson (1959), this study implemented the methodology proposed by Garrick (2005) to estimate the r_E between EBVs of the same sires evaluated using different data sets, and assuming true genetic correlations between the same trait expressed in two different environments.

Although an r_G equal to 1.0 was assumed, the mean r_E for each trait was less than 1.0 as indicated in Notter & Díaz (1993). Expected correlations were < 1.0 because these values were a function of reliabilities of two separated genetic evaluations (Garrick 2005). The critical values of r_E obtained in this study were lower than the observed r_S between OAD and TAD EBVs, confirming little evidence of sire re-ranking in New Zealand dairy cattle when progeny were evaluated based on progeny milked OAD or TAD.

However, some potential bias of the r_E simulated is assumed, which is attributable to the fact that r_E were derived as a function of the true number of progeny per each sire in each MF rather than effective number (Notter & Díaz 1993). They indicated that r_E should be obtained using reliabilities (or accuracies) of EBVs computed from elements of the inverse matrix of the mixed model equations.

This study reveals a scaling effect as is indicated by the regression coefficients being lower than unity. In the scaling effect, sires maintain their ranking across MF, but only differences in the magnitude of their EBVs are observed (Hammami et al. 2009). In agreement with this study, Hammami et al. (2009) indicated that most studies conducted to evaluate G×E in dairy cattle within country, have found a scaling effect instead of re-ranking.

The regression coefficients presented in Tables 7.4-7.7 indicate that evaluations made under TAD, over-predict realized responses in OAD milking systems and that response to selection in the OAD herds will be smaller compared to the TAD herds. Suboptimal progeny performance of F and F×J sires is supported by lower observed r_S of those breed groups compared to J sires, suggesting that the J breed is a more appropriate breed under OAD systems, than the other breeds. Previous studies have indicated that in general, F and F×J cows milked OAD were more affected than J cows because those breeds had decreased milk production (MY and MS yield) per cow and per hectare to a greater extent than J cows when they were compared to their TAD-milked counterparts (Clark et al. 2006; Cooper 2000).

Considering herd average of MS (or PL) as two different environments, Bryant et al. (2007) also reported a low degree of re-ranking in New Zealand. Observed r_S and mean r_E found by those authors were lower for milk yields compared to the results in Table 7.7. (r_S and r_E were 0.76 and 0.53; 0.50 and 0.43; 0.83 and 0.43 for MY, FY and PY, respectively). Although that study cannot be compared directly with the present study, considering herds milked OAD and TAD as low and high-MS-yield respectively, the findings in Bryant et al. (2007) support the results of this study for milk yields.

Conclusions

The results obtained in this study confirm a scaling effect but no evidence of sire re-ranking for milk traits in the New Zealand sire dairy cattle population with progeny at OAD and TAD milking frequencies. A joint selection program using adjustment factors for each MF environment is recommended.

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Appendix 7.1. Derivation of (co)variance matrix **V**

A matrix **V** of designed (co)variance for each sire between true and estimate breeding values for m traits in each environment can be represented as:

$$V = \begin{bmatrix} V_i & Cov_{i,j} & \cdots & Cov_{i,m} \\ Cov_{i,j} & V_j & \cdots & Cov_{j,m} \\ \vdots & \vdots & \ddots & \vdots \\ Cov_{i,m} & Cov_{j,m} & \cdots & V_m \end{bmatrix}$$

Derivation of each sub-matrix included in **V** can be represented as:

$$V_i = \begin{bmatrix} \sigma^2_{g_{i_1}} & \sigma_{g_{i_{1,2}}} & r^2_{i_1}\sigma^2_{g_{i_1}} & r^2_{i_2}\sigma_{g_{i_{1,2}}} \\ \sigma_{g_{i_{1,2}}} & \sigma^2_{g_{i_2}} & r^2_{i_1}\sigma_{g_{i_{1,2}}} & r^2_{i_2}\sigma^2_{g_{i_2}} \\ r^2_{i_1}\sigma^2_{g_{i_1}} & r^2_{i_1}\sigma_{g_{i_{1,2}}} & r^2_{i_1}\sigma^2_{g_{i_1}} & r^2_{i_1}r^2_{i_2}\sigma_{g_{i_{1,2}}} \\ r^2_{i_2}\sigma_{g_{i_{1,2}}} & r^2_{i_2}\sigma^2_{g_{i_2}} & r^2_{i_1}r^2_{i_2}\sigma_{g_{i_{1,2}}} & r^2_{i_2}\sigma^2_{g_{i_2}} \end{bmatrix}$$

$$Cov_{i,j} = \begin{bmatrix} \sigma_{g_{i_1,j_1}} & \sigma_{g_{i_2,j_1}} & \sigma_{g_{i_1,j_1}}, r^2_{i_1} & \sigma_{g_{i_2,j_1}}, r^2_{i_2} \\ \sigma_{g_{i_1,j_2}} & \sigma_{g_{i_2,j_2}} & \sigma_{g_{i_1,j_2}}, r^2_{i_1} & \sigma_{g_{i_2,j_2}}, r^2_{i_2} \\ \sigma_{g_{i_1,j_1}}, r^2_{j_1} & \sigma_{g_{i_2,j_1}}, r^2_{j_1} & \sigma_{g_{i_1,j_1}}, r^2_{i_1}, r^2_{j_1} & \sigma_{g_{i_2,j_1}}, r^2_{i_2}, r^2_{j_1} \\ \sigma_{g_{i_1,j_2}} r^2_{j_2} & \sigma_{g_{i_2,j_2}} r^2_{j_2} & \sigma_{g_{i_1,j_2}}, r^2_{i_1}, r^2_{j_2} & \sigma_{g_{i_2,j_2}}, r^2_{i_2}, r^2_{j_2} \end{bmatrix}$$

Where $r^2_{i_1}$ and $r^2_{i_2}$ are reliabilities of trait i in environments 1 and 2, respectively; $\sigma^2_{g_{i_1}}$ and $\sigma^2_{g_{i_2}}$ are the genetic variance of trait i in environments 1 and 2, respectively; $\sigma_{g_{i_{1,2}}}$ is the co(variance) of a same trait i between environment 1 and 2; $\sigma_{g_{i_1,j_1}}$ is the co(variance) between traits i and j in environment 1; $\sigma_{g_{i_1,j_2}}$ is the co(variance) between traits i and j in environment 1 and 2.

CHAPTER 8

Selection scheme designs for dairy cattle milked once daily in New Zealand: a deterministic approach

Abstract

In New Zealand, a specific selection scheme for the dairy cattle population milked once-a-day (OAD) has not been implemented. This study aims to investigate estimated genetic progress for different selection objectives and selection scheme designs using progeny testing (PT) and genomic selection (GS) on OAD herds. Under a PT-scheme, estimated genetic progress ranged 32-43 kg milk/year, 1.69-1.95 kg fat/year, and 1.56-1.76 kg protein/year. Conversely, genetic gain resulting from the selection of bulls generated in twice-a-day (TAD) milking systems and used to inseminate cows in OAD herds ranged between 33 and 43 kg/year (milk), 1.56 and 1.67 kg/year (fat) and 1.36 and 1.64 kg/year (protein). Correlated responses tend to be greater in the yield traits when the emphasis on fertility and residual survival was reduced in the selection objective, and when udder-related type traits were included in the objective of selection. After 25-years of implementation of a PT-selection scheme for the OAD population, the genetic gain was greater compared to selecting bulls tested in TAD and used in OAD systems. However, it takes several years before this advantage is realised. A more immediate and profitable alternative might be the implementation of a GS-scheme for OAD herds, which is cheaper than a PT-scheme, and would result in a faster genetic gain in the aggregate breeding value or merit for all the traits included in the selection objective.

Keywords: once-a-day milking; dairy cattle; genetic gain; selection scheme; New Zealand

Introduction

The breeding goal indicates the direction of a genetic improvement program. In New Zealand dairy cattle, this corresponds to the conversion of feed into farm profit. The industry has developed a selection index called Breeding Worth (BW), which measures the genetic superiority or inferiority of an animal to convert 5 tonnes of feed dry matter into farm profit. The BW index is calculated by weighting the estimated breeding values (EBVs) for lactation yields of milk (MY), fat (FY) and protein (PY), somatic cell score (SCS), live weight (LW), fertility and residual survival, with their respective economic values.

The selection index theory (Hazel 1943) is a method for calculating EBV of an animal by combining all the information available on the animal and its relatives. It is the basis of which the animals are ranked for selection. The optimal selection index maximizes the correlation between the selection index and the selection objective (Mrode 2014). Therefore, selection indices are used as a predictor of the selection objective, which is focused on traits that influence the breeding goal. In New Zealand, the traits included in the selection objective are the same as those included in BW (López-Villalobos & Garrick 2005).

The estimation of genetic progress using selection index theory has been well documented by Spelman & Garrick (1997) and Sneddon et al. (2016) in New Zealand dairy cattle which are mostly milked twice-a-day (TAD). In these studies, the genetic progress of traits in BW were estimated from selection schemes developed for populations milked TAD, based on the four pathways of selection (Rendel & Robertson 1950). These pathways are: cows to breed cows (CC), cows to breed bulls (CB), bulls to breed cows (BC) and bulls to breed bulls (BB). The annual rate of genetic progress (ΔG) for a typical dairy cattle selection scheme results from the following formula, proposed by Rendel & Robertson (1950):

$$\Delta G = \frac{\sum_{i=1}^{4} i_i r_i \sigma_g}{\sum_{i=1}^{4} L_i}$$

where σ_g, i, r, L are the genetic standard deviations of the selection objectives, intensity of selection, accuracy of selection and generation interval, respectively in the *i*th selection pathways.

So far, a selection scheme for the cattle population milked once-a-day (OAD), has not been implemented. Therefore, it is of interest to design a specific selection scheme for the population milked OAD, because it dictates the potential genetic progress that can be achieved in the traits of the selection objective, and it has considerable influence on the cost-effectiveness of the selection program (López-Villalobos & Garrick 2005).

Since the implementation of artificial insemination technology, progeny testing (PT) is the main method of evaluating bulls in a dairy selection scheme (Pryce & Daetwyler 2012), but genomic selection (GS; Meuwissen et al. 2001) creates an opportunity to modify the conventional PT selection scheme. Schaeffer (2006) indicated that under the GS scheme, rates of genetic gain could be doubled compared to PT-scheme.

This study aims to evaluate selection schemes by estimating genetic progress in the traits of different selection objectives for New Zealand dairy herds milked OAD based on PT or alternatively through GS.

Materials and methods

Population structure of the population milked once a day

The total New Zealand dairy cattle population milked in the 2014/15 season was 5.018 million cows (LIC & Dairy NZ 2015). Assuming that 3% of these cows were milked OAD (McPherson et al. 2007) the OAD population would be approximately 150,500 cows. Generally, herds milked OAD have been reported to have better health and fertility performance than herds in TAD systems (Stelwagen et al. 2013), which can allow for a lower replacement rate. Consequently, for the OAD population, it was assumed that a lower replacement rate is required (López-Villalobos & Holmes 2010). Using the assumed replacement rate, the theoretical age structure for OAD herds can be calculated as follows: 15.0% 2-year-olds, 13.9% 3-year-olds, 12.8% 4-year-olds, 11.8% 5-year-olds, 10.9% 6-year-olds, 10.0% 7-year-olds, 9.3% 8-year-olds, 8.5% 9-year-olds, and 7.8% 10-year-olds.

Selection scheme model for the population milked once a day

A deterministic simulation approach was used to evaluate different selection schemes and selection objectives to estimate the genetic changes in the OAD population. The schemes investigated were based on traditional PT methodology, and the use of GS as an alternative. Also, genetic progress was evaluated when bulls were progeny tested in TAD systems and used in OAD herds. The schemes investigated considered the four pathways of selection proposed by Rendel & Robertson (1950), as indicated in the introduction.

Derivation of cow and bull paths for the separate once-a-day selection scheme

Cows available for selection as bull mothers were defined as active cows, corresponding to cows in their second, third and fourth lactations. It was assumed that 70% of these cows could be potentially active cows. The number of cows required for contract mating (cows needed to produce one bull for PT) for this population was assumed to be 6.6 times the number of bulls required to be progeny tested (López-Villalobos et al. 2000).

The proportion of cows selected in herds milked OAD was derived assuming an 80% pregnancy rate (results from seasons 2013/14 and 2014/15 in one herd milked OAD at Massey University, results not presented). Spontaneous abortion and mortality during first year were assumed to be 5% and 15%, respectively. Assuming a low replacement rate for herds milked OAD, on the theoretical age structure, 18% correspond to female calves (26,412 calves). Based on these assumptions, the population selected for the CC path was 81,297 cows. It was assumed that there were two records for cows in the CB and CC pathways (Spelman & Garrick 1997).

Assuming that 1.5 services are required per pregnancy per cow in the total cow population, and assuming that 600 frozen doses of semen can be collected weekly per bull (30,000 doses per bull/year) (Schuh 1992), eight five-year old bulls are required to service the OAD population. To avoid inbreeding, the selected proportions of 2% and 10% in the BB and BC pathways respectively, which are used in the New Zealand dairy TAD PT-scheme (Sneddon et al. 2016), were increased to 10% and 20% in the OAD

BB and BC pathways, respectively. Each bull was assumed to be evaluated on the performance of 85 daughters (Spelman & Garrick 1997).

Generation intervals calculated for the OAD population were based on the age structure of OAD herds for the CC pathway. For the CB path, it was based on selecting bull calves born from cows at 4-years of age (80%) and 5-years of age (20%). For the BB and BC paths, the generation intervals correspond to those reported by Sneddon et al. (2016).

Progeny testing of bulls evaluated in twice-a-day milking system

Farmers operating under OAD systems select semen from bulls evaluated on their progeny's performance under TAD conditions. Therefore, it is important to describe the national (assumed TAD) dairy cattle selection scheme. The assumptions used in the four pathways of selection for a PT-selection scheme in the national dairy cattle are similar to those in Sneddon et al. (2016) and are presented in Table 8.1.

Table 8.1. Population size, population selected, proportion selected and selection intensities for a progeny testing selection scheme for the dairy cattle population milked twice-a-day.

Pathway	Population	Population selected	Proportion selected	Intensity of selection	Generation interval
BB	440	9	0.02	2.42	6.5
BC	440	44	0.10	1.75	7.0
CB	1,056,000	3,168	0.003	3.033	4.2
CC	4,800,000	4,790,400	0.98	0.02	6.1

BB=bull to breed bull; BC=bull to breed cow; CB=cow to breed bull; CC=cow to breed cow.

Currently, as there is no selection scheme for the OAD population, farmers operating a OAD system generate cow replacements by selecting bulls from the TAD population selected (proven) from the BC path in the national PT-selection scheme. Figure 8.1 describes the national dairy cattle selection scheme and the selection system for OAD herds.

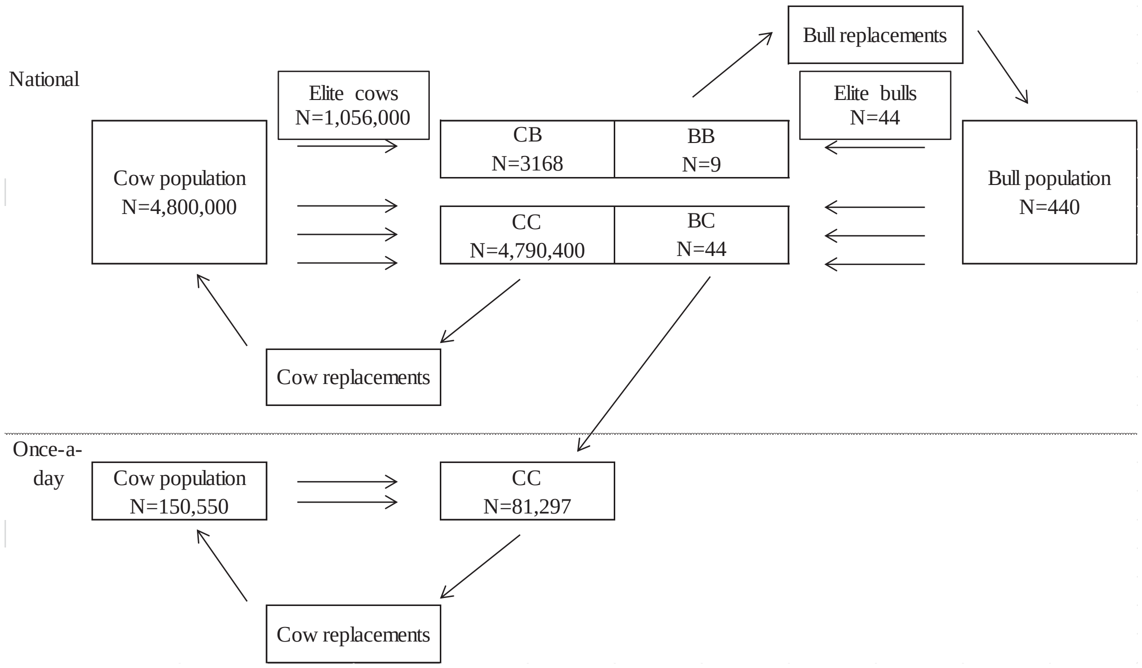

Figure 8.1. Structure of the national progeny testing selection scheme and the selection system for once-a-day herds. Bull replacements originate from mating elite bulls (BB) and elite cows (CB). Cow replacement resulted from cows selected to breed cows (CC) mated with bulls selected to breed cows (BC).

In the selection system described above, OAD farmers can select bulls ranked on either BW or an OAD selection index. Until 2015, the BW index included four production traits (MY, FY, PY and LW) and three robustness traits (SCS, fertility and residual survival). However, the LIC OAD index included only four traits (MY, FY, PY and SCS). The OAD index re-ranks proven bulls based on BW according to OAD EBVs and was developed by Livestock Improvement Corporation using EBVs of bulls whose daughters are milked TAD to develop a predictive equation to estimate OAD EBVs (Stelwagen et al. 2013).

Progeny testing of bulls tested in once-a-day milking system

Based on the description detailed in the derivations of cow and bull paths section, the bull population required for PT in a separate OAD selection scheme is 38. The assumptions used in the PT selection scheme in the OAD population are detailed in Table 8.2 and illustrated in Figure 8.2.

Table 8.2. Population size, population selected, proportion selected and selection intensities for a progeny testing selection scheme in the population milked once-a-day.

Pathway	Population	Population selected	Proportion selected	Intensity of selection	Generation interval
BB	38	4	0.10	1.75	6.5
BC	38	8	0.20	1.40	7.0
CB	40,573	248	0.0061	2.83	4.2
CC	150,550	81,297	0.54	0.74	6.1

BB=bull to breed bull; BC=bull to bred cow; CB=cow to breed cow; CC=cow to breed cow.

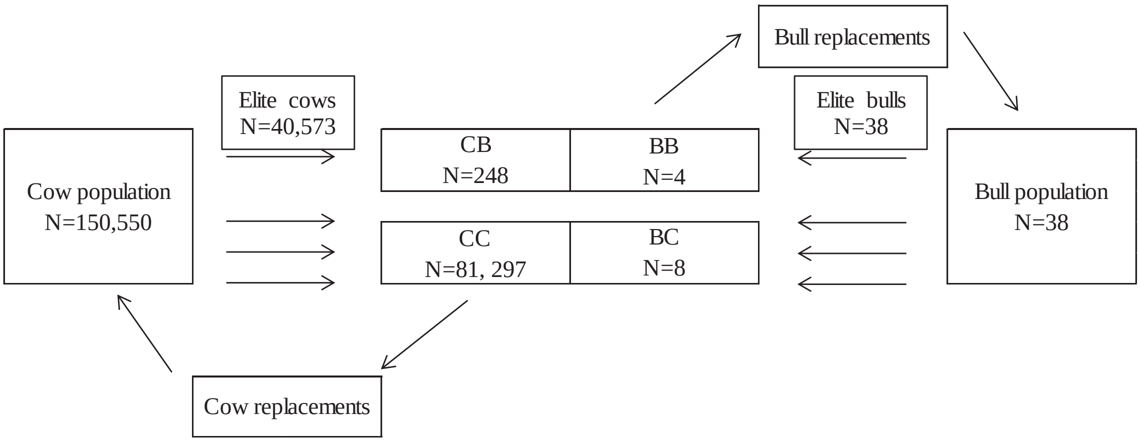

Figure 8.2. Structure of the proposed once-a-day progeny testing selection scheme. Bull replacements originate from mating elite bulls (BB) and elite cows (CB). Cow replacement resulted from cows selected to breed cows (CC) mated with bulls selected to breed cows (BC).

Genomic selection approach for once-a-day milking systems

In this selection scheme, it was considered that 2,000 of the active cows with the highest EBVs according to the breeding goal were screened annually. These cows were assumed to be inseminated, producing 500, genotyped bull calves. Then, 15 bulls were selected for BB and BC and having progeny according to their genomic EBVs. Hence, this approach considers a proportion of bulls of 3% in the BB and BC paths and 5% in the CB path. This approach assumed reliabilities (R^2) of 40%, 50% and 60%, and a two-year interval in the BB and BC paths (bulls reaching sexual maturity at 15 months). Therefore, this scenario modified the assumption presented in Table 8.2. Those modifications are presented in Table 8.3 and illustrated in Figure 8.3.

Table 8.3. Population size, population selected, proportion selected and selection intensities for a genomic selection scheme in the population milked once-a-day.

Pathway	Population	Population selected	Proportion selected	Intensity of selection	Generation interval
BB	500	15	0.03	2.27	2.0
BC	500	15	0.03	2.27	2.0
CB	40,573	2,000	0.05	2.07	4.2
CC	150,550	81,297	0.54	0.74	6.1

BB=bull to breed bull; BC=bull to breed cow; CB=cow to breed cow; CC=cow to breed cow.

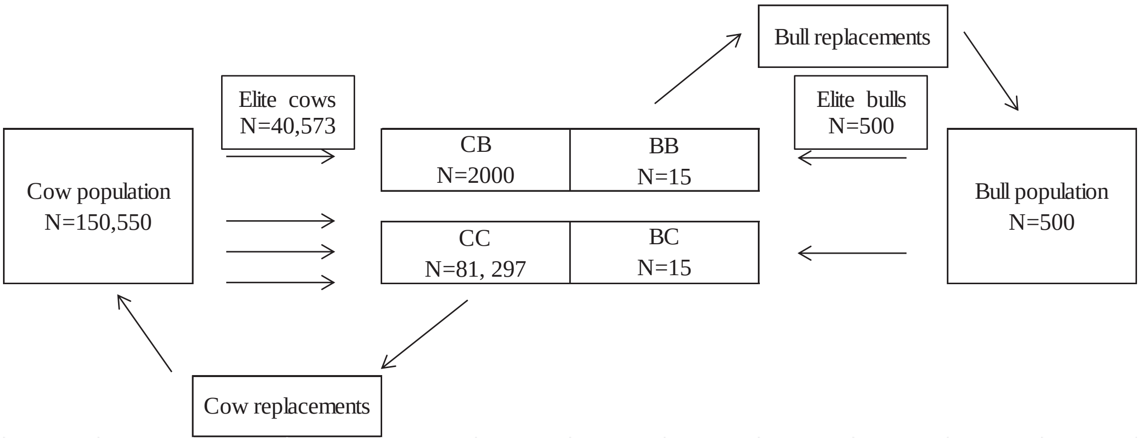

Figure 8.3 Structure of the proposed once-a-day genomic selection scheme. Bull replacements originate from mating elite bulls (BB) and elite cows (CB). Cow replacement resulted from cows selected to breed cows (CC) mated with bulls selected to breed cows (BC).

Selection indexes and selection objectives

Bulls tested in twice a day system

In this study, two selection objectives when bulls were tested in TAD systems and used in OAD herds were:

1. TAD_{SO1}, which corresponds to same traits as those included in BW (MY, FY, PY, LW, fertility, SCS and residual survival).
2. TAD_{SO2}, which included the same traits as those included in BW plus udder support and milking speed.

In this study, TAD_{SO2} is a theoretical selection objective where udder-related type traits were included due to their greater perceived importance under OAD systems

(McPherson et al. 2007). These traits are important because the OAD system requires a faster milking speed, to facilitate removal of the increased milk volume and reduce electrical power cost and labour time. Udder support is proposed to be included in the $\mathrm{TAD}_{\mathrm{SO2}}$, because of the increased stress placed on the udder due to the milk weight of the udder by the end of the 24h interval.

Separate once-a-day selection schemes

In the design of the separate selection schemes (PT and GS) for the population milked OAD, selection index theory (Hazel 1943) was used to investigate three different selection objectives. The selection objectives proposed for the separate OAD-selection scheme were:

1. Selection objective 1 ($\mathrm{OAD}_{\mathrm{SO1}}$), which included the same traits as those in $\mathrm{TAD}_{\mathrm{SO1}}$.
2. Selection objective 2 ($\mathrm{OAD}_{\mathrm{SO2}}$), which included the same traits as those in $\mathrm{TAD}_{\mathrm{SO2}}$. The relative weights of fertility and residual survival were both reduced to 2%, and an emphasis of 1.8% was assigned to both udder support and milking speed. Those relative emphases were assigned arbitrarily.
3. Selection objective ($\mathrm{OAD}_{\mathrm{SO3}}$), traits were the same as in $\mathrm{OAD}_{\mathrm{SO2}}$, but fertility and residual survival were restricted in the selection objective, using the method described by Cunningham et al. (1970), preventing any genetic change in these traits. The restricted selection index methodology proposed by Cunningham (1970) is detailed in Cameron (1997). The $\mathrm{OAD}_{\mathrm{SO3}}$ objective was investigated because fertility and residual survival are considered to be less of an issue in OAD herds, given a theoretical improvement in the overall energy balance of cows milking OAD (Stelwagen et al. 2013). Deleting these traits from the selection objective would result in an undesirable reduction in fertility given its antagonistic relationship with milk yields (Pryce & Harris 2006). Therefore, restriction to prevent any genetic change seemed more appropriate.

Selection index theory

The selection index (I) is a method for predicting the selection objective (H) in which several valuable traits are selected simultaneously, such as I=H. These expressions can be represented as follows (adapted from Cameron 1997):

$$\mathrm{I} = \sum_{\mathrm{i}=1}^{\mathrm{m}} \mathrm{b_i X_i} = \mathbf{x}'\mathbf{b} = \mathrm{H} = \sum_{\mathrm{i}=1}^{\mathrm{n}} \mathrm{v_i g_i} = \mathbf{g}'\mathbf{v}$$

Where $\mathbf{x}'$ is a row vector of m known and adjusted phenotypic values, $\mathbf{b}'$ is a row vector of m weight's coefficient to estimate, $\mathbf{g}'$ is a row vector of n unknown true breeding values and $\mathbf{v}$ is a row vector of n known relative economic values. The measured traits in the selection index are also referred to as selection criterion (Cameron 1997).

The vector $\mathbf{b}$ was calculated with the following equation:

$$\mathbf{b} = \mathbf{P^{-1}Gv}$$

Where $\mathbf{G}$ is the genetic (co)variances matrix, $\mathbf{P^{-1}}$ is the inverse phenotypic (co)variances matrix, and $\mathbf{v}$ and $\mathbf{b}$ are vectors defined previously for H and I, respectively. For all the selection objectives investigated in this study, traits in the selection index were the same as those included in each objective.

In the selection index theory, true breeding values of traits included in H are weighted according to their economic values. In this study, those values corresponded to the 2014/2015 dairy season. The economic values and their relative emphasis are shown in Tables 8.4. Economic values used in $\mathrm{OAD_{SO1}}$ were the same as $\mathrm{TAD_{SO1}}$, while the economic values used in $\mathrm{OAD_{SO2}}$ and $\mathrm{OAD_{SO3}}$ were re-calculated keeping the same relative emphasis used in the $\mathrm{TAD_{SO2}}$. The relative emphasis was calculated as described by Van Raden (2002).

Table 8.4. Economic values (EV) and relative emphasis (RE) for traits in breeding worth, the theoretical once-a-day selection index, and different selection objectives investigated for the dairy cattle milked once-a-day.

	Bull evaluated in TAD systems				OAD selection schemes					
	TAD_{SO1}		TAD_{SO2}		OAD_{SO1}		OAD_{SO2}		OAD_{SO3}	
	EV($)	RE (%)	EV($)	RE (%)	EV($)	RE (%)	EV($)	RE (%)	EV	RE (%)
Milk (kg)	-0.097	18.5	-0.097	18.5	-0.097	16.4	-0.109	18.5	-0.109	19.3
Fat (kg)	1.81	13.9	1.81	13.9	1.81	12.6	2.0	13.9	2.0	14.5
Protein (kg)	8.18	43.5	8.18	43.5	8.18	41.8	8.53	43.5	8.53	45.3
Live weight (kg)	-1.63	9.4	-1.63	9.4	-1.63	11.2	-1.37	9.4	-1.37	9.8
Fertility (%)	7.23	3.8	3.85	2.0	7.23	4.5	3.23	2.0	0.0	0.0
Somatic cell score (units)	-38.61	7.1	-38.61	7.1	-38.61	9.0	-30.71	7.1	-30.71	7.4
Residual survival (days)	0.14	3.8	0.07	2.0	0.14	4.5	0.06	2.0	0.0	0.0
Udder support (units)			9.54	1.8			8.0	1.8	8.0	1.9
Milking speed (units)			13.16	1.8			11.03	1.8	11.03	1.9

TAD_{SO1} = selection objective that includes lactation yields of milk, fat and protein, live weight, somatic cell score, fertility and residual survival; TAD_{SO2} = selection objective that includes the same traits as TAD_{SO1} plus udder support and milking speed; OAD_{SO1} = once-a-day selection objective with the same traits as TAD_{SO1}; OAD_{SO2} = once-a-day selection objective with the same traits as TAD_{SO2}; OAD_{SO3} = once-a-day selection objective with the same traits as TAD_{SO2} with restriction in fertility and residual survival.

Calculation of genetic gain

The expected correlated response in each trait was calculated with the following formula (Cameron 1997):

$$\mathrm{CR_j} = \mathrm{i}\frac{\mathbf{b'G_i}}{\sqrt{\mathbf{b'Pb}}}$$

Where $\mathrm{CR_j}$ is the correlated response for the *j*th trait in the selection objective, $\mathbf{G_i}$ is the *i*th column of the genetic (co)variances matrix $\mathbf{G}$, and i is the intensity of selection. Matrix **P** and row vector **b** were defined in the previous section.

Estimated genetic and phenotype parameters (heritability, repeatability, correlation and variance) used in the selection index were from Lembeye et al. (2016) for MY, FY, PY and SCS; and the same as used by Sneddon et al. (2016) for LW, fertility, residual survival; and Berry et al. (2004) for the udder-related type traits. These parameters are presented in Table 8.5.

All variances and (co)variances were formulated separately for the four pathways because of the differences in their sources of information. The formulas used to calculate elements of the matrices $\mathbf{P}$ and $\mathbf{G}$ were derived using the methodology presented by Cameron (1997) (Appendix 8.1).

For the alternatives when bulls were tested in TAD and used in OAD herds, ($\mathrm{TAD_{SO1}}$ and $\mathrm{TAD_{SO2}}$), correlated responses for the milk production traits in the OAD population were computed by expanding the matrix $\mathbf{G}$ with columns that contained (co)variances between traits in the index and the additional traits (Appendix 8.2). Approximations of genetic correlations required to calculate those (co)variances were obtained as the linear correlations between EBVs of bulls evaluated with their daughters in OAD and TAD systems. These correlations are presented in Table 8.6.

Table 8.5. Genetic (below the diagonal) and phenotypic (above the diagonal) parameters among traits in the breeding worth and udder traits of dairy herd populations milked once- or twice-a-day.

Trait	MF[1]	σ_g	h^2	Rep	MY	FY	PY	SCS	LW	Fertility	RS
MY	OAD	300.74	0.33	0.48		0.74	0.93	-0.13	0.25	-0.002	0.0
	TAD	404.22	0.36	0.52		0.68	0.91	-0.09			
FY	OAD	12.37	0.21	0.40	0.40		0.82	-0.14	0.24	0.02	0.0
	TAD	16.27	0.26	0.43	0.35		0.78	-0.06			
PY	OAD	9.07	0.22	0.42	0.85	0.60		-0.13	0.30	0.02	0.0
	TAD	11.29	0.25	0.44	0.84	0.54		-0.06			
SCS	OAD	0.412	0.12	0.35	0.07	0.02	0.1		0.04	0.04	0.0
	TAD	0.391	0.12	0.32	-0.04	0.1	0.07				
LW	-	12.24	0.39	0.65	0.28	0.33	0.36	-0.01		0.05	0.0
Fertility	-	1.10	0.03	0.05	-0.15	-0.06	-0.05	-0.10	0.03		0.0
RS	-	5.74	0.07	0.11	0.0	0.0	0.0	0.0	0.0	0.0	
US[2]	-	0.40	0.11	0.11	0.36	0.14[3]	0.31[3]	0.45	0.12	0.12	0.0
MS[2]	-	0.29	0.12	0.12	0.69	0.28[3]	0.59[3]	0.24	0.36	-0.15	0.0

MY= milk yield; FY= fat yield; PY=protein yield; SCS=somatic cell score; LW=live weight; RS= residual survival; US= udder support; MS= milking speed; σ_g=genetic standard deviation; h^2= heritability; rep=repeatability.

[1] MF = milking frequency, OAD = milking once-a-day and TAD = milking twice-a-day.

[2] Repeatability of US and MS were assumed equal to heritability. Phenotypic correlations of US and MS with the other traits were assumed equal to genetic correlations.

[3] Assumed values.

Table 8.6. Approximation of genetic correlations among milk yields and somatic cell score (SCS) under once- and twice-a-day milking systems.

OAD TAD	Milk yield	Fat yield	Protein yield	SCS
Milk yield	0.93	0.12	0.81	0.29
Fat yield	0.12	0.66	0.34	0.22
Protein yield	0.81	0.34	0.84	0.33
SCS	0.29	0.22	0.33	0.60

OAD=once-a-day milking; TAD=Twice-a-day milking.

In the GS-scheme proposed to the population milked OAD, a single-trait studied was the aggregate breeding value or merit for all the traits included in the selection objective (H; Mrode 2014). Therefore, response under GS on OAD was calculated with the formula proposed by Rendel & Robertson (1950):

Results

Progeny testing selection systems

Predicted responses per year in the population milked OAD through the different scenarios investigated based on PT-schemes are presented in Table 8.7. Estimates of genetic progress in the OAD population resulting from a specific OAD selection scheme (OAD_{SO1}) were; MY 35.89 kg/year, FY 1.86 kg/year, PY 1.56 kg/year, LW 0.44 kg/year, fertility 0.006%/year, SCS -0.003 units/year and residual survival 0.926 days/year. Compared to OAD_{SO1}, estimated genetic progress in the OAD population resulting from TAD_{SO1} were 9.4% to 16.1% lower for the yield traits, slightly greater for LW and SCS, and a similar increase in fertility and residual survival.

Under the scenario where udder-related type traits were included in the selection objective (OAD_{SO2}), the greatest increases in milk yields were predicted (43.35, 1.95 and 1.76 kg of MY, FY and PY, respectively). The estimated genetic progress in milk yield traits resulting from TAD_{SO2} would result in lower progress compared to OAD_{SO2}, but greater than OAD_{SO1}, OAD_{SO3} and TAD_{SO1}. Both TAD_{SO2} and OAD_{SO2}, however, resulted in a small decrease in fertility.

Genetic progress under OAD_{SO3} compared to OAD_{SO1} and OAD_{SO2} was lower for MY and FY. The increase in milk solids would be similar to that expected from the current situation (3.3 kg). However, this would be the only scenario in which LW would decrease (330 g/year).

The simulated genetic trend for milk yields and LW in 25 years in the OAD population associated with PT scenarios of OAD_{SO1} compared with TAD_{SO1}, and OAD_{SO2} compared with TAD_{SO2} are shown in Figure 8.4 and Figure 8.5, respectively. The analyses indicated that an OAD selection scheme showed zero increase for milk yield traits in the first eight years of implementation, contrasting with just two years resulting from the utilisation of TAD_{SO1} and TAD_{SO2}.

Table 8.7. Correlated response per year in the New Zealand dairy population milked once-a-day (OAD) resulting from selecting bulls progeny tested under twice-a-day (TAD) systems, and for a separate progeny testing OAD selection scheme based on alternative selection objectives[1].

	Bull evaluated in TAD systems		OAD selection scheme		
	TAD_{SO1}	TAD_{SO2}	OAD_{SO1}	OAD_{SO2}	OAD_{SO3}
Milk yield (kg)	32.51	42.94	35.89	43.35	31.61
Fat yield (kg)	1.56	1.67	1.86	1.95	1.69
Protein yield (kg)	1.36	1.64	1.56	1.76	1.61
Live weight (kg)	0.55	0.80	0.44	0.75	-0.33
Fertility (%)	0.008	-0.005	0.006	-0.006	0.000
Somatic cell score (units)	0.016	-0.023	-0.003	0.004	0.003
Residual survival (days)	0.921	0.447	0.926	0.378	0.000
Udder support (units)	0.015	0.016	0.013	0.013	0.013
Milking speed (units)	0.026	0.026	0.020	0.023	0.016

[1] TAD_{SO1} = selection objective that includes lactation yields of milk, fat and protein, live weight, somatic cell score, fertility and residual survival; TAD_{SO2} = selection objective that includes the same traits as TAD_{SO1} plus udder support and milking speed; OAD_{SO1} = once-a-day selection objective with the same traits as TAD_{SO1}; OAD_{SO2} = once-a-day selection objective with the same traits as TAD_{SO2}; OAD_{SO3} = once-a-day selection objective with the same traits as TAD_{SO2} with restriction in fertility and residual survival.

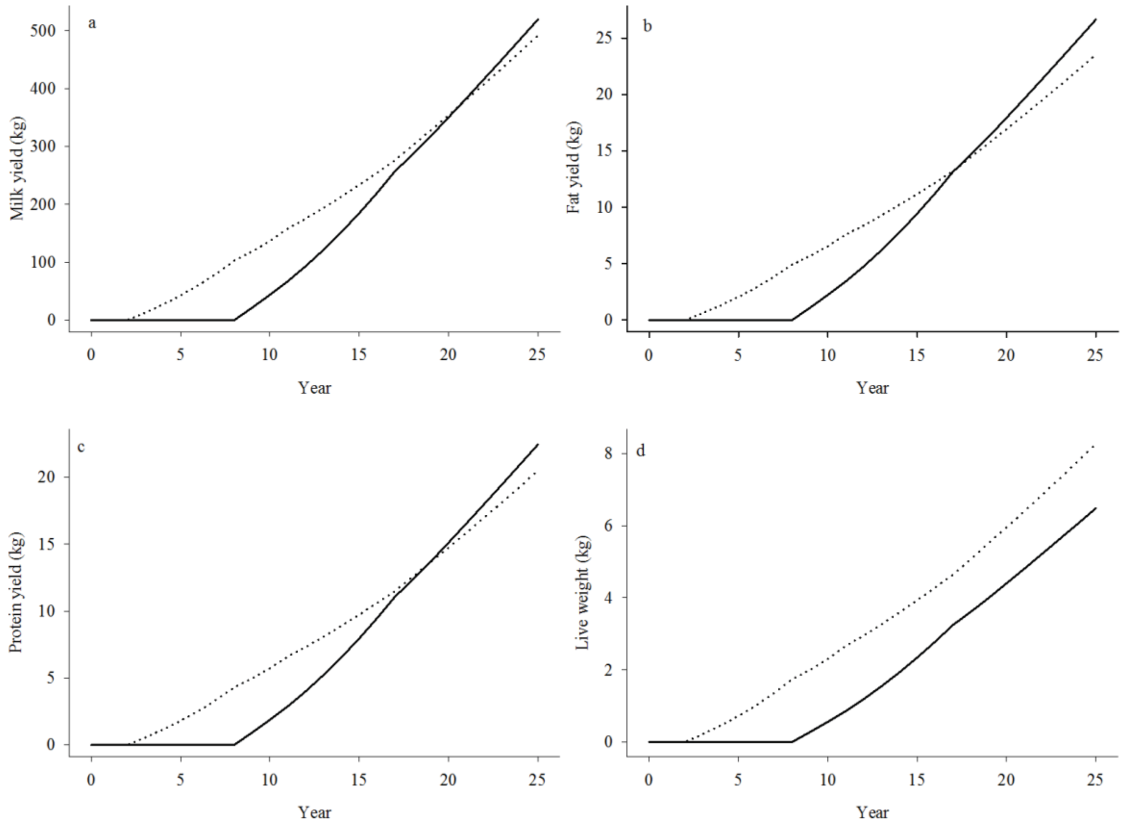

Figure 8.4. Estimated genetic trends in milk yield (a), fat yield (b), protein yield (c) and live weight (d) in the once-a-day population resulting from the $\mathrm{OAD}_{\mathrm{SO1}}$ progeny testing selection scheme (solid line) and bulls selected by $\mathrm{TAD}_{\mathrm{SO1}}$(dotted line) over a 25 year-period. $\mathrm{TAD}_{\mathrm{SO1}}$= bulls selected under TAD systems which selection objective includes selection objective that includes lactation yields of milk, fat and protein, live weight, somatic cell score, fertility and residual survival. $\mathrm{OAD}_{\mathrm{SO1}}$= once-a-day selection objective 1 that includes same traits as those in $\mathrm{TAD}_{\mathrm{SO1.}}$

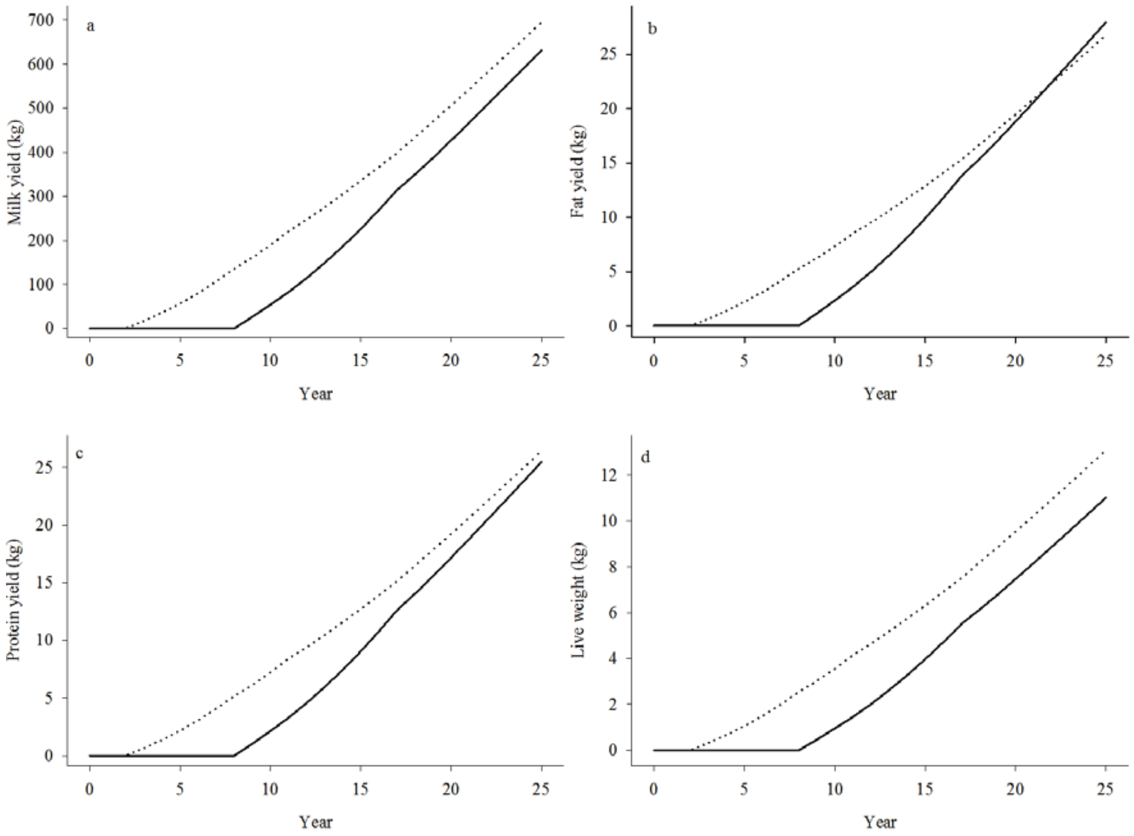

Figure 8.5. Estimated genetic trends in milk yield (a), fat yield (b), protein yield (c) and live weight (d) in the once-a-day population resulting from the OAD_{SO2} progeny testing selection scheme (solid line) and bulls selected by the TAD_{SO2} (dotted line) over a 25 year-period. TAD_{SO2} = bulls selected under TAD systems which selection objective includes lactation yields of milk, fat and protein, live weight, somatic cell score, fertility, residual survival, udder support and milking speed. OAD_{SO2} = once-a-day selection objective 2 with the same traits as those in TAD_{SO2}.

Genomic selection approach

Table 8.8 shows predicted genetic gains in overall selection objectives based on the conventional PT and the simulated GS on OAD herds. Overall, simulations which considered GS were approximately 50% to 80% greater than genetic gain predicted in the conventional PT scheme. The greater predicted genetic gains increase as R^2 increased.

Figure 8.6 shows the predicted genetic trend in the overall true (aggregate) breeding value based on traditional PT and alternative GS on OAD scenarios for OAD_{SO2} in a 25-

year horizon. Genetic gain ($ expressed in σ_g) increased to 2.818, 4.001, 4.302 and 4.574 in PT and at 40%, 50% and 60% of R^2 in the GS on OAD scenario, respectively.

Table 8.8. Asymptotic annual response (ΔG) of the aggregate breeding value ($ expressed in genetic standard deviation [σ_g] per year), in the New Zealand dairy population milked once-a-day based on the traditional progeny testing and an approach to genomic selection.

Scheme	OAD_{SO1}		OAD_{SO2}		OAD_{SO3}	
	ΔG (σ_g/yr)	Relative to PT (%)	ΔG (σg/yr)	Relative to PT (%)	ΔG (σ_g/yr)	Relative to PT (%)
PT	0.189		0.197		0.215	
GS-40% reliability	0.296	157	0.304	154	0.329	153
GS-50% reliability	0.320	169	0.328	166	0.352	164
GS-60% reliability	0.341	180	0.349	177	0.374	174

PT= progeny testing; GS= genomic selection; OAD_{SO1}= selection objectives include selection objective includes selection objective that includes lactation yields of milk, fat and protein, live weight, somatic cell score, fertility and residual survival; OAD_{SO2}= same as $OAD_{SO1}$with additional traits udder support and milking speed; OAD_{SO3}= same as OAD_{SO2} with restriction in fertility and residual survival.

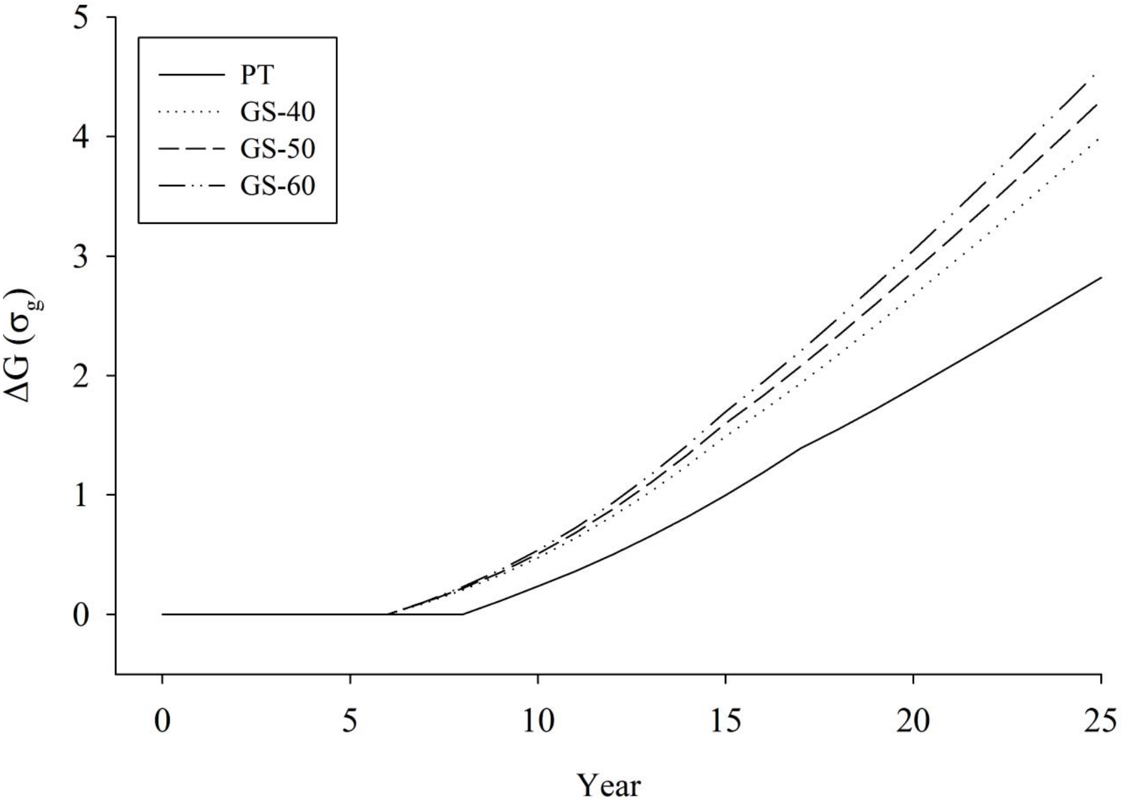

Figure 8.6. Estimated genetic trends for the aggregate breeding value ($ expressed in σ_g) in the once-a-day population under OAD_{SO2} (once-a-day selection objective 2 that includes lactation yields of milk, fat and protein, live weight, somatic cell score, fertility, residual survival, udder support and milking speed) resulting from traditional progeny testing (PT) and genomic selection. GS-40 = genomic selection, 40% reliability GS-50 = genomic selection, 50% reliability GS-60 = genomic selection, 60% reliability.

Discussion

Progeny testing selection systems

The results presented in Table 8.7 indicate that the greatest response in milk yield traits would result when the udder-related type traits are included in the selection objectives (TAD_{SO2} and OAD_{SO2}) due to a moderate and favourable genetic correlation between yield and udder-related type traits (Table 8.5). Nevertheless, a small decrease in fertility is expected due to less emphasis on these scenarios (Table 8.4), and the antagonist genetic correlation between milking speed and fertility (Table 8.5).

The current BW index leads to increases in milk yield traits, small increases in non-productive traits, and an undesired increase in LW in dairy cattle assumed to be milked TAD (Sneddon et al. 2016). The results in Table 8.7 indicate that a similar outcome would be expected in herds milked OAD under the scenario that bulls selected for $\mathrm{TAD}_{\mathrm{SO1}}$ under TAD system are used to OAD, suggesting that high BW cows and bulls are also generally suitable for OAD dairying.

Although a separate selection scheme for the OAD dairy population results in a greater response for FY and PY compared to using bulls tested in TAD systems, the utilization of the theoretical $\mathrm{TAD}_{\mathrm{SO2}}$ would result in similar increases compared with $\mathrm{OAD}_{\mathrm{SO2}}$ for milk solids (FY + PY) (only 11% less). This suggests that developing an OAD index with the inclusion of udder-related type traits would be advised to select bulls for future replacements in OAD herds.

The theoretical $\mathrm{TAD}_{\mathrm{SO2}}$ and $\mathrm{OAD}_{\mathrm{SO2}}$ would result in a decrease in fertility, for this reason, the $\mathrm{OAD}_{\mathrm{SO3}}$ proposed in this study would be worth considering if a OAD selection scheme is implemented. Investigating this scenario ($\mathrm{OAD}_{\mathrm{SO3}}$), the constraints might be the limited response in milking speed and the unfavourable response in SCS. It could be argued that an increased emphasis on SCS should be included in the OAD selection index, because generally, there is an increase in this trait in herds milked OAD (Clark et al. 2006), although this occurs mostly during the transition period. Theoretically, a selection scheme dedicated to OAD herds should not increase SCS (as would result under $\mathrm{OAD}_{\mathrm{SO2}}$ and $\mathrm{OAD}_{\mathrm{SO3}}$). Because in this study the emphasis in fertility, residual survival and the udder-related type traits was assumed arbitrarily, a future target would be to adequately derivate economic values for these traits in the selection objective for OAD herds.

The accumulated trend of genetic gain in the OAD population resulting from a PT OAD-selection scheme or selecting bulls from TAD and using them in OAD herds started to increase eight and three years after implementation, respectively (Figures 8.4 and 8.5). In the separate PT-OAD scheme, the timing (eight years) corresponds to the five-year period required for bulls to gain a daughter-proof from PT, plus the time required for their daughters in commercial herds to complete their first lactation (~3 years of age). The time required for accumulated genetic gains through the $\mathrm{TAD}_{\mathrm{SO1}}$ and

TAD_{SO2} in the OAD population is reduced as bulls are already available to be selected or proven from the TAD system.

The time elapsed between the scheme implementation and the realised genetic gain will be a disincentive for implementing an OAD PT-selection scheme. Further, during the first 15 years, BW accumulates greater benefits than the alternative OAD scheme for FY and PY (Figure 8.4), and TAD_{SO2} would theoretically accumulate greater increases of MY and PY than OAD_{SO2} during a 25-year period (Figure 8.5).

Genomic selection approach

Previous studies (Schaeffer 2006; Pryce et al. 2010; Buch et al. 2012; Thomasen et al. 2014a) reported greater rate of genetic gain and net profit under GS compared to the conventional PT scheme by nearly halving the generation interval. Harris (2005) suggested that due to the lack of financial resources to implement a separate selection scheme for herds milked OAD, it may be advisable to rationalise resources to enable across-breed selection schemes instead of within-breed schemes (López-Villalobos & Garrick 2005) using molecular tools such as GS. Consequently, the advantages of the GS approach on OAD systems should be investigated. There are several possible strategies where GS can be incorporated (Pryce et al. 2010) in the population milked OAD, but the success of a GS scheme will depend on the cost of genotyping and having a large reference population (Hayes et al. 2009).

The relationship of genomic EBVs (GEBVs) with true breeding values is assumed to have a R^2 of 60% (Meuwissen et al. 2001). In New Zealand, however, the R^2 obtained was less than 60% (Harris & Johnson 2010). Hence, in this study, the genetic gain was explored assuming lower R^2. Low accuracy levels generally occur when the young bulls selected are not in the reference population or they are not progeny from proven bulls (Harris & Johnson, 2010; Thomasen et al. 2014b). Reference populations are mostly produced from PT bulls and they have low R^2 if they belong to a small dairy cattle population (Thomasen et al. 2014b) as would be the case in herds milked OAD.

Pryce & Daetwyler (2012) suggested that genotyping cows, as in this study, may be crucial in expanding a reference population. This not only would increase R^2 and genetic gain, but also decrease inbreeding. In a stochastic simulation for a small dairy population (Danish Jersey), Thomasen et al. (2014b) compared the effect of annually adding 2,000 first-lactation cows randomly selected to the reference population versus adding 60 tested bulls each year. They reported increased R^2 (0.20 after 4 years and 8,000 cows genotyped vs. 0.07 after 15 years and with 900 PT bulls).

For the simulated period between 20 and 30 years, Thomasen et al. (2014b) found an increased R^2 of 0.19 to 0.27 of GEBVs for a scheme with only bulls added to the reference population. In contrast, for the same period, the increased R^2 was 0.30 to 0.60 when 2,000 first-lactation cows were added, and no difference was observed when it was simulated adding 4,000 cows to the reference population. Considering a cost of €60 (equivalent to ~ $94 in May 2016) per animal used in the study of Thomasen et al. (2014b), the alternative proposed in that study had the greatest profit when animals were selected based on GEBVs and used when they were sexually mature.

Considering a cost of $30,000 per bull under PT in five years (housing, feeding, semen collection and storage, test mating, and incentives for farmers [Holmes et al. 2002]), the cost to breeding companies to implement a specific PT selection scheme would be approximately 1.14 million/year (testing 38 bulls/year, Table 8.2.). Given the theoretical genetic progress in the overall selection objective (expressed in genetic standard deviation [σ_g]) shown in Table 8.8, for an increase of one σ_g change, breeding companies would spend between 5.30 and 6.03 million with the traditional PT scheme. Assuming the cost of genotyping per animal is $100, the annual cost of the GS approach would be ~ $317,500 (genotyping 2000 dams, 500 bulls, keeping them for 15 months, and slaughtering them as soon as semen had been collected). This represents 28% of the cost of traditional PT selection scheme. Hence, the increase of one σ_g change under GS, the cost of breeding companies might potentially drop to 0.97-1.07 million assuming 40% R^2. Further, the timing to observe the benefits of a GS-selection scheme on OAD is two years shorter than with conventional PT, and the trend of genetic gain is, theoretically, greater (Figure 8.6).

Consequently, a GS selection scheme might be a preferred option in the implementation of an OAD selection program. The results of this study might lead to consider this scheme to be more feasible for the OAD population, above a conventional PT scheme, even though the number of the herds under OAD milking have increased moderately over the years.

Conclusion

Genetic progress is expected to be slightly greater in a separate PT selection scheme for the OAD milking system compared to using bulls tested under TAD systems. Reduced emphasis on fertility and residual survival, and additional emphasis on udder-related type traits would increase genetic response in milk yield traits but decrease fertility slightly. The long lag between the implementation of the OAD selection scheme and the realization of its genetic benefits suggest that other alternatives such as a GS selection scheme should be considered. Further simulations are required to predict separately long-term genetic response based on GS in economically important traits in the population milked OAD.

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Appendixes

Appendix 8.1. Derivation of co(variance) matrices in bull and cows pathways of selection

$\sigma^2_{P_i}$ =phenotypic variance for trait i.

$\sigma^2_{g_i}$ =genetic variance for trait i.

$\sigma_{P_{ij}}$= phenotypic covariance between trait i and j.

$\sigma_{g_{ij}}$= genetic covariance between trait i and j.

n= number of records per animal (own performance in cow pathways, performance of daughters in bull path).

r= repeatability.

p= number of animals in progeny group.

k= relationship among animals in progeny groups (half-siblings=0.25).

a= relationship among animals in progeny groups and animals to evaluate (bull to daughter =0.5).

Derivation of phenotypic and genetic (co)variances in cow pathways

Elements in matrix **P**

$$\sigma^2_{P_i} = \left[r + \frac{1-r}{n}\right] \times \sigma^2_{P_i} \text{ ,}$$

$$\sigma_{P_{ij}} = \frac{\sigma_{P_{ij}} + (n-1) \times \sigma_{g_{ij}}}{n}$$

Elements in matrix **G**

$$\sigma^2_{g_{ii}} = \sigma^2_{g_{ii}},$$

$$\sigma_{g_{ij}} = \sigma_{g_{ij}}$$

Derivation of phenotypic and genetic (co)variances in bull pathways

Elements in matrix **P**

$$\sigma^2_{P_i} = \frac{[r+(1-\frac{r}{n})]+(p-1)k\times h^2_i}{p} \times \sigma^2_{P_i} \text{ ,}$$

$$\sigma_{P_{ij}} = \frac{[\sigma_{P_{ij}}+(n-1)\times\left(\frac{\sigma_{g_{ij}}}{n}\right)+\left(k\times\sigma_{g_{ij}}\right)]}{p}$$

Elements in matrix **G**

$$\sigma^2_{g_i} = \sigma^2_{g_i} \times a,$$

$$\sigma_{g_{ij}} = \sigma_{g_{ij}} \times a$$

Appendix 8.2. Construction of matrix G in bull pathways when they are tested in twice-a-day and used in once-a-day systems

$$\mathbf{G} = \begin{bmatrix} \sigma^2_{g_{i_1}} \times a & \sigma_{g_{i_1,j_1}} \times a & \cdots & \sigma_{g_{i_1,n_1}} \times a & \sigma_{g_{i_1,p_2}} \times a & \cdots & \sigma_{g_{i_1,r_2}} \times a \\ \sigma_{g_{i_1,j_1}} \times a & \sigma^2_{g_{j_1}} \times a & \cdots & \sigma_{g_{j_1,n_1}} \times a & \sigma_{g_{j_1,p_2}} \times a & \cdots & \sigma_{g_{j_1,r_2}} \times a \\ \vdots & \vdots & \ddots & \vdots & \vdots & \ddots & \vdots \\ \sigma_{g_{i_1,n_1}} \times a & \sigma_{g_{j_1,n_1}} \times a & \cdots & \sigma^2_{g_{n_1}} \times a & \sigma_{g_{n_1,p_2}} \times a & \cdots & \sigma_{g_{n_1,r_2}} \times a \end{bmatrix}$$

Where $\sigma^2_{g_i}$ is the genetic variance of the i trait in environment 1; $\sigma_{g_{i_1,j_1}}$ is the co(variance) between trait i and j in the same environment; $\sigma_{g_{i_1,p_2}}$ is the co(variance) between trait i and p in different environments and a is the relationship among bulls and daughters (a =0.5).

CHAPTER 9

General discussion

The main goals of this thesis were firstly, to test sire by milking frequency (MF) interaction (S×MF); secondly, to design a specific selection scheme for the population milked once-a-day (OAD) in New Zealand; and thirdly, to investigate production, efficiencies and crossbreeding parameters for traits of economic importance under OAD systems. The specific objectives proposed to achieve these goals were:

1. A comprehensive review of literature relating pasture-based systems of dairy cattle milked OAD.
2. To investigate feed conversion and gross efficiencies; production and lactation persistency; and estimation of crossbreeding parameters for traits of economic importance under OAD pasture-based systems.
3. To estimate genetic parameters (heritability, genetic correlations and genetic variances) of milk production traits for OAD milking.
4. To determinate the effect of MF environments on the genetic evaluation of dairy sires and to test for evidence of sire re-ranking for milk production traits across MF in grazing systems.
5. To evaluate alternative selection schemes by estimating genetic progress in the traits of different selection objectives for New Zealand dairy herds milked OAD.

Review of dairy cattle milked once-a-day during whole lactation

A comprehensive review of literature discussing pasture-based systems of dairy cattle milked OAD during the entire lactation was presented in chapter 2. The review identified that cows milked OAD had reduced milk yields and lactation persistency compared to their counterparts milked twice-a-day (TAD). The studies indicated that, in general, Holstein-Friesian (F) cows had greater reductions for milk (MY), fat (FY) and protein yield (PY) (kg/cow) than Jersey (J) cows when they were compared with their equivalent TAD counterpart, suggesting the existence of a breed by MF interaction.

In New Zealand, there have been two studies (McPherson et al. 2007; Stachowicz et al. 2014) that estimated the correlations between estimated breeding values (EBVs) for milk production traits in sires with progeny in both OAD and TAD MF systems. These correlations were medium-high for milk traits (0.47-0.85). However, the findings were inconclusive as to whether re-ranking of sires was significant across MF.

Comparative efficiency and production performance for milk production traits

In chapter 3, production, gross and feed efficiency performances of F, J and F×J cows were examined using data of cows milked OAD during two seasons at Massey University dairy farm No. 1. The findings were:

- Total milk solid (MS) yields (kg/cow) were slightly greater in F and F×J compared to J cows.
- Jersey cows were more efficient per 100 kg of live weight (LW) than F or F×J cows.

Chapter 4 described the analysis of yield performance of milk traits of commercial cows milked OAD, compared with an equivalent TAD dairy cattle population. This chapter concluded that:

- The relative difference in production traits between OAD and TAD systems were smaller than those reported in experimental trials.

Chapter 5 examined the expression of breed and heterosis effects for yield traits (MY, FY and PY) in cows milked OAD and the equivalent TAD dairy cattle population. Main findings were:

- With an average of five lactations, breed effect (F-J) increased with production levels (PL; FY + PY) and in both OAD and TAD, but the increase was greater in TAD systems. These finding suggest that J cows are better adapted than F cows to OAD systems.
- In absolute values, heterosis increased with PL and in both MF, but in percentage values, heterosis effects were greatest at medium and low PL in cows milked OAD and TAD, respectively.

The findings of this thesis will have significant practical implications for farmers operating OAD milking systems, or for those thinking of switching from TAD to OAD. Under OAD systems, smaller cows, like Jerseys, are preferred over larger cows, such as F, because J cows had greater feed and gross efficiencies (chapter 3) and had smaller reductions of milk yields compared to their counterparts milked TAD (chapter 4). The next target for Massey University dairy farm No.1 should be comparing breed profit and efficiency per ha instead of per cow (as were indicated in this thesis), which would lead to the determination of the most suitable breed to operate under OAD systems. Nevertheless, this will require significant logistical and management changes on the farm to execute the research.

The percentage of crossbred cows in the national herd has increased in the last 20 years because of crossbred herds using crossbreeding systems to achieve higher profit per hectare than herds using pure breeds. The national herd in New Zealand for the year 2014 was comprised of F×J cows (46%) followed by F (35%) and J (10%) (Livestock Improvement Corporation [LIC] & Dairy NZ 2015). This may be a consequence of favourable heterosis for fertility and survival traits (López-Villalobos et al. 2000) which gives greater production potential to herds with F×J crossbred cows. Given the results obtained in chapter 5 (smaller breed effect in OAD compared to TAD systems), it is hypothesized that the productive potential of F×J cows under OAD conditions might be relatively higher than their counterparts milked TAD because the benefits of crossbred animals are generally achieved when the genetic differences between purebreds are low (Falconer & Mackay 1996).

The results of this thesis suggest that J cows could be a more profitable breed under OAD milking. However, long-term studies including rotational crossbreeding and selection from a larger dairy population are needed to confirm the expected advantage of J cows over F and F×J crossbreds under OAD milking system.

Interaction between genotype and milking frequency

The effect of MF on the genetic evaluation was investigated and is described in chapters 6 and 7. Genetic parameters and S×MF interactions for total milk production from 2008 to 2012 lactation records were estimated in chapters 6 and 7, respectively.

Chapter 6 presents the first attempt at the estimation of genetic parameters in dairy cattle milked OAD. The estimated parameters allow calculation of genetic progress in milk production traits for the population milked OAD if a selection scheme was implemented. Similar trends and directions would be expected in herds milked OAD compared to the New Zealand national herd under a TAD milking system. Nevertheless, the genetic progress, in absolute values, is expected to be lower than the national selection program because genetic variances for milk production traits are lower in OAD compared to TAD dairy cattle.

In contrast, the genetic progress expressed in genetic standard deviations might be more similar in the two MF populations. It is hypothesized, however, that a progeny testing (PT) selection scheme for the OAD population would apply lower selection intensities in the selection pathways (Rendel & Robertson 1950) compared to the current PT-selection scheme of the New Zealand dairy cattle. These assertions are based on the small OAD dairy population (<5% of the national herds of New Zealand dairy cattle), hence, the proportion of selected animals would be greater (reduced selection intensities), in order to avoid inbreeding. Further, the genetic parameters estimated in chapter 6 were slightly lower in the OAD than the TAD population, leading to lower accuracies of the selection pathways in a separate OAD selection scheme. Therefore, genetic progress would be greater in the TAD population even though it is expressed in genetic standard deviations.

Regression coefficients (b_s) and observed rank correlation (r_S) between EBVs of sires with progeny in both MF were calculated in chapter 7. The regression coefficients were lower than unity, and the correlations ranged between 0.41 and 0.85 for somatic cell score (SCS) and milk yields. In general, the r_S values found in chapter 7 are in agreement with previous values reported in chapter 2, but this thesis is the only study that has tested observed r_S with an expected correlation (r_E), assuming that the expression of the same trait in the two MF environments is the same ($r_G = 1.0$) as suggested by Notter & Díaz (1993). The results of this thesis indicate that there is a scaling effect ($b_s < 1.0$), but no significant sire re-ranking in New Zealand dairy cattle across MF, since the r_S were in all cases greater than the critical values of the distribution r_E calculated. The latter means that differences in the EBVs of sires is greater in the more favourable environment (TAD) compared to the less favourable environment (OAD; Bryant et al. 2005). Therefore, the best sires selected under TAD would still perform best under OAD systems.

Hammami et al. (2009) summarized studies that were conducted to evaluate genotype by environment interaction (G×E) in dairy cattle. In that paper, within-country studies have demonstrated only a scaling effect instead of sire re-ranking, as was the main conclusion of chapter 7. This scaling effect is the consequence of heterogeneity of variances, as was found in chapter 6 and would not implicate detrimental consequences on selection for milk production traits.

Genetic correlation across milking frequency

A limitation in chapter 7 is that the r_G between the same traits expressed in the two MF were not estimated. If the r_G is substantially lesser than unity, the degree of re-ranking would be large (Cromie et al. 1998). Although this thesis found no evidence for S×MF, observed r_S of FY, PY SCS were only moderate; therefore, it was advised to calculate the r_G between MF environments. Preliminary r_G estimations of the same milk production trait in the two MF environments were calculated using only first-lactation records with the data available. The resultant r_G values were 0.90±0.02, 0.91±0.03, 0.85±0.04 and 0.77±0.05 for MY, FY, PY and SCS, respectively. Those values were lower than unity, but for the yield traits, were no less than 0.80, a threshold level suggested by Robertson (1959) to interpret if the interaction is expected to cause important reductions in the efficiency of selection programs.

Those preliminary estimates of r_G for milk yields are consistent with most estimates of r_G for the same trait between environments within-country ($r_G > 0.80$) (environments defined as regions, herd PL, herd size, feeding regimes) (Hammami et al. 2009). For example, research carried out in Ireland (Cromie et al. 1998) and in New Zealand (Bryant et al. 2007) indicated $r_G > 0.86$ for MY, FY and PY with different feeding regimes (Cromie et al. 1998) and herd PL (Bryant et al. 2007), providing little support for sire re-ranking. These preliminary r_G indicate that the magnitude of the G×MF interaction is low and MF environments are not dramatically different (Cromie et al. 1998), hence the responses to selection in herds milked OAD are not significantly affected when selection is based on TAD systems (Montaldo 2001).

Implications for breeding

The implementation of a separate OAD-selection program would not be justified. Mulder et al. (2006) and James (1961) estimated that the r_G needed to be below the range of 0.61-0.70 when comparing selection programs, before there was any advantage in implementing a dedicated selection scheme based on PT. The “break-even correlation” was defined as the intersection of r_G when the genetic gain of different selection strategies is equal (Sae-Lim et al. 2013).

Nevertheless, Namkoong (1985) postulated that, although single-traits may not have exhibited different expressions in different environments, a true G×E may exist by a value of a composite trait that is derived from the combination of those single-traits that do not exhibit any G×E interaction. For example, Charagu & Peterson (1998) found a significant interaction for economic efficiency (a composite trait of MY, FY, PY and LW) measured among daughters of Canadian and New Zealand F sires according to the payment system of British Columbia and Ontario (Canada) and the New Zealand payment system. The interaction was significant in both strain by environment and in sires within strain by environment.

Therefore, it is advised that future research addresses the estimation of the r_G in a composite index across MF environments. This composite index might initially include only milk production traits (MY, FY, PY and SCS), and when enough data is available it can be extended to other traits of breeding worth (BW; LW, fertility, residual survival and body condition score).

Selection scheme for once-a-day milking herds

A selection scheme based on PT and an alternative of genomic selection (GS) for the OAD population was investigated and results discussed in chapter 8. Three selection objectives were included in chapter 8 (OAD_{SO1}= same trait as those included in BW; OAD_{SO2}= same as OAD_{SO1} with additional traits of udder support and milking speed; OAD_{SO3}= same as OAD_{SO2} with restriction in fertility and residual survival). Further, correlated responses in the OAD dairy population resulting from selecting bulls by PT in TAD systems and used in OAD herds based on the current selection objective of the New Zealand dairy cattle, and a specific OAD selection objective were also investigated.

Selection scheme based on progeny testing

Estimates of genetic progress in milk yield traits for the OAD population arising from a specific OAD selection scheme were slightly greater than those resulting from selecting bulls under TAD systems and used in OAD-herds when the selection objectives mimicked the BW and a theoretical OAD-selection objective ($\mathrm{TAD_{SO1}}$ and $\mathrm{TAD_{SO2}}$).

Chapter 8 also shows that under a selection scheme specifically designed for the OAD-herds, the predicted genetic trend in the cow population based on the PT occurs after seven years of its implementation. Therefore, the time between the scheme implementation and the realised genetic gain may be a disincentive for implementing an OAD selection scheme.

Mulder et al. (2006) advised that a specific selection program for environments of low importance, as is the case of the OAD population, is not justified when only a small amount of semen is sold. In addition, Vargas & van Arendonk (2004) reported that when there is no significant G×E (as was discussed previously), the practice of semen importation from a large environment-specific selection program resulted in a greater (33%) rate of economic response compared to the implementation of a local PT selection scheme. That advantage was mainly due to higher selection intensities for the selection paths, which is the result of the differences in population size.

Given the results from chapter 8 and the evidence presented by Mulder et al. (2006) and Vargas & van Arendonk (2004), it is concluded that a small genetic advantage results from a separate selection scheme for the population milked OAD compared to bulls selected based on BW ($\mathrm{TAD_{SO1}}$) or the theoretical $\mathrm{TAD_{SO2}}$ and used in OAD herds. The latter indicates that high BW cows and bulls are also suitable for OAD dairying, and the $\mathrm{TAD_{SO2}}$ proposed in chapter 8 could be recommended as a useful tool to select bulls for future replacement.

Selection scheme based on genomic selection

Predicted genetic gain in the overall selection objective based on GS was in all cases greater than the conventional PT (50-80%). This is due to a shorter generation interval in the GS-scheme compared to the PT-scheme.

Another advantage of implementing a GS scheme is the lower cost compared with a PT scheme. In the conventional PT-scheme, it was assumed that breeding companies should keep 38 bulls till they are 60 month-old, in contrast in the GS-scheme the number of bulls required is reduced to fifteen bulls at 15 month-old. These results suggest that if OAD-farmers require a separate selection scheme, GS would be a more profitable option compared to a PT scheme, even though the number of OAD herds does not increase. The cost of genotyping per animal is, therefore, a crucial factor when considering GS as a more practical technology for genetic improvement of the New Zealand OAD population.

Another crucial factor for small dairy cattle populations, as would be the case in herds milked OAD, is the low reliability of genomic predictions (Thomasen et al. 2014a). Low reliability is a consequence of small reference populations (Hayes et al. 2009), which are mostly produced with PT bulls (Thomasen et al. 2014b). In this case, cow genotyping is an important factor for expanding the reference population (Pryce & Daetwyler 2012).

A possible alternative to reduce costs (compared to the implementation of a PT scheme) and to increase reliability is the pre-selection of young bulls based on GEBVs for PT (hybrid scheme). The hybrid scheme can potentially increase genetic gain compared to the conventional PT scheme (~30%; Buch et al. 2012; Thomasen et al. 2014a; Winkelman et al. 2015). The generation interval, however, is unaffected, which negates the main advantage of GS. However, the advantage of this scheme is that the number of young bulls submitted to PT can be limited to the number needed (Pryce & Daetwyler 2012).

In chapter 8, an arbitrarily lower limit of 40% of reliability of the aggregate breeding value was assumed. The study of Thomasen et al. (2014a) suggests that selecting bulls based on GS as age one-year-olds, and with a reliability lower than 30%, cannot compensate the reduced generation interval compared to the hybrid scheme available for Danish Jersey. The latter emphasizes that a GS-scheme might be a primary alternative in the implementation of a separate selection scheme, but the challenge is to have a reference population that guarantees high reliabilities. For the New Zealand OAD population, this can be achieved more effectively by genotyping cows.

Limitations of this thesis

In chapter 3, it was assumed that pasture contained a constant value of 10.5 MJ of metabolisable energy (ME) per kg^{-1} of dry matter and that cows could consume the pasture needed to achieve their specific energy demands. However, the content of ME in the pasture varies during the grazing period (Holmes et al. 2002), indicating that DMI estimates used in determining production efficiency might be biased. Feed conversion efficiency and DMI reported in chapter 3, however, were in agreement with results of Prendiville et al. (2009) under grazing conditions with same breed groups as used in the chapter, who measured individual DMI at different stage of the lactation period.

The approach shown in chapter 7 included only four traits of the national New Zealand dairy cattle selection objectives (MY, FY, PY and SCS). The calculated r_E was achieved by simulating true sires and simultaneously estimating BVs for the four traits for both MF. Then, correlations between EBVs were only in sires selected according to an economic index (EI) of the simulated EBVs for TAD. This EI index did not include live weight (LW). Hence, the EI values were higher in F sires and F×J sires with a large proportion of F genes compared to J sires, due to a greater breed effect of F. Under pasture-based systems, the economic value of LW has a negative sign (NZAEL 2016) to avoid increasing LW. The latter resulted in fewer J sires being selected in the across breed analysis of chapter 7. Although it is recognized that the expected values might be biased, previous studies in New Zealand also concluded that there was no sire re-ranking for milk yield traits in low and high PL of the herd (Bryant et al. 2007). Considering herds milked OAD and TAD as low and high PL herds respectively, the study of Bryant et al. (2007) supports the results of the analysis across breeds.

In the analysis undertaken in chapter 8, the selection objective did not include body condition score (BCS) as a trait of economic importance. From 2016, BCS is included as a new trait in BW. The economic value of this trait is $98.40, but the initial impact on BW will be relatively small (NZAEL 2016). The relative emphasis of BCS on BW is 7%. However, this emphasis is reduced to 2% in the actual LIC OAD selection index (LIC 2016). Therefore, excluding BCS would have little impact on the overall genetic progress estimated in chapter 8 where several selection objectives were considered.

The LIC OAD selection index comprises the same traits included in BW plus four functional type-traits: milking speed, udder support, body capacity and front teat placements. In this thesis, only milking speed and udder support were considered within the selection objectives investigated (OAD_{SO2} and TAD_{SO2}). The major implication of this omission is that there is a different relative emphasis in the traits included as selection objective in chapter 8 compared with the actual LIC OAD index, which might lead to different genetic progress than those reported in the chapter.

To reiterate, the true r_G between the same production traits in the two MF were not estimated in chapter 7. It would be prudent to extend the preliminary estimates of r_G of a milk trait measured in different MF environments indicated previously, with the estimation of r_G of the same trait across MF including lactation from several age classes. These correlations and the r_G of milk production traits measured in OAD and TAD systems can be used to compute correlated responses in the OAD population in scenarios where bulls are selected under TAD and used in OAD herds. Instead of the r_G, linear correlation values between EBVs of sires with progeny in both systems were used. Although these correlations were lower than the true r_G presented above, these values are high enough to adequately reveal the direction of the correlated responses. Therefore, the genetic progress for milk production traits in OAD herds, when the selection of bulls is based on TAD_{SO1} or in the theoretical TAD_{SO2} is unlikely to be significantly biased.

This thesis did not investigate a specific bio-economical farm model for the typical herd milked OAD. Some of the results in chapter 3, 4 and 5 can be used as input components of a specific OAD production-system (biological and nutritional parameters), to simulate income and cost in an OAD farm. The development of a bio-economical farm model would have allowed derivation of economic values for the traits included in the selection objective in chapter 8. This is important because deriving economic values is the first step in the development of a selection objective (Ponzoni & Newman 1989). Instead of a farm model, economic values used in chapter 8 were derived based on an arbitrarily relative emphasis. In New Zealand, economic values of traits in the selection objective are derived from a farm model and updated annually (Harris 1998), and those values represent the additional profit per 5 tonnes of dry matter. It is possible; therefore, that estimation done in this thesis might not accurately reflect the additional farm profit per 5 tonnes of dry matter of OAD milking systems.

Future work

Some aspects derived from this thesis may lead to future research projects. Firstly, the development of a bio-economic farm model would allow determining economical values as outlined above. Additionally, simulations aiming to evaluate the effect of straight-breed or crossbreeding on the profitability of dairy herds could elucidate the long-term effect of selection and crossbreeding on the rate of genetic gain and productivity of the New Zealand dairy cattle milked OAD.

Secondly, as concluded in chapter 8, a GS selection scheme should be cheaper and more profitable than the implementation of a PT scheme. This thesis investigated only one possible GS scheme. However, there are several possible selection schemes or strategies where GS can be incorporated (Pryce et al. 2010). Further research should attempt to evaluate the effect of GS on genetic gain and inbreeding through a hybrid scheme or through a nucleus scheme where more intense selection can be applied in the female pathways.

Lastly, data analysed in chapters 5, 6 and 7 came from 298 farms operating OAD milking, which is equivalent to 2.5% of dairy herds in New Zealand (LIC & Dairy NZ 2015). Although the proportion of herds under OAD systems is low, studies concerning OAD systems in New Zealand have shown that farm staff working on OAD farms could enjoy better working conditions and lifestyle compared to those working in TAD milking farms. Hence, modelling the effect on the New Zealand dairy industry from an increasing proportion of OAD herds is worth investigating. As milk production and calving are seasonal, the industry processes high volumes of milk at peak lactation and it is under-capacity after peak of lactation, and therefore, lactation persistency is of economic importance to the milk processing industry (Morris et al. 2008). Changes in the volume of milk to process and in the shape of the lactation curves (less defined peak but more persistent lactation curves; chapter 4) would have important implications in the operational logistics of dairy companies in New Zealand. In the literature review of this thesis (Chapter 2) it was pointed out that OAD-milking can potentially affect the processing characteristics (reduced levels of free fatty acids and more plasminogens) of the milk used in the production of butter, cream and cheese. Further, greater concentration of lactoferrin is observed in cows milked OAD compared to TAD (Farr et al. 2002). Lactoferrin is a component of milk whey, valuable for its properties as an iron-binding, bacteriostatic and anti-bacterial protein, representing an opportunity worth exploring from a marketing viewpoint (Stelwagen et al. 2013). Modelling changes in total milk produced in the shape of OAD lactation curves, and on milk processing would assist the industry to adapt if the proportion of OAD herds increased substantially.

General conclusions

The central findings of this thesis are:

- Breed by MF interactions for milk yield traits across MF are not sufficient to warrant a separate selection scheme across MF environments since S×MF was not significant. The observed breed by MF interaction suggests that J cows are better suited to low PL in pasture-based systems milking OAD. It is possible that OAD herds composed of F×J cows might be more profitable. This, however, needs further investigation.
- Farmers operating OAD can rely on selecting bulls based on BW or an OAD selection index, which includes udder-related type traits, because genetic progress resulting from separate OAD-selection scheme based on PT is low compared to using bulls tested under TAD and dedicated to OAD systems.

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Statement of Contributions

Statements of contributions to doctoral thesis containing publications fort chapters: 3, 4, 5 and 6.

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Name of Candidate: Felipe Lembeye Illanes

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Name of Published Research Output and full reference:

Lembeye F, López-Villalobos N, Burke JL, Davis SR, Richardson J, Sneddon NW & Donaghy DJ (2016): Comparative performance in Holstein-Friesian, Jersey and crossbred cows milked once daily under a pasture-based system in New Zealand, New Zealand Journal of Agricultural Research, DOI: 10.1080/00288233.2016.1207669

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  The candidate analyzed data provided by Massey dairy farm No.1, performed the analysis with input from Prof. Nicolas Lopez-Villalobos on the models used and wrote the first draft of paper then under took changes with guidance from supervisors and input from other co-authors.

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