

Chapter I

General Introduction

Throughout history, breeders have developed various methods to identify superior individuals in domestic livestock populations. This is because the selection of replacement stock, especially sires, has a tremendous impact on the livestock population, effectively disseminating their superiority through the population by mating with several or even hundreds of females. Sires not only have an impact on the resulting progeny, but these choices also affect the performance of later generations of the population if daughters of the sires themselves are kept as replacement breeders. Every farm owner would like to select sires of desirable genetics for improvement in economically important traits. Fortunately, the concept of breeding value estimation provides breeders a means by which sires with desirable genetics are identified thus, presenting an avenue to make useful selection decisions. Estimated breeding values are used to rank and select replacement animals to achieve genetic improvement.

1.1 Genetic evaluation system

The breeding value can be defined as the value of an individual to the genetic merit of its offspring. Parents transfer a random sample of half of their genes to their offspring. Thus, to obtain genetic improvement, parents carrying desirable genes should be selected and used for breeding. Unfortunately, we only see phenotype, but in reality we want to estimate the value of the genes an individual carries. The breeding value of animals must be estimated from phenotypes (that which can be observed or measured e.g. milk yield, coat color) of the animals themselves and/or those of their relatives. Phenotype is an expression of all genes for a certain trait with the environment influencing its expression upward or downward. Thus, the biggest challenge to breeders is how to sort the effects of environment (non-genetic) from the effects of genetics or, more specifically, the additive genetic effects.

Best Linear Unbiased Prediction (BLUP) is the most widely used method for genetic evaluation and breeding value estimation in livestock. The methodology simultaneously estimates systematic environment effects and predicts breeding value of individual animals included in the analysis based on phenotypic information. The phenotypes may be performance records on the prospective replacement stock or records on their relatives. Visual evaluation is not recommended for traits which can be measured. For example, using a scale to measure milk yield to evaluate milk production performance gives more accurate evaluation than would visual appraisal of the animal. Therefore, to achieve genetic progress, recording of performance, identification of replacement animals based on genetic merit or breeding value and effective dissemination of superior genetics are necessary.

The dairy cattle sector provides a good example of effective use of performance records and wide use of sires to disseminate superior genetics through artificial insemination. The history of the American dairy cattle industry documented that cows from herds with recorded individual milk production had a higher average lactation yield than herds with no such records. The American Dairy Science Association, through a committee, established a set of rules and guidelines for measuring milk yield in dairy herds that a "Cow Testing Association" adopted in 1926. The name of the association was changed to Dairy Herd Improvement Association (DHIA) in 1927. The average milk production of U.S. dairy cows in 1930 was 2,049 kg per lactation (Voelker, 1981) whereas the average yield of cows enrolled in the DHIA milk recording program was 3,474 kg per lactation. From 1930 to 1970, average production increased to 5,795 kg and 4,428 kg per lactation for the enrolled cows and the wider U.S. dairy cow population, respectively. This was equivalent to 66.8% and 116.1% increase in average production in enrolled cows and the total cow population in a 40-year period. In the same time period, the percentage of recorded cows in the testing program increased from 2.4% to 17.2%. By 1980, 26.8% of all cows were enrolled in the DHIA milk recording program. The total cow population benefitted the most from this recording program as evidenced by the higher increase in average milk yield. The marked

improvement was attributed to the production of increasing number of cows recorded in testing program and as source of superior genetics through sire and cow evaluation program (Voelker, 1981). The U.S. DHIA credits their recording program as a tool for sound breeding management (King & Miller, 1965). An accurate measure of individual lactation performance is essential to a good genetic evaluation system. The implementation of a genetic evaluation system paved the way for identification of superior breeding stocks while the use of artificial insemination disseminated the superior genetics to the whole of the dairy cow population and increased further the rate of genetic gain (Voelker, 1981).

The review by Voelker (1981) of the history of the U.S. Dairy Herd Improvement Association pointed to some very important aspects responsible for the accelerated increase in production potential of the US dairy cattle population. These are the establishment of an organized structure for herd recording, a genetic evaluation system and the availability of artificial insemination (AI) to disseminate good genetics to the general population. Specifically, genetic evaluation can be viewed as several components, with each component dependent upon each other in order to provide a good result. Genetic evaluation needs to be planned, consistent with the kind of population at hand, to cover identification of traits of interest and their economic value; recording of performance and pedigree; identification of environmental and genetic effects; development of an appropriate genetic evaluation model for estimating genetic parameters and breeding values; selection of breeding animals based on genetic predictions made; and lastly, development of a breeding program and mating strategy in order to maximize the use of superior genetics into as wide the population as possible (Elzo, 2001). The various components of a genetic evaluation system in the dairy sector mentioned above were essential as milk production traits are expressed only in females but the males are more efficient in disseminating superior genetics as they can be mated to many females at any given time, especially with the use of artificial insemination. The bulls are evaluated based on their daughters' performance through progeny testing. On the average, 20 – 40 daughters per bull need to be recorded to achieve good accuracy and it

takes about 5 – 6 years to produce a progeny-tested dairy bull. Since proving of bulls is a long and expensive process, superior bulls identified through this system are used to the maximum. While such components can easily be seen in most countries with developed dairy industry, it may not necessarily be the same in the dairy buffalo populations located in various developing countries, even though these components are just as applicable and needed for genetic improvement in a similar manner as dairy cattle. The Philippines is one of the developing countries with a program that aims to improve the milk production potential of its dairy buffalo population.

1.2 The water buffaloes.

There are two types of water buffaloes, the swamp type commonly found in South East Asia and the riverine type found in the Americas, Eastern Europe, Asia and near East. Buffaloes are tropically adapted animals, able to tolerate hot, humid conditions and generally fare well under less optimum and intensive conditions compared with dairy cattle. Under ordinary conditions, milk production is hardly different from better breeds of local cattle (Van Den Berg, 1990). It is estimated that 85% of the water buffalo population is in Asia and the near East. Swamp-type buffalo is almost exclusively found in Asia and is known to be a source of meat, milk and draft. Milk production of the swamp buffalo is very low, averaging only 1.5 – 4 kg/day (PCARRD, 1978) under Philippine conditions. The riverine buffaloes, on the other hand, are a better milk producer, averaging 8 kg/day. An average of 10 kg/day is now more commonly seen in countries such as Italy with a more intensive production system with the Mediterranean breed of buffalo. The riverine buffaloes are now selected and bred for increased milk production, but selection is quite recent relative to dairy cattle breeds. The cross between the riverine and swamp buffalo is fertile and averages 3.6 kg/day (Mamuad et al.,1981), with average production going up with higher proportion of riverine blood under Philippine conditions. As of April 2010 (BAS, 2011b), there were about 2,991,713 buffaloes in the Philippines and out of the total buffalo population, 31,708 may be considered of the dairy type (purebred riverine and their crosses with the swamp type).

1.3 Constraints in breeding program implementation for Philippine dairy buffaloes

Currently, in the breeding program for Philippine dairy buffaloes, milk yield is the only trait being selected on. Genetic evaluation and progeny testing is limited only to the nucleus and other institutional herds. The current population consists of a closed nucleus; a second tier of multiplier herds (institutional herds) and the base consisting of purebred riverine cows in various dairy cooperatives and crossbred cows within and outside dairy cooperatives. Young bulls are nominated to become AI bull and into the progeny testing program based on parent average first parity milk yield EBVs. Elite cows (bull mothers) and proven bulls identified based on first parity milk yield EBVs are used to produce young bulls. Cows in the multiplier herds are used to produce daughters of progeny test bulls. At the same time, frozen semen of test bulls are stored for future use. There are approximately ~500 and ~600 cows that are being recorded per year in the nucleus and multiplier herds, respectively. There are actually more purebred dairy buffalo cows in the hands of farmers in several dairy cooperatives (~1,500 cows) that could potentially be enrolled in the program but are not yet included in the genetic evaluation nor participate in progeny testing. The cows in the base are not part of an official milk testing scheme due to cost considerations, among others. This is unfortunate as the breeding program being implemented and the eventual recipient of the improved genetics are actually for these cows in the villages. A simple and cost effective milk testing and recording system for the dairy cooperatives that uses a combination of owner recorded and few supervised milk tests is necessary. The constraints under the present situation are that 1) there is a very small nucleus to select replacement bulls from, selection intensity is not optimum; 2) the number of bulls that the AI station can accommodate limits the number of candidate bulls recruited every year; 3) the number of daughters that could be evaluated per bull under progeny testing is small (7 -8 daughters on average) due to the small percentage of recorded population, maximum accuracy can only be achieved if bulls are used for longer period of time thus, rate of genetic

gain is not maximized; 4) AI diffusion rate towards the base population is low, there are more daughters sired by natural service than by AI sires hence, diffusion of superior genetics to the base population is slow.

Given the breeding program constraints above with the current situation in Philippine dairy buffalo population, the conventional progeny-testing scheme will be costly and hard to implement. Tobias (2010) reported that in developing countries, conventional progeny-testing scheme may not be cost efficient when the costs are weighed against possible genetic gains considering the use of net present value in a 25-year period. Exploring alternative breeding schemes may be warranted, such as use of young bulls rather than proven bulls. It was also recommended that under Philippines situation, elite matings be limited to the nucleus herd in the conventional dairy breeding structure but the aim is to produce bulls for natural mating that will service the base population (Bondoc & Bantoc, 1996). There are advantages and disadvantages to these suggestions but these alternative breeding schemes should be analysed with regards to benefits/gains versus cost.

1.4 The breeding objective in dairy buffaloes

Milk is priced and sold by volume but recently there has been interest in putting value to milk components. Milk protein and milk fat are actually more valuable due to the “niche” market” of buffalo milk for processing into cheese and other dairy products. It has been shown that milk yield is negatively correlated with milk component traits (fat and protein concentration) such that selecting for milk yield alone (as what is currently being done with Philippine dairy buffaloes) will bring about lower milk fat and protein percentage (Wilcox et al., 2003). A balance in selection has to be put in place that will allow increase in milk production potential but avoid deterioration of milk fat and protein percentage.

The experience in dairy cattle population is that breeding for increased milk yield while largely disregarding functional and fertility traits results in a deterioration of reproductive performance; cows became harder to impregnate post-partum. In the UK, days-to-first service was reported to be 83 days in 1999 compared with 74 days in 1984 (Esslemont & Kossaibati, 2001). Calving interval, on the other hand, was reported by the same authors to be 397 days when the ideal should be less than 370 days. In the Netherlands, it was reported that the average calving interval in 2001 was 402 days and that in the period between 1995 and 2001, there was an increase in calving interval by 2 days per year (De Jong, 2001). While calving interval and other fertility traits are largely affected by management, the same author, as well as other researchers reported that selection for fertility is possible as there is enough variation to do so. Fertility traits were reported to have an unfavourable genetic correlation with milk yield (Lindhé, 2001). Feedback from farm managers of the different institutional buffalo herds in the Philippines report of high-yielding buffalo cows being harder to impregnate post-partum (personal communication). Therefore, it is probable that deterioration of fertility in dairy cattle is also true for dairy buffaloes. Buffaloes have an inherently poor reproductive performance (Barile, 2005). Kumaresan and Ansari as cited by Barile (2005) reported conception rates from artificial insemination (AI) following natural estrus in riverine buffaloes from 16.67% to 33.33%. The low success rate in AI is partly due to weak estrus signs and variable estrus period. Despite this report, buffalo cow reproductive performance in nucleus herds in the Philippines show that there are individual cows with exceptional performance that give a calf once a year. This observation though, needs to be validated but nevertheless supports the report (de Jong, 2001) that there is enough variation in the cow population to select on fertility traits. While managers and researchers try to improve reproductive performance in the short term through management strategies, selection for fertility traits may also complement this effort with small but permanent change in the population.

The low buffalo conception rate and eventual long calving interval, a 10-month gestation period, in combination with short lactation length result in prolonged dry periods. Any additional day that a cow is dry will cost the dairy farmer in terms of maintenance and opportunity costs (due to loss of potential sale of calves, culls and milk). Selection for persistency can partially address the issue of short lactation length and poor reproductive performance due to prolonged post-partum anestrus. A persistent cow has been described as having a flatter lactation curve with a lower peak that occurs at a later date than average and a slow rate of decline after the peak has been reached (Cole & Null, 2009). Lower peak yield may result in higher probability of a cow returning to estrus earlier post-partum due to a less negative energy balance at the beginning of lactation and a longer lactation period due to slower rate of decline after peak. It has been shown in dairy cattle that lactation persistency is heritable and can be selected for (Cole & Null, 2009; Cole & VanRaden, 2006). It is likely probable that the same is true for dairy buffaloes as well. Persistent cows are therefore especially desirable in dairy buffalo population as feeding of high grain (i.e. 60:40 or 50:50 ratio) diet is not a common practice and farmers rely on daily milk sales to sustain their daily living expenses in between crop harvests.

1.5 Scope of the thesis

To address the concerns mentioned above, additional traits need to be added to the breeding program. These traits for consideration, however, are negatively correlated with milk yield. It will therefore be difficult to achieve genetic progress but, selection indices can be drawn up to balance the response. The small number of participating cows in the nucleus and multiplier herds and the absence of participation of cows in the various cooperatives are issues of concern. As recording cows in dairy cooperatives is expensive and difficult, often resulting in records with incomplete or irregular intervals between tests, a method for yield calculation suitable for milk and milk components situation must be implemented. The aim of this research therefore, is to be able to lay the foundation for a comprehensive breeding program.

The succeeding chapters try to address some of these issues. Chapter 2 is a review of literature that discusses the different methods used for calculating production yields of dairy cows, genetic evaluation and predicted response to selection.

Chapter 3 presents a system for calculating and standardizing milk production yields appropriate for use in genetic evaluation and farm management. Two methods of yield calculation are compared: Test Interval Method (TIM) and a multiple trait procedure that utilizes lactation curve functions and covariances among test day yields within and across traits for prediction of lactation yield in terms of accuracy of prediction of complete and partial lactations. The advantages of multiple trait procedure for use in test day milk recording are discussed.

Chapter 4 deals with the estimation of genetic parameters for milk production traits using the 305D lactation yields calculated based on the method developed in Chapter 2 as well the use of test day records directly in univariate and multi-variate analyses. It discusses the response to multi-trait selection on milk yield and milk components by selection index. Furthermore, the implication of long-term selection on yield traits on fat and protein concentration is explored in this chapter.

Chapter 5 deals with univariate and multi-variate analyses by random regression of test day records for the five milk production traits. It examines the fit of different models using varying orders of polynomial functions fitted to fixed and random effects in terms of Bayesian information criterion, variance estimates across the lactation trajectory, genetic correlations between adjacent test days within and between traits as well as heritability estimates.

Chapter 6 deals with determining the response to selection from altering the shape of the lactation curve through selection on the leading eigenvalues of the genetic covariance matrix estimated by random regression test day model from Chapter 5. It discusses selection for a more persistent curve, characterized as having a lower peak and slower rate of decline after peak, and the effect on milk

production as a consequence. The improvement/deterioration in lactation persistency from selection on total lactation as well as the use of persistency indices is determined as the ratio of the response or genetic gain at 240D over 90D in lactation. Furthermore, the correlation of calving interval to milk yield at different stages of lactation is estimated.

Chapter 7 is the general discussion of this thesis. It discusses several points arising from this research work. These are: 1) suitability of test day and 305D lactation records for genetic evaluation; 2) consequence of selection for higher milk yield on fat and protein concentration; 3) suitable random regression model for use in genetic evaluation; 4) balancing the response to selection on milk production, milk components and lactation persistency in Philippine dairy buffaloes.

Chapter II

Review of literature

This chapter will first present relevant information on the dairy buffalo industry and the current breeding structure in the Philippines to gain better appreciation of the research topics to be undertaken. Related studies on dairy cattle and buffaloes that may be applicable to the research to be undertaken such as to milk yield calculation/prediction, parameter estimation and various genetic evaluation models, development of selection indices and breeding program optimization are also presented and reviewed in this chapter. These studies will provide valuable information and a guide in identifying areas for research and development that should be undertaken to address the objectives presented in the previous chapter.

2.1 Dairy buffalo production in the Philippines

In the Philippines, the swamp type is the indigenous breed of water buffalo (carabao) with a population of approximately 2.99 million (BAS, 2011b) 99% of which are owned by smallholder farmers. It is a major large ruminant species in the Philippines, where there more buffaloes than cattle. The cattle population number is about 2.62 million (BAS, 2011b) as of 2010. Among the water buffalo population, a small percentage are dairy animals of riverine blood. The riverine buffalo breed is an introduced breed in the Philippines. Murrah buffaloes have been imported from India since the Spanish times (19th century). Subsequent importation of 940 head was done after the Second World War, consisting mostly of the Murrah breed for dairy purposes and for crossbreeding with the swamp-type buffalo although exact records regarding these importations are not available (Villegas, 1958). Frozen semen of Nili-ravi buffaloes from Pakistan as well as Murrah buffaloes from India were also imported in the 1980s (Bondoc, 1998). These were used in the breeding program of an FAO funded project of the Philippine

Carabao Research and Development Center (PCRDC). Infusions from Bulgaria were done more recently; from 1994 to 1999. Bulgaria imported Murrah buffaloes from India in 1962 and 1975 and used these genetics to upgrade their Mediterranean breed of buffaloes (Alexiev, 1998). Continuous backcrossing to the Murrah breed was done until the 4th generation before *inter se* mating was done. Progeny from this breeding program, called Bulgarian Murrah, were the stocks that were imported into the Philippines.

The increasing trend in mechanization in rice-producing areas of the Philippines is slowly replacing the carabao with hand tractors as provider of draft power. The carabao is also a traditional source of liquid milk in rural farming communities. However, due to its the low milk production potential, the swamp-type breed is not suitable for developing a buffalo-based dairy enterprise. In rice-producing areas wherein the hand tractor has largely replaced the carabao as source of draft power, the introduction of riverine blood in the swamp buffalo population and establishment of dairy buffalo cooperatives have brought about a renewed interest in buffalo-based dairy enterprises that provide farmers a daily source of income especially in between rice/crop harvests. There are currently approximately 31,708 head of dairy buffaloes located in various villages and government farms (BAS, 2011b). The number includes purebred riverine buffaloes and crosses between the swamp and the riverine buffalo breed.

The domestic milk production is only able to account for approximately 2% of domestic demand. Nevertheless, there has been continuous growth in the dairy sector for the past several years. Currently, buffalo milk accounts for about 38% of the domestic milk production; 61% by dairy cattle and 1% by dairy goats. The volume and value of production is shown on Table 2.1 below.

Table 2.1 Volume and value of milk production, 2009

Species	Inventory, hds.	Volume, M Liters	Percentage, contribution	Raw milk, PhP/Liter
Cattle	21, 260	8, 645	60.6	20
Buffalo	31, 708	5, 400	38.1	46
Goat	14, 151	185	1.3	36

Source: Philippine Bureau of Agricultural Statistics, 2011

According to the Bureau of Agricultural Statistics (BAS, 2011a), the dairy buffalo sector grew by 1.93% while the dairy cattle sector grew by 12.44%, due mainly to the herd build-up program of the government, which includes importation of crossbred heifers from New Zealand. In contrast, the dairy buffalo sector has had very limited opportunity to import genetics from other countries and must rely on the local population for growth in production. There are currently more dairy buffalo cows than dairy cattle cows. To increase the number of dairy buffaloes, swamp buffaloes are inseminated or bred to riverine buffalo bulls and followed up by continuous backcrossing (upgrading) to the riverine breed.

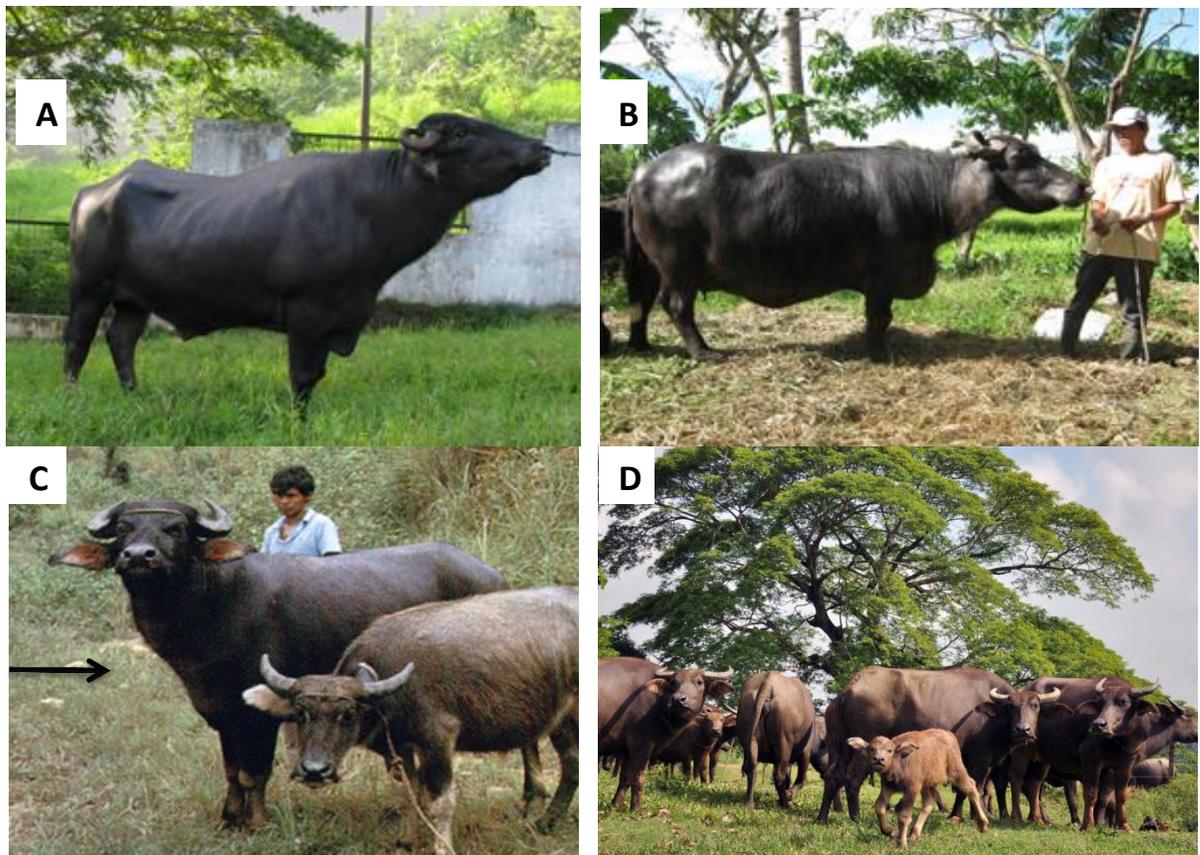


Figure 2.1 Common buffalo breed groups in the Philippines. (A) Philippine dairy buffalo bull - riverine type, (B) Philippine dairy buffalo cow from one of the dairy cooperatives, (C) Yearling Philippine Carabao heifer (foreground) and a heifer cross of swamp and riverine type (arrow) of the same age as the swamp type, (D) Mature Philippine Carabao – swamp type

2.1.1 Dairy buffalo sector breeding structure. Like most Asian countries, landholding is small in the Philippines. Farmers typically raise 2-5 carabaos for draft or source of meat/milk. Currently, farmers with dairy buffaloes are normally organized into cooperatives in each village or villages that are close together. Cows in these dairy cooperatives are mainly purebred riverine breed. Cows are normally grouped together in a small locality to facilitate milk collection from individual farmers. The number of dairy buffalo cows a farmer owns is limited by feed resources and his family's ability to care for them. Milk recording and appreciation of good genetics, however, are not given priority. Less than optimum government resources and reluctance by the farmers to pay for supervised milk recording of village dairy buffaloes on a monthly basis hinder establishment of individual milk production recording for evaluation of dairy animals. However, there is a small percentage of dairy buffalo farmers that record daily yields. These are often written on a calendar or notebook. A consolidated monthly record is provided to the Philippine Carabao Center (PCC), the government agency mandated to carry out development programs pertaining to the water buffaloes. Unfortunately, farmers are more concerned with having milk to sell on a daily basis than to record accurately, making it difficult to get a complete set of records per lactation. In this kind of set up, genetic improvement through managed breeding, culling and selection is quite impossible to be undertaken by a single farmer or even a cooperative. It is fortunate that artificial insemination (AI) is an accepted technology among dairy buffalo farmers. The government, through PCC, has taken the initiative to undertake a genetic improvement program for dairy buffaloes. This is done by setting nucleus and multiplier farms where recording of performance and evaluation of individual animals for milk production is being done. Bulls from best performing sires and dams based on EBVs (sire for sires and dams for sires) are selected to become AI sires for use in the nucleus and multiplier herds. Frozen semen of senior or proven bulls is used on village cows. Breeding material from the nucleus herds are brought to the multiplier farms and villages through provision of frozen semen and live animals for breeding. Bulls for natural service from nucleus and multiplier farms complement

artificial insemination service especially in remote areas. The breeding structure is very pyramidal – a small nucleus, a slightly bigger second tier (multiplier herds) and a larger base. The flow of genetics is mainly downward. There is very minimal movement of genetics upward to the nucleus. Progeny of exceptionally good cows from the village (based on phenotype – milk yield) are the rare instances wherein genetic material is brought back into the nucleus. Culling and selection of cows in the nucleus and multiplier herds is done based on first parity milk yield EBVs (Sarabia, et al., 2009).

Every year, about 12 young bulls are selected from the nucleus to be sent to the AI station for semen collection. After training and semen quality evaluation, approximately half remain to become semen donor. These young bulls are used on multiplier herds to produce daughters and sons. Excess frozen semen is stored for future use. For use in nucleus, all available AI bulls (young and senior) are ranked based on first parity milk yield EBV and the top three are selected for use in producing the next crop of young bulls for breeding. Other bulls (senior or proven) are assigned to be used on cows in the base. Thus, the AI bulls are used to service three breed groups but the bulk of inseminations are on swamp buffaloes as these are the most in numbers. There are approximately 30,000 inseminations per year nationwide. The current structure is shown in Figure 2.2 below:

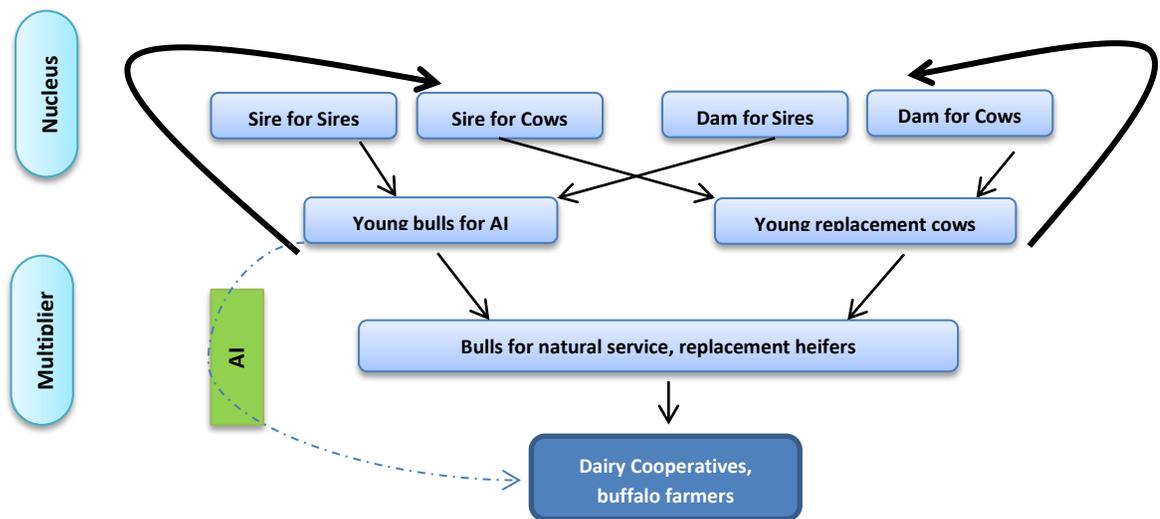


Fig. 2.2 Current breeding structure of the dairy buffalo sector

2.1.2 Traits of economic interest in the local buffalo population. While milk production is the primary trait of interest, there are other traits that should be considered that are correlated to and in support of milk production. Fertility, health/fitness traits support or complement the expected increase in production due to selection. Table 2.1 below presents the lower and upper range of means of some production traits gathered from reports of various authors from different countries. Only the lowest and highest means reported are shown:

Table 2.2 Reported milk production and reproductive performance of dairy buffaloes from the Philippines and various countries

Trait	Reported range of means from other countries		Means from Philippine dairy buffaloes
	Min.	Max.	
305D Milk yield, kg	1,496 ^d	2,286 ^a	1,537.7
305D Fat yield, kg	119.6 ^b	197 ^a	109
305D Protein yield, kg	77.4 ^b	104.7 ^a	62.5
Fat concentration, %	6.8 ^b	8.6 ^a	7.5
Protein concentration, %	4.3 ^b	4.6 ^a	4.1
Lactation length, d	267 ^c	302.7 ^e	276
Calving interval, d	385 ^d	472 ^e	480.8
Age at first calving, mos	39 ^d	41 ^e	42

^aRosati & Van Vleck, 2002; ^bAspilcueta-Borquis et al., 2010a ^c; Khan et al., 2005; ^dTonhati et al., 2000; ^eKumar et al., 2008

Compared with the reported figures from other countries, Philippine dairy buffaloes have lower performance and suggest these traits should be selected on. The dairy buffaloes inherently have poor reproductive performance (Barile, 2005) such that serious effort in improving the trait should be done. There is a need to emphasize the use of selection on reproductive performance traits that have considerable genetic variation. Otherwise, the low performances can be enhanced by improving the environmental and husbandry conditions. Milk yield, fat percentage and lactation length are the only traits that are within range of those reported. Lactation length, though within range, is still short and needs to be longer. It is generally perceived that dairy buffalo cows have lower persistency than cattle. This is evidenced by a much shorter lactation length relative to dairy cattle. The combination of a 10-month gestation period, a short lactation length and long calving interval results in a long dry period wherein a cow is unproductive. Improving fertility traits and persistency to lengthen lactation period will

shorten calving interval and are thus also important traits for improvement. Shortening the number of days dry will benefit the dairy farmer indirectly through lower opportunity costs and higher lifetime milk production potential.

2.1.3 Buffalo milk products and market. Payment of milk produced is based on milk volume rather than milk component yield. However, the price is two to three times higher than cattle milk depending on the area. Buffalo milk is preferred for processing into dairy products, such as soft cheese, milk candy, yoghurt, ice cream and flavoured milk. This is because buffalo milk has more total solids, milk protein and milk fat, thus, better cheese yield. The higher milk fat gives creaminess to yoghurt, ice cream and other dairy products. The traditional soft white cheese and mozzarella cheese are made almost exclusively from buffalo milk in the Philippines. Similarly in Italy, “Mozzarella di Buffala” is a premium cheese product. Thus, the price of buffalo milk is an appreciation of its inherent qualities. Buffalo milk has a “niche” market and is not expected to compete with cattle in the liquid milk market. This indicates that milk components are traits of value in dairy buffaloes and should be selected for. Under less intensive production system in the Philippines, the buffalo will fare well or even better than dairy cattle if maintenance and production cost are taken into consideration. It is not expected, however, to compete with dairy cattle under a more intensive production system. If the dairy cattle population was able to increase production potential from 2,000 kg/lactation in the early 1900s to more than 8,000 kg/lactation currently, it is also probable that the dairy buffaloes could increase its milk production potential to a level close to that of dairy cattle if an effective recording and genetic evaluation system is put in place. Selection should be for multiple traits for a more “rounded” buffalo cow and given the constraint mentioned in the preceding paragraphs, efforts should be exerted to include cows in the villages to help increase rate of genetic gain. This will only come about if there is a more labour-efficient and systematic recording system to be able to calculate lactation measure of individual cows.

2.2 Calculation and prediction of lactation yield

A genetic evaluation model is only as good as the quality of animal performance record. Knowing the lactation measure of cows has proven to be useful for management and genetic evaluation in dairy cattle. In dairy production system, milk production is the most useful information, along with reproductive performance, for the farm manager in deciding whether a cow gets inseminated or is culled. A standard lactation measure is important so that cows get compared fairly within herd. Individual milk performance record is also useful for evaluating feeding and management practices in the herd. Market planning and industry situation will also find these records useful. However, recording daily milk yield is tedious and impractical such that various methods of calculating milk yields based on once-a-month record have been adopted. The International Committee for Animal Recording (ICAR, 2010) has recommended several methods for calculating lactation yields for dairy cattle and similarly for dairy buffaloes based on monthly records. These methods to predict whole lactation yields can be grouped into linear interpolation, use of lactation curve function and prediction of yields utilizing covariances between test day records and complete lactation record within and between traits (milk yield, fat and protein).

2.2.1 Test Interval Method (TIM). To date, several methods to calculate lactation yields have been accepted and recommended by ICAR. Test Interval Method (TIM) remains to be the reference method for yield calculation. The U.S. Dairy Herd Improvement Association (DHIA) has used this method since 1969 (Voelker, 1981) and has proven to be suitable for genetic evaluation. Yield is estimated by connecting “dots” (test day measure) at approximately 30-day intervals by interpolation. Due to the curvilinear nature of the lactation curve, first to second month of lactation is not adequately explained by TIM. The addition of linear and quadratic coefficients (Shook factors) for the first, last and the test day around peak production was adopted by DHIA in order to increase accuracy of estimating lactation

yield based on monthly samples (Shook et al., 1980). The formula for calculating lactation yields based on monthly test day measure is (ICAR, 2010):

$$MY = I_0M_1 + I_1 \frac{(M_1+M_2)}{2} + I_2 \frac{(M_2+M_3)}{2} \dots + I_{n-1} \frac{(M_{n-1}+M_n)}{2} + I_nM_n$$

$$FY = I_0F_1 + I_1 \frac{(F_1+F_2)}{2} + I_2 \frac{(F_2+F_3)}{2} \dots + I_{n-1} \frac{(F_{n-1}+F_n)}{2} + I_nF_n$$

$$FP = \frac{FY}{MY} * 100$$

Where:

M_1, M_2, M_n are the weights in kilograms, given to one decimal place, of the milk yielded in the 24 hours of the recording day.

F_1, F_2, F_n are the fat yields estimated by multiplying the milk yield and the fat percentage (given to at least two decimal places) collected on the recording day.

I_1, I_2, I_{n-1} are the intervals, in days, between recording dates.

I_0 is the interval, in days, between the lactation period start date and the first recording date.

I_n is the interval, in days, between the last recording date and the end of the lactation period.

The formula applied for fat yield and percentage can be applied for any other milk components such as protein and lactose.

ICAR also recommends similar linear interpolation for yield calculation in dairy buffaloes. Due to the shorter lactation period, standard lactation length for buffaloes is set at 270D rather than 305D. There are two test intervals recommended: 28 – 33 days interval (A4 method) and 38-46 days interval (A6 method). Thus, a standard lactation measure for dairy buffalo is 2x-a-day 270D record. No multiplicative adjustment factors are used or reported by buffalo-rearing countries for the first, last and test day spanning the peak yield similar to DHIA. Italy has adopted the 270D standard lactation length while other countries such as India (Gandhi, 2003), Pakistan (Khan et al., 2005) and Brazil (Tonhati et al., 2000) calculate lactation yields based on 305D standard lactation length.

2.2.2 Lactation curve functions for predicting 305D milk yield. Use of lactation curve functions and some mathematical functions have been used for analysis of lactation yield by several researchers (Ali & Schaeffer, 1987). A cow's lactation, when plotted through time, is best described as having a short rising phase followed by a slow linear decline. Mathematical models to describe the lactation curve have

been proposed for prediction of total and peak yields, determining effect of environmental factors and for modeling genetic effects (Swalve & Guo, 1999). An exponential gamma function proposed by Wood (1967) is the most common model used to describe the lactation curve due to its simplicity.

$$y_t = at^b \exp^{-ct}$$

where:

Y_t represents milk yield on day t after calving;

a is the initial milk yield;

b is the inclining rate of milk yield;

c is the declining rate of milk yield after peak production and

\exp is the base of natural logarithm.

t is number of days after calving

Sherchand (1994), citing Wood, stated that the parameter a is a scalar directly related total milk production, b is an index of an animal's capacity to utilize energy for milk production, and c is a decay rate. Peak yield is estimated by $a(b/c)^b \exp^{-b}$ at b/c weeks after calving. Parameters are estimated by iterative non-linear regression because the parameters are intrinsically non-linear. Summing up predicted daily yields to 305D derives predicted total milk yield. The function can be linearized by transformation of the data by taking natural logarithms of both sides of the equation, $\ln(y_t) = \ln(a) + b \ln(t) - ct$. Linearization requires less computing time than iterative non-linear techniques (Congleton & Everett, 1980a) however, this does not give very good fit compared to non-linear regression (France & Dhanoa, 1984). This was validated by Cobby & Le Du (1978) when they compared linear and non-linear techniques for estimating the parameters of Wood's gamma function and reported smaller mean square error for non-linear techniques. Fitted to monthly milk yield data of Holstein cows, Wood's model gave a good fit; but a better fit was observed for lactation records of ≥ 44 weeks compared with those less than 44 weeks in duration (Kellogg et al., 1977).

Other functions describing the lactation curves have been reported aside from Wood's gamma function.

These are:

1. An inverse quadratic polynomial (IP) developed by Nelder (1966) have been reported to fit Hariana cattle and Friesian crosses well (Bhat et al., 1981).

$$y_t = \frac{t}{a + bt + ct^2}$$

It was reported to fit well with lactation records that start low and peak early, such those seen in dairy buffaloes. Peak yield is computed from $\frac{1}{2\sqrt{ac+b}}$ and predicted to occur at $\sqrt{\frac{a}{c}}$ month.

2. Functions termed “Linear cum log model” and “Quadratic cum log model” by Singh and Gopal (1982)

$$y_t = a - bt + c \ln(t)$$

$$y_t = a + bt + ct^2 + d \ln(t)$$

The two models were fitted to bi-weekly lactation records. The linear cum log model describes a linear declining function, $y = a - bt$ and an increasing function, $y = c \ln(t)$. The quadratic cum log model has an increasing function, $y = d \ln(t)$, while the function, $y = a + bt + ct^2$ is responsible for the linear decline. Peak yield was reported to occur at $\frac{-b \pm \sqrt{b^2 - 8cd}}{4c}$ week after calving. When fitted to Indian dairy buffalo records, it was reported to fit better than gamma, IP and linear cum log models.

3. Wilmink’s exponential model (Wilmink, 1987a)

$$y_t = a + bt + c \exp^{-0.05t}$$

4. A quadratic polynomial regression by Ali and Schaeffer (1987)

$$y_t = a + bt + ct^2 + d \log(t) + k \log(t)^2$$

5. A mixed log model by Gou and Swalve (unpublished)

$$y_t = a + b\sqrt{t} + c \log(t)$$

Catillo et al. (2002) fitted five linear or “linearized” models of lactation curve to Italian buffaloes with the intent of including these equations as covariates in TD models applied to genetic evaluations. The

models used include Wood's exponential model and Nelder's inverse polynomial, Wilmink's exponential, and Gou and Swalve's mixed log. The study indicated that Ali and Schaeffer's five-parameter model fitted bi-weekly buffalo lactation records consistently in all age groups although differences in goodness of fit measures were small among the models. However, like other polynomial models, the curve tend to turn upward rather than downward at the beginning and end of lactation indicating poor fit especially if the interval between beginning/end of lactation and test day is longer than 15 days (Flores, 2003). The incomplete gamma function and inverse polynomial were the more common equations used to model milk production. Some limitations reported are that milk production is forced to zero at DIM 0; milk production is overestimated in early lactation and underestimated at peak production; residuals are autocorrelated and model parameters are highly correlated (Scott et al., 1996). Model parameters that are highly correlated result in unstable models. Studies comparing different models in describing the lactation curve in dairy cattle have indicated the simplest functions were more robust (Tozer & Huffaker, 1999). For 305D milk yield prediction based on partial records, linearized Wood's model was compared with test interval method and was shown to have better performance (Congleton & Everett, 1980b). Criteria used for comparing the models were bias, $\frac{1}{m} \sum_{t=1}^m (y_t - \hat{y}_t)$ and mean square error (MSE), $\frac{1}{m} \sum_{t=1}^m (y_t - \hat{y}_t)^2$ where m is the number of observations, \hat{y}_t is the predicted yield for the day in milk t , and y_t is the actual daily milk. These criteria are often used when a non-linear fitting procedure is used. Comparison using adjusted squared correlation coefficient (R^2 adj.) was also used as criteria for goodness of fit with linear regression (Catillo et al., 2002; Olori et al, 1999). In this manner, models with different numbers of parameters could be compared directly. Other criteria include mean absolute value and distribution of residuals, defined as the difference between actual and predicted milk yield, and Durbin-Watson (DW) statistic. The Durbin-Watson statistic measures the presence of first-order autocorrelation in the unobserved errors of regression expressed on a scale of 0 to 4 (Foster et al., 1998). Values near 0 suggest positive autocorrelation, while values greater than 2 indicate negative

autocorrelation. However, this statistic is not a good indicator (inconclusive) when there are less than 15 data points and is therefore not good when fitting test day records. Assumptions in regression are that, residual errors are normally distributed, independent, with zero mean and equal variance. The presence of autocorrelation is a violation of one these assumptions. Plotting the residuals over time is one way of determining if residuals track over time if DW statistic was not determined. These should be randomly distributed about their mean. Hence, previous studies include residual mean and variance (Scott et al., 1996) as measures in assessing fit of the model and plotted over time (Olori et al., 1999). The correlation between residuals and actual yield was also calculated to determine the dependence of the residuals on level of production. The same authors (Olori et al., 1999) stated that the goodness of fit of a lactation curve model might depend on whether the objective is to predict the cumulative yield or individual daily yield. In prediction of cumulative yield, the magnitude of residuals is not important as long as they sum to zero whereas in predicting individual daily yield, the magnitude and distribution of residuals are important. To assess the performances of models in their ability to predict individual daily and total milk yield based on limited test day yields, mean square prediction error (MSPE) for each lactation was calculated and averaged for each model in the study of Ruiz et al. (2000). The best fitting model was selected to estimate the total milk yield. This was done by first fitting the model to test day yields of 30-d intervals to determine parameter estimates. The estimates were used to predict daily yields between intervals and summed up over a lactation to determine total milk yield. The residuals, determined as the difference between predicted and actual daily yields, were used to compute MSPE. In most studies comparing the performances of various models, those with more parameters will generally fit better and more consistently. In a more recent study, Koçak & Ekiz (2008) fitted several functions on milk yield records of Anatolian dairy cattle that included Wood's incomplete gamma function, Wilmink's exponential function and Nelder's quadratic polynomial. Lactation curve parameter estimates were significantly different between parities. The same study also reported that Ali and Schaeffer's five

parameter polynomial had the best fit in terms of root mean square error (RMSE), coefficient of determination (R^2) and difference between actual and predicted lactation yield. Lactation yield deviations were almost close to zero for all lactations using Ali & Schaeffer's, Wilmink's and Guo & Swalve's models. The RMSE and lactation yield deviations were not significantly different among the three models for all lactations indicating comparable performance with models having more parameters. Wilmink's and Guo & Swalve's model gave the best fit among the three parameter functions. Generally, three-parameter models did not fit as well as models with more parameters in the initial and late stages of lactation. However, the three parameter models were more robust, can handle varied conditions, and for 305D yield prediction, the magnitude of residuals may not matter much provided they sum up close to zero.

The shape of the lactation curve is also influenced by environmental factors. Cows in pasture-based dairy production systems that calved in spring were reported to have a "normal" curve, a peak followed by a slow decline. Autumn calving cows on the other hand, produced a different shape that was longer in length with a lower yield at peak lactation but higher yield at mid and late period (Garcia & Holmes, 2001). Keown et al. (1986) analyzed the effect of calving season on the lactation curve. Peak yield was reported to be lowest but persistency greatest in July to August and in the first versus later lactations. Peak yield was highest, but persistency the least, with January to March calving. Metry et al. (1994) reported that herd-year-season of calving significantly affected milk yield and persistency in Egyptian buffaloes consistent with those reported in dairy cattle. The lactation curve of winter calving cows differed due to changes in feeding regimen. The effect of age at first calving on mean milk yield was not significant though, contrary to what is reported in dairy cattle. On the other hand, Catillo et al. (2002) reported that there were significant differences in milk yield and shape of lactation curve among cows calving at different ages. Least squares estimate of test day milk yield was lowest for cows calving as 3 yr old or younger and maximum for cows calving at 4 to 5 yr of age. Production gradually declined

for older cows. These differences in estimated test day milk yield were also evident in the shape of the lactation curve. Initial and peak yield increased with age at calving. However, the rate of linear decline also increased with age. Younger cows had a flatter lactation curve suggesting more persistency; hence, even though cows calving at ≥ 6 yr had higher initial and peak yield than cows calving as 4 and 5 yr, their average milk yield was estimated to be lower due to faster rate of decline after peak production. Summer calving cows had significantly lower milk yield than winter calving cows and that was attributed to high ambient temperatures at this time of the year. They did not find any differences in the average shape of the lactation curves among cows calving at different season though, contrary to the report of (Metry et al., 1994). There were observed differences between parities in terms of the estimated parameters. Kellogg et al. (1977) reported that parameters **a** and **c** of Wood's incomplete gamma function were lower for first than subsequent lactations. In later studies (Congleton and Everett, 1980b), the incomplete gamma function was used to generate lactation curves from Holstein-Friesian lactation records. Factors that might have an effect on the estimated parameters, such as month of calving, days open, intra and inter-herd variations in cumulative yield, were analyzed by linear regression for the first, second and third lactations. Most variations in lactation curves were due to parameter **a**. Adjustment of this parameter made predictions of cumulative yield from partial records closer to observed yields than those generated by test interval method (TIM). These studies suggest that the shape of the lactation curve is influenced by environmental and physiological factors that should be taken into account in modeling lactation curve function. It may be possible to create groups of cows with similar curves depending on parity, age, season of calving, region or even management type.

The shape of the lactation curve is not only influenced by environmental factors, but genetic factors as well. Genetic parameters for factors that describe the shape of the lactation curve have been estimated in previous studies. Heritabilities for curve parameters of the linear cum log model reported by Singh and Gopal (1982) have been estimated (Sherchand, 1994). Parameter **d**, which is concerned

with increasing function, and parameter **b** had low heritability estimates at 0.08 and 0.04 respectively. Parameters **a** and **c** which are concerned with decreasing function had moderate heritability estimates, 0.27 and 0.21 respectively. This finding supports the view of Togashi and Lin (2004) that the shape of the lactation curve could be changed through selection. A cow with a flatter curve due to reduced rate of decline was said to be more persistent.

2.2.3 Linear Interpolation using Standard Lactation Curves (ISLC). The study by Koçak & Ekiz (2008), which compared various lactation curve functions, indicated that the fit of the three parameter models (Wilmink's and Guo & Swalve) were comparable in performance with models having more parameters and were more robust for 305D yield prediction. Methods for calculating lactation yields based on some lactation curve function that allow flexibility and missing test day measure compared with TIM have been accepted by ICAR in official milk recording. This include among others, interpolation of standard lactation curve (ISLC) using a standard lactation curve for a group of cows pertaining to certain class of herd-age-month/season of calving and yield trait utilizing Wilmink's model (Wilmink, 1987a). The curvilinear nature of lactation is better accounted for by non-linear functions than linear interpolation with TIM. Standard lactation curves for different classes were fit by Wilmink's function:

$$y_t = a + bt + ce^{-0.05t} + \epsilon$$

Where:

y_t = represent an average test-day production per herd

t = the number of days after calving

e = the base of the natural log

a, b, c = are parameters describing the lactation curve

ε = random errors

Predicting missing test day yields and projection to 305D is possible. The daily yields are predicted for fixed days of the lactation: day 0, 10, 30, 50 etc. Yield calculation is separate for milk and milk components. The cumulative yield is calculated as follows (ICAR, 2010):

$$\sum_{i=1}^n [(INT_i - 1) * y_i + (INT_{i+1}) * y_{i+1}] / 2$$

where:

y_i = the i^{th} daily yield;

INT_i = the interval in days between the daily yields y_i and y_{i+1} ;

n = total number of daily yields (measured daily yields and predicted daily yields)

The Netherlands use this method for yield calculation where monthly test day intervals have a length of ~20 days. However, few countries adopt interpolation of standard lactation curve (ISLC) for yield calculation.

2.2.4 Prediction of lactation yield by multiple trait procedure (MTP). Recent advances in computing consideration as well as variations in sampling protocols have brought about different ways of yield calculations. ICAR also recommends MTP developed by Schaeffer and Jamrozik (1996) to predict milk, fat and protein yields. This method is particularly suitable if there is data from only a few test day records. The methodology incorporates information about lactation curve function and covariances within and across milk, fat and protein yields in 305D yield calculation. Standard lactation curve for a group of cows pertaining to certain class of region, breed, lactation number, age and season of calving is modelled using Wood's exponential model:

$$y_t = at^b \exp^{-ct}$$

where:

y_t represents milk yield on day t after calving;

a is the initial milk yield;

b is the inclining rate of milk yield;

c is the declining rate of milk yield after peak production and

\exp is the base of natural logarithm.

The formula can be linearized by taking logarithms to $\ln(y) = \ln A + B \ln t - Ct$. Parameters a , b , c are estimated for each yield trait for each known cow class. Test day yields are weighted by their relative

variances, and standard lactation curves of cows from similar class for the estimation of lactation curve parameters for each cow. Schaeffer and Jamrozik (1996) details MTP calculations below:

The vector c for parameters to be estimated for one cow is:

$$c = \begin{bmatrix} \ln A_M \\ B_M \\ C_M \\ \ln A_F \\ B_F \\ C_F \\ \ln A_P \\ B_P \\ C_P \end{bmatrix}$$

and the data is in:

$$y_k = \begin{bmatrix} \ln(y_{Mk}) \\ \ln(y_{Fk}) \\ \ln(y_{Pk}) \end{bmatrix}$$

The parameters are solved using the model: $y_k = X_k c_k + e$ hence,

$$X_k = \begin{bmatrix} 1 & \ln t & t & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & \ln t & t & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & \ln t & t \end{bmatrix}$$

The solution is a generalized least squares estimate:

$$\hat{c} = (X'R^{-1}X + G^{-1})^{-1}(X'R^{-1}y + G^{-1}c_0)$$

where:

$$R_k = \begin{bmatrix} r_{MM^t} & r_{MF^t} & r_{MP^t} \\ r_{MF^t} & r_{FF^t} & r_{FP^t} \\ r_{MP^t} & r_{FP^t} & r_{PP^t} \end{bmatrix}$$

where:

$$X'R^{-1}X = \sum_{k=1}^n X_k' R_k^{-1} X_k$$

$$X'R^{-1}y = \sum_{k=1}^n X_k' R_k^{-1} y_k$$

and R_k would be determined by:

$$r_{ij}(t) = \beta_{0ij} + \beta_{1ij}(t) + \beta_{2ij}(t^2)$$

where:

M, F, P , represents milk, fat and protein respectively

Vector c is to be estimated from test day records

c_0 represent corresponding curve parameters estimated across cow-class similar to the cow in question

y_k = vector of natural logarithms of the yield traits on test k at day t of the lactation

X_k = the incidence matrix

n = number of test days for that cow

R_k = is matrix of order 3 that contains variances and covariances among test day yields on test k of the lactation at day t of the lactation

G = is a 9x9 matrix containing variances and covariances among the parameters in c and represents the variation between cows in these parameters which include genetic and permanent environmental effects

MTP, like ISLC, can predict 305D yield from partial records, thus, a separate procedure for extending part lactation using extension factors is no longer needed unlike that of TIM. It was reported that the accuracy of the MTP is the same as that of TIM with more records but may be higher than TIM with less number of test day records. Milk fat and protein yields can still be predicted with higher accuracy even if some test day yields are missing maybe due to covariances among the three traits. Furthermore, MTP can accommodate long intervals between test days, unevenly spaced test day measurements, milk only test day data and less number of test day record in making 305D prediction better than TIM. Yield calculation using TIM may become erroneous if test intervals are not close to 30-days, hence, MTP is more advantageous in this aspect. Lactation curve parameters for each cow can be obtained even with only one test day record. Due to the flexibility of MTP, this will suit situations where organizational structure, resources and manpower for conducting official milk testing are less ideal as should be as cows may be tested less frequently than the standard A4 method, a 2x-a-day AM-PM 4-week interval test plan. This will be very ideal in the current situation in the dairy buffalo sub-sector in the Philippines. A study compared the accuracy of predicting 305D milk yield using TIM, MTP and Best Prediction (BP) (VanRaden, 1997) in Japan Holstein cattle population (Hagiya et al., 2004) using test day records from 771 first lactation cows. It was reported that the use of MTP that incorporates Wilmink's model to

describe the lactation curve had better accuracy over that of MTP that incorporates Wood's model or Best Prediction (BP). Legendre polynomials were also used to model the lactation curve of Black and White cows in Poland (Ptak et al., 2004) in one study. It was reported in that study that with MTP, the use of Legendre polynomials had better performance compared with Wilmink's and Ali and Schaeffer's curve function except when fitting protein lactation curves. The study also looked at the accuracy of predicting 305D lactation yield from part lactation with lactation length of 60, 100 and 200 days. The authors reported that the accuracy of predicting 305D yield from part lactation using MTP is best if part lactation is 200 days or longer. It is therefore important that the mathematical function to use in this procedure is the one that best describes the lactation curve of the various cow-classes in the population. The same may also be true when we try to fit lactation curves of dairy buffaloes.

2.2.5 Best Prediction (BP) model. The move to use other methods for yield calculation is due to proliferation of various milk testing plans other than the standard A4 method. Best Prediction (BP) is a computational method derived from selection index theory. It is almost similar to MTP as the procedure also takes into consideration covariances between test days and between milk, fat and protein yields but without the lactation curve function. VanRaden (1997) states that test day yields are assumed to have a multivariate normal distribution, and it assumes that variances and means are known and they can be combined into a 305D yield by best prediction. The selection index procedures can be used to predict missing test day measures from their covariances with the measured test day yields. VanRaden (1997) details the formula as:

$$\hat{y} = \mu + c'V^{-1}t$$

where:

\hat{y} = the mean 305D yield

μ = mean 305D yield

c = covariance between lactation and observed test day yields for single trait

V^{-1} = inverse of the variance for observed test day yields for single trait

t = test day deviations

Dimensions of \mathbf{t} and \mathbf{V} are usually <30 with multi-trait prediction and <10 with single-trait prediction of 305-d yields for milk, fat, or protein based on a maximum of 10 test days per lactation. Single trait prediction can be done for single traits or multivariate for more than one trait which was reported to be more accurate especially if there are missing component samples. Lactation to date, 305D, 365D and projected yields are possible. Adjustment factors for the first, peak and last test day and for projecting part lactations used with TIM is no longer needed with Best Prediction similarly with multiple trait procedure. With short lactations, MTP and BP have distinct advantage over TIM due to inclusion of covariances among test day yields in prediction.

The accuracy of BP and MTP has been compared in Japanese Holstein cattle by Hagiya et al. (2004). MTP was reported to have better performance than BP if Wilmink's model was used in MTP as against other lactation curve functions. This finding suggests that the choice of lactation curve model that could adequately describe the various shape of the lactation curve of different cow-class groups is critical to achieve better accuracy. A distinct advantage of using MTP over BP is that other information that could possibly be useful to the farm manager can be derived from MTP, such as prediction of peak yield and day of peak yield using individual cow lactation curve parameters. Nutritionists will find this useful in formulating ration for high yielding and lower yielding cows. Lactation curve parameters can also be used in genetic evaluation to select for persistency as it has been shown in previous studies that it is possible to select for persistent cows.

2.2.6 Production index. Recent developments in genetic evaluation system use the test day yields directly in analysis rather than the 305D lactation measure. These are test day models and in particular, random regression test day model estimates lactation curve parameters and a bull's future daughters' lactation curves are predicted from these parameters. This renders a standard 305D ME lactation

measure unnecessary for genetic evaluation if test day models are used. However, standardized lactation measure also has uses other than for genetic evaluation. Farm managers, veterinarians, nutritionists, industry monitors and other researchers still need to have a means by which cows' lactation measure can be compared fairly for a variety of purposes. The availability of alternative methodology for calculation of lactation yields, such as ISLC, MTP and BP that can accommodate various milk sampling schemes, may potentially reduce labor and milk-testing cost without sacrificing accuracy in prediction and will benefit the dairy industry, be it cattle or buffaloes.

2.3 Standardization of lactation yields.

Once the lactation yield has been calculated using the methodology/ies described above, there is another step that needs to be done prior to use of lactation records for genetic evaluation. Lactation yields are standardized to a uniform length and adjusted to mature equivalent so that cows can be compared fairly. This is because in predicting genetic merit of individual animals, non-genetic systematic environmental effects that influence milk production must be removed. A standard lactation measure for dairy cattle is 2x-a-day ME 305D yield while that of a dairy buffalo is a 2x-a-day 270D yield.

2.3.1 Extending /projecting lactation yields to 305D. Extending or projecting yields to 305D is done for on-going part lactations, for cows leaving the herd prior to lactation termination or discontinuation of testing. Records are standardized to a 305D length such that cows that have started lactations but not completed can be used in genetic evaluation. If standardization of lactation length is not done, this creates bias in genetic evaluation for sires whose daughters have short lactation or incomplete lactations. Thus, main reasons for standardization of lactations into a single length would be so that cows may be compared fairly; reduce bias in evaluating genetic merit of sires and earlier data on bulls' progeny, potentially reducing generation interval (Miller et al., 1972). Inclusion of extended part lactation will result in higher estimates of heritability and repeatability (Wilmink, 1988a; Norman,

Dickinson & Wright, 1985). Various methods to extend part lactation include ratio factors (Cilek & Tekin, 2006), single regression, multiple regression and factor analysis. Factor estimates of the proportion of part to whole lactation requires estimates with weighing ratio based on correlation between part and whole lactation increases the accuracy. The use of regression is more commonly adapted to extend part lactation to 305D. Multiple regression and factor analysis utilizes all test day information while single regression utilizes only the last test day information (Miller et al., 1972). The accuracy increases by incorporating herd means in predicting the unknown part of the lactation (Wilmink, 1987a). However, single regression is much simpler and needs less data to be stored in order to compute for the remaining unknown portion of part lactation. This might be the reason why DHIA has adopted a single regression with slope and intercept in extending part lactations to 305D. Lactations 155 days or shorter also incorporate mature equivalent herd means in the equation. The formula that DHIA adopted is as follows (Wiggans & Dickinson, 1985):

$$\hat{Y}_{305} = Y_{DIM} + (\hat{Y}_D)(305 - DIM)$$

where:

\hat{Y}_{305} = predicted 305D yield

Y_{DIM} = yield for partial record

\hat{Y}_D = estimated average daily yield for the remainder of the lactation

(305 – DIM) = days remaining

\hat{Y}_D is estimated as :

$$\hat{Y}_D = [\alpha_s + \beta_s(DIM)](Y_s) + \alpha_F + \beta_F(DIM) - \text{if part lactation is longer than 155 days}$$

$$\hat{Y}_D = [\alpha_s + \beta_s(DIM)](Y_s) + \frac{\alpha_F + \beta_F(DIM)}{1000} (Y_H) - \text{if part lactation is shorter than 155 days}$$

where:

Y_H = is mature equivalent herd average yield

Y_s = sample day yield

$\alpha_s + \beta_s$ = sample day intercept and slope

$\alpha_F + \beta_F$ = factor intercept and slope. Factors for class of cows based on season of calving, parity number region of country and breed. Separate factors are developed for milk and fat.

Fat yield utilizes the same formula but have different factors for cow class and sample yield. Calculation of projected protein yield is almost similar to the formula above but factor is a function of days in milk:

$$F_p = a_1 + a_2(\text{DIM}) + a_3(\text{DIM}^2)$$

$$\hat{Y}_{305} = Y_{\text{DIM}} + \left(\frac{P\%_{\text{LS}}}{100}\right) (F_p)(\hat{Y}_R) = \text{if lactation is 240 days or longer}$$

$$\hat{Y}_{305} = Y_{\text{DIM}} + \left(\frac{\overline{P\%}}{100}\right) (F_p)(\hat{Y}_R) = \text{if lactation is shorter than 240 days}$$

where:

F_p = protein factor

a_1, a_2, a_3 = are estimated coefficients

$P\%_{\text{LS}}$ = is last sample day protein percentage

\hat{Y}_R = estimated remaining milk yield

$\overline{P\%}$ = average protein percentage of test days so far

The method of Miller et al. (1972) in deriving extension factors based regression on last test day yield is simpler, termed "Method P". The procedure was reported to be equally precise using multiple regression on all known test day yields:

$$y_t = y_n + \bar{y}_{t-n} + \beta_{(t-n)x}(x - \bar{x})$$

where:

y_t = estimated total lactation yield

y_n = sum of the total production for the first n months

\bar{y}_{t-n} = population mean for the unknown segment of lactation

x = is some function of the n known test day yields

\bar{x} = is the population mean of x

$\beta_{(t-n)x}$ = is the appropriate regression of the yield from the unknown portion of the lactation on x

Calculation of milk and component yields are dependent on herd means, which are influenced by several environmental and non-genetic effects, such as region, season of calving and herd. Thus, it is necessary that factors to be used are derived from the target population of interest.

The methodologies for extending part lactations mentioned above are needed if lactation measure is calculated by TIM. The use of extension factors to project part lactation to uniform length of 305D is no longer necessary if methodologies in calculating lactation yields, such as ISLC, MTP and BP, are used giving these methodologies distinct advantage over TIM in terms of accuracy in calculation and standardization of lactation yields.

Some major buffalo-rearing countries, like India and Pakistan, do not adhere to the 270D standard lactation length but instead use 305D lengths (Gandhi, 2003; Khan et al, 2005). In fact, Italy is the only country that adopted the 270D standard lactation length. Parameter estimation for milk, fat, protein and mozzarella yields of Italian buffaloes by Rosati and Van Vleck (2002) used lactation records standardized to 270D. On the other hand, most genetic evaluation work on dairy buffaloes truncate lactation length to 305D but do not project short or part lactations to 305D (Aspilcueta-Borquis et al, 2010a). The same is true when lactation records of dairy buffaloes in the Philippines are analyzed. These are truncated to 305D, but short or part lactations are not projected. Studies to derive extension factors in buffaloes similar to Shook factors may be limited if not lacking. Tonhati et al. (2004) published correction factors to adjust lactation length in Brazilian dairy buffaloes but these are only to predetermined lengths of 90D, 240D, 270D and 305D. The methodologies for extending part lactation used in dairy cattle mentioned above may most likely be applicable to dairy buffaloes as well. There have been no reported studies on dairy buffaloes that compared the estimation of genetic parameters and breeding value prediction using adjusted and unadjusted lactation measure to see if there are significant differences in the values parameters estimated and if the use of projected lactation yields would result in re-ranking of bulls' estimated breeding values.

2.3.2 Age-month of calving adjustment of lactation yields. After calculating part and whole lactation yields, the next step in standardizing lactation measure is to adjust these for age and month of

calving. Lactations normally increase and reach maximum production at maturity. Production gradually goes down as the cow ages further. Because of this, younger cows may be unfairly compared with older cows within the same parity effect. Effect of age on milk production is larger with younger cows while month of calving is more important for older cows (Khan & Shook, 1996; Keown & Everett, 1985). The average age-month class when maximum production is achieved is normally determined to be the mature age of the cow and lactation yields are adjusted to this age-month class. Thus, a young cow's adjusted lactation yield is its production had the cow calved at mature age. It was reported that factors developed for age-month adjustment needs to be re-estimated periodically on at least a regional basis as production potential of cows change over time due to selection, changes in management and feeding, and rate of maturity in different regions (Khan & Shook, 1996). Age adjustment factors can be additive, multiplicative or both. The U.S. DHIA use multiplicative adjustment factors in adjusting yields to mature equivalent. Adjustment factors to adjust for age and month of calving can be additive or multiplicative. Age-class solutions (adjustment factors) to milk yield are usually obtained using mixed model equation (Everett et al., 1982), the animal model (Khan and Shook, 1996; Mostert, Theron, & Kanfer, 2001), or the repeatability model (Wilmink, 1987b). Results of these studies found that separate factors should be obtained for different parities. The solutions to age-class were used to derive adjustment factors. Khan and Shook (1996) details the calculation of adjustment factors as:

Additive correction factor: $a_j = c_o - c_j$

Multiplicative correction factor: $m_j = (\mu + c_o) / (\mu + c_j)$

Combination correction factor: $Y_{jn}^* = Y_{jn} + \lambda(m_j Y_{jn} - Y_{jn}) + (1-\lambda)a_j$

where:

a_j = is the additive correction factor

c_o = is solution for the base class of age, lactation, season and period

c_j = is solution for class j of age, lactation, season and period

m_j = multiplicative correction factor

μ = is overall mean

Y_{jn}^* = is the adjusted milk yield

Y_{jn} = is the uncorrected milk yield

λ = is the relative weight of multiplicative adjustment

The decision on the use of additive or multiplicative adjustment factors may depend on the population concerned. Additive adjustment factors affect only means for age and season, but multiplicative adjustments also modify variances in proportion to the square of the adjustment factors hence, Khan and Shook (1996) compared additive, multiplicative and combined additive and multiplicative factors for adjusting lactation yields to mature equivalent yields. The authors reported that the combination of multiplicative and additive adjustment factors was optimal in minimizing heterogeneity (variation) of standard deviations within age-class. Their study pointed out that the prediction of genetic merit is sensitive to the kind of adjustment method used. Multiplicative adjustment of milk yield was reported to bias the estimates of good sires upward and poor sires downwards. This might be because low-yielding cows are under corrected while high-yielding cows are overcorrected and that this observation affects young sires more. Thus, in their study, additive adjustment factors are recommended for first, second and third parity as variation in standard deviation was minimal with the use of additive adjustment factors. On the other hand, multiplicative adjustment factor was recommended for parity 4 and 5. The various studies on age adjustment suggest that a single set of adjustment factors cannot adequately address different cow-class groups. Factors may need to be estimated separately within each age groups in each parity and that both additive and multiplicative factors need to be investigated. The optimum adjustment factor therefore, may differ among various dairy populations and thus have to be derived separately. It is recommended that age adjustment factors be continuously re-estimated (Wilmink, 1987c; Keown & Everett, 1985).

The use of age-month adjustment factor to standardize lactation yields to mature equivalent or standard age prior to genetic evaluation is not universally used or reported in recent works done on dairy buffaloes. The effect of age on lactation yield is accounted for in the genetic evaluation model with

age of cow at calving as linear and quadratic covariate (Tonhati, et al., 2004). There is also no age adjustment factor being used on lactation records of dairy buffaloes in the Philippines and the same procedure as Tonhati et al (2004) is being done in analysis as well. Again, there have been no studies to compare the use of age adjusted and unadjusted lactation yields in genetic evaluation and its effect on ranking of bulls. The method of adjusting age-month effect impacts the accuracy of genetic evaluation as well as ranking of cows in production index being used by farm managers for decision making in the herd.

2.4 Genetic evaluation models in dairy cattle and buffaloes

As mentioned earlier, any farm owner and breeder would like to rank animals based on genetic merit or “true” breeding value. However, we cannot determine true breeding value but can estimate this breeding value based on observed/measured phenotype or animal performance. Other than the measured performance of an animal, we can also draw upon the information from the animal’s parents, siblings and other relatives. Thus, the correct measurement and recording of animals’ performance record is very critical in estimating animals’ genetic merit. The standardization of lactation measure, as detailed in the previous paragraphs above, is a means by which bias is minimized. If non-genetic effects, such as age and month of calving, are not adequately corrected, cows may not be compared fairly and bulls’ breeding value and eventual ranking may be affected. Good animal recording goes hand in hand with a suitable genetic evaluation model in any animal breeding program. Estimation of genetic merit utilizes a statistical procedure that is able to provide a Best Linear Unbiased Prediction (BLUP) of breeding values (Henderson, 1974). This procedure is a linear model that is able to simultaneously estimate systematic environment effects (fixed effects) and predict genetic merit of animals (random effects). By having both fixed and random effects, the linear model is essentially a mixed model. Accounting for fixed effects that influence measurement is important as breeding value estimation will be biased by these effects. This is particularly useful if data is not balanced as what is commonly seen in

practice or in the field. The use of BLUP linear models in animal breeding was first seen in evaluating dairy bulls' genetic merit (Mrode, 1996) but has now evolved into more complicated models especially with the increase in computing capacity. The basic mixed model is given as:

$$y = Xb + Zu + e$$

Where:

y = is the vector of record of animals or observations

b = is the vector of identifiable environmental fixed effects such as herd management, sex, year of birth, season of calving, etc.

u = is the vector of random additive genetic effects

e = is the vector of random residual effects

X and Z refer to incidence matrices relating to fixed and random effects, respectively

BLUP has selection index properties and works as a linear model that utilizes all information from all possible relatives and correlated traits and proper weights on information used when estimating breeding values of animals. Besides accounting for fixed effects that might create bias in breeding value prediction, BLUP also accounts for culling, selection across generations and non-random mating due to accounting of relationship of animals with each other included in the analysis through the relationship matrix (A). Animals can be compared across herds with proper linkage and genetic trends can be estimated.

The most commonly used model in various livestock industries is the animal model. Unlike the sire model wherein only the sires are given breeding values and the dam side is ignored, the animal model has the ability of simultaneous genetic evaluation of male and female animals with pedigree records. The simple animal model can be expanded to incorporate random maternal or permanent environment effects for single trait or multiple traits (Quaas & Pollak, 1980). The model has been applied on several domestic livestock species, such dairy and beef cattle, sheep, goats and buffaloes. With proper sire linkage in different herds, animals can be compared fairly across herds. Animal models

can utilize standardized 305D lactation measure or use test day yields directly rather than summing these test day yields into a single 305D measure.

2.4.1 Analysis of 305D lactation records. In dairy cattle, production traits included in genetic evaluation reported are 305D milk yield, fat yield, protein yield, milk fat percentage and protein percentage. Other traits that are correlated or otherwise support production that have been analysed using an animal model separately or together with milk production traits include somatic cell count (Norberg et al., 2009), functional/type traits (Tarres et al., 2009), and fertility traits (Liu, et al., 2008; Weigel & Rekaya, 2000) such as 60D and 90D non-return rate, calving to first service interval, confirmed pregnancy rate at 60D and 90D.

The model for analysing lactation data can be a single-trait repeatability model wherein 305D lactation measures from different parities are considered repeated measures of the same trait, e.g., fat yield. The milk production traits can then be combined into a multiple trait model with repeated measures from different parities. Lactation measures from different parities can also be analysed as separate traits altogether. The genetic evaluation for milk production traits of dairy cattle in the U.S. is best described by a paper by Wiggans et al. (1988) of the Animal Improvement Program Laboratory of the U.S. Department of Agriculture Agricultural Research Service (AIPL, 2010). The model for genetic evaluation is a single-trait BLUP repeatability animal model with three random effects: animal additive, permanent environment and herd x sire interaction. Traits analysed include milk (yield), fat (yield and percentage), and protein (yield and percentage). Records up to five parities are included in the analysis. Pre-adjustment (multiplicative) of records for age and month of calving, number of times milked, previous days-open and heterogenous variance are done. Among the pertinent fixed effects included are: herd-year-season management group, registry status for Holstein, parity x age, regression on

inbreeding and general heterosis, among others. Estimated breeding values from the production trait group are then combined with EBVs from other traits into a Total Merit Index.

Only a few studies have reported on procedures for genetic evaluation and parameter estimation in dairy buffaloes. Studies on parameter estimation and genetic evaluation in dairy buffaloes used repeatability animal model and restricted maximum likelihood (REML) for parameter estimation. The earlier work by Tonhati et al. (2000) is a multi-trait animal model that involved production (milk yield, lactation length) and reproductive traits (calving interval, age at first calving) in Brazilian dairy buffaloes. Work on dairy buffaloes in Pakistan (Thevamanoharan et al., 2001) was also done almost similarly using the same model and REML for parameter estimation but involved more traits, e.g. 305D milk yield, total milk yield, lactation length, dry period, service period, gestation period and calving interval. The inclusion of milk fat and protein percentage and yield was first reported by Rosati and Van Vleck (2002) working on Italian buffaloes. Their work also involved estimating heritability estimates for mozzarella yield. Calculation of mozzarella yield is a function of milk yield, milk protein percentage and milk fat percentage. Thus, use of mozzarella yield as a trait optimally puts selection pressure on milk yield, fat and protein percentage. Milk yield and protein percentage have greater influence on mozzarella yield. All milk produced from Italian buffaloes is almost exclusively made into mozzarella cheese or some other kind of cheese, hence, the impetus to select animals based on mozzarella yield. Estimates of heritability for milk, fat and protein yields were reported to be 0.14, 0.11 and 0.14, respectively.

Relatively small data set for analysis is a common issue in dairy buffaloes' studies with records numbering only in the thousands (approx. 1,000 – 5,000). Small contemporary group size is also often encountered. In 2010, the genetic parameters for somatic cell count in dairy buffaloes were first reported in a work by Aspilcueta et al. (2010a). The study also included Fat%, Protein%, milk, fat and

protein yields of Brazilian dairy buffaloes. The analysis used a repeatability animal model and parameters were estimated by Bayesian inference via Gibbs sampling. The authors mentioned that for small data set, Bayesian methods may be better as negative estimates of variance (non-positive definite covariance matrices) may occur with REML or ML. Gianola and Fernando (1986) cited Lehman in that ML or REML have no “small sample” justification. Furthermore, the authors wrote that with Bayesian methodology, because the data are based on posterior distribution, inferences are exact for any sample size, be it large or small. But, the problem with small data set is that the posterior depends quite a bit on the prior (assumption). Estimates of heritabilities reported by Aspilcueta et al. (2010a) for milk, fat and protein yield using Bayesian inference were 0.22, 0.21 and 0.23, respectively. Work that combines milk yield with reproductive traits in a multi-trait model (calving interval, age at first calving) on the same population of Brazilian buffaloes was reported in the same year but parameter estimation was done using REML (Seno et al. 2010).

Almost all the genetic evaluation and parameter estimation work reported on dairy buffaloes using 305D lactation measure do not project part lactations but nevertheless truncate to standard 305D lactation length without correction for lactation length. Records less than 90D (Seno et al., 2010; Aspilcueta-Borquis et al., 2010a), 120D (Rosati & van Vleck, 2002) or 150D (Thevamanoharan et al., 2001) are discarded from the analysis. Records of Italian buffaloes more than 120D in lactation are nevertheless projected to a standard 270D length. Pre-adjustment of lactation yield or test day yield are done for systematic environment effects such as age-season of calving (2 seasons), previous days open or stage of lactation, among others. Eliminating short lactations may cause upward bias for some sires if their daughters with short lactations are not included in the analysis. The effect of age at calving on yield is accounted for in the model by putting age of cow at calving as covariate (linear and quadratic). It may be worthwhile to investigate if pre-adjustment of records prior to analysis could increase estimates of genetic parameters or their accuracies. There have not been any studies on multi-trait evaluation that

includes milk production and fertility traits except the one reported by Seno et al. (2010), but the analysis did not include milk component yields. Studies on lactation persistency in dairy buffaloes is also lacking even though lactation lengths are quite short. Dairy buffaloes in the Philippines are evaluated and ranked on the basis of first lactation yield alone. Although milk fat and protein test day yields are already available, the number of records is small and has not been analyzed. Estimation of parameters in a multi-trait model together with milk yield and fertility traits for Philippine dairy buffaloes has not been done and needs to be investigated.

2.4.2 Analysis of test day records. The use of test day records directly rather than standardized 305D lactation records in genetic evaluation has been developed. The paper by Bilal and Khan (2009) gives a good description of the development of a test day (TD) model for genetic evaluation of dairy cattle and summarizes the salient points of the various TD models. The use of test day record directly has advantages over that of 305D lactation records. Test day yields are affected by systematic environmental effects on the test day itself and test day measure but accounts for these more accurately on each test day compared with that of the 305D lactation record as there is no averaging of the effects over the entire lactation. Also, those test day effects can change over time. Fixed effects, such as herd-test day (HTD), parity and days in milk, are modelled directly. As test day measure is used directly rather than aggregating these into a single measure, there is no need to adjust or standardize lactation yields to 305D. Instead of a single lactation measure, more information (test day yields) is available maximizing information available per animal for genetic evaluation, increasing the accuracy of prediction. The test day model allows flexibility in recording scheme as it can handle varying intervals between test days; varying number of test day record; milk only records or milk with milk fat and protein percentage recorded, coming into the evaluation with appropriate weight by considering covariances among test day yields. It was reported that there is a 4% - 8% increase in accuracy from using test day yields in genetic evaluation over that of 305D yields (Schaeffer et al, 2000). The authors

also mentioned that persistency can be estimated genetically. As even few test day records can be used for evaluation, an animal can be evaluated earlier, thus, potentially increasing rate of genetic gain. However, with projection of part lactation yields to 305D, an animal can also be evaluated earlier with an animal model using 305D lactation yields. Swalve (2000) presented a summary on computational methods for various test day models. There are two ways by which test day yields are used in a model. The first is a TD model with a fixed regression (FRM) on days in milk. It is a repeatability model wherein test day yields from the same lactations are treated as repeated measures of the same trait. The permanent environment effect is fitted to account for the similarities among test day yields within the same lactation. Pre-adjustment of records are done on test day yields prior to use, such as age, days in milk, month of calving and pregnancy status, among others. This model assumes that covariances are the same with regard to days in milk. The basic model in scalar notation as cited by Swalve (2000) is:

$$y = \text{HTD} + \sum b_i x_i + a + pe + e$$

where:

HTD = fixed effect of herd-test-day

a = is random animal genetic effect

pe = permanent environment effect

e = residual term

$\sum b_i x_i$ = lactation curve function to fit several coefficients of fixed regression of yield on DIM

It was emphasized that the fixed regressions should be nested within cow-classes that have similar lactation curves and that heterogeneity of residual variance should be accounted for. The model can be extended into multiple traits wherein parities are considered separate traits.

The U.S., as cited by Swalve (2000), has adopted a two-step TD model beginning in 2000 wherein TD records are pre-adjusted for age-season, previous days-open, milking frequency, stage of lactation, age at milking and days pregnant. TD records are pre-adjusted and then used to derive 305D lactation measures and finally breeding value estimated using BLUP animal model procedure as

described section 2.5.1. This process takes advantage of the fact that a systematic environmental effect is better accounted for using test day yields. This two-step procedure is recommended for countries that did not have previous TD records stored but would like to shift to TD model to avoid drastic changes in ranking of animals with the shift.

2.4.3 Random Regressions (RR). Further development in test day modelling was proposed by Schaeffer and Dekkers as cited by Swalve (2000) wherein a fixed regression are used to account for the shape of the lactation curve of cows in the same cow-class groups and individual cows' animal genetic and permanent environment effects is accounted for by random regressions. This permits individual cows to deviate from the standard lactation curve and permits covariance structure among regression coefficients. Functions used in various studies to model the shape of the lactation curve include, among others, Ali and Schaeffer's curve, Woods's model and Legendre polynomials (Swalve, 2000; Guo et al., 2002). Canada formally shifted from a single-trait repeatability animal model to multiple-trait random regression test day animal model in 1999 (Schaeffer et al., 2000) using Wilmink's function to model the shape of the lactation curve both for fixed and random regressions. In scalar notation, the model is given as:

$$y = HTD + \sum bz + \sum az + \sum pz + e$$

where:

y = test day record

HTD = fixed herd test day effect

z = are covariates associated with days in milk

b = are fixed regression within region, age and season

a = random regression genetic coefficients specific for each animal

p = random regression coefficients for the permanent environment effect for each cow

e = residual effect for each cow

The model includes 4 milk traits (yield, fat and protein yield, somatic cell count) and 3 lactations. Thus, there are 12 traits with test days within lactations. The covariance matrices are of the order 36 (12 traits

x 3 parameters of the sub-model). Random regression test day models become computationally demanding as there are more parameters to be estimated compared with 305D lactation animal model and the fixed regression test day model. The fit of random regression models is better with higher order functions, such as 4th, 5th or 6th order Legendre Polynomials, as these can better describe the shape of the lactation curve but increases further the number of parameters to be estimated especially so as (co)variances are needed at least for residual and animal genetic effects, making the model more computationally demanding. Several methodologies have been presented to model the variance-covariance structure and estimate parameters (Bilal & Khan, 2009; Sawalha et al., 2005). Jensen (2001) states that covariance functions can be estimated by generalized least squares. But coefficients can also be estimated directly from the data using restricted maximum likelihood (REML) as described by van der Werf, et al. (1998).

Test day models have also been applied to dairy buffaloes' milk yield traits. Aspilcueta-Borquis et al. (2012a) described a random regression test day model for analyzing milk yields using Legendre polynomials (LP) to model the additive and permanent environment effects while (co)variance components were estimated by REML. Fifth and sixth order LP for additive and permanent environment random effects and a step function with six classes for residual variance was adequate model to describe the covariance structure. The use of six classes for residual variance was important to account for heterogenous residual variance (V_e) across lactation. However, their results reported negative genetic correlations between the middle of lactation and the beginning and end of lactation. This observation was supported by the report of Strabel & Jamrozik (2006) wherein they mentioned that random regression models may perform poorly in estimating dispersion parameters at early and late stages of lactation and could have negative genetic correlations or unreasonable high estimates of daily variances and heritabilities. The use of higher order polynomials creates strange variances "at the edge" (Meyer, 2005). It could also be that such observations could be due to lack of information to properly

describe variability, especially at the end of lactation (small number of records). Thus, the RR test day model may not be advisable for use with small data set. However, the use of RR TDM applied on tropical milking Criollo cattle with 15,377 test-day records from 1,438 lactations (356 first lactation, 282 second, 238 third, and 562 \geq fourth lactation), of 467 cows has been reported. Legendre polynomials and Wilmink's function was used to model the random coefficients. Estimates of correlations and heritabilities were variable depending on the lactation curve function used but negative genetic correlations were not reported at the extremes of lactations perhaps because only lower order polynomials were applied. Fitting RR test day model in small data set may be possible but there are compromises, such as the use of lower order polynomial.

2.4.4 Analysis of lactation persistency. One main advantage of a test day model is that lactation persistency of individual cows can be evaluated using the parameters of the lactation curve function. Previous studies have shown that curve parameters can be influenced by genetics (Sherchand, 1994). A cow with good lactation persistency is characterized as having a slow decline in milk production after the peak has been reached. Cole and Null (2009) citing Dekkers, et al. (1997) note that average cows with higher persistency are more profitable when yield and persistency are correlated and that the difference between a persistent and non-persistent cows is small unless reproductive performance is poor. There are other benefits to having good persistency. Persistent cows have flatter lactation curves and lower peak yield that occur at a later stage in lactation. A flatter curve requires less energy at the beginning of lactation. This reduces the negative energy balance that cows experience during peak lactation and thus, there is less metabolic and health problem encountered. It follows that high yielding but less persistent cows are more likely to suffer from metabolic problems. Harder et al. (2006) did report that there is a favourable correlation between persistency and health traits. However, metabolic disease is unfavourably correlated with persistency; thus, reports are conflicting in this aspect. Nevertheless, with the hypothesis that persistent cows require less energy at the beginning of lactation

due to a lower and later occurring peak, cows are more likely to come into heat and get pregnant earlier post-partum. Such are the reasons that authors reported favourable correlations between persistency and some measure of fertility traits, such as 56D non-return rates (Muir et al., 2004). But, selection for milk yield invariably selects for cows that peak high, hence, the observed deterioration of fertility performance. This is because genetic correlation between 305D milk yield and peak yield has been estimated at 0.91 (Ferris et al., 1983). Nevertheless, it has been shown that cows can be selected for persistency and this can be included in routine genetic evaluation programs. Heritabilities and genetic correlations with milk yield, fertility and health traits have been estimated (Cole & Null, 2009; Verbyla & Verbyla, 2009; Cole & VanRaden, 2006). Genetic correlations among yield traits and persistency are low to moderate.

There are various methods or ways to estimate persistency. It can be expressed as ratios of partial yields and total yields, normally the first trimester divided by the total yield. More common are measures associated with the shape of the lactation curve. It can be the difference between peak yield and yield at some arbitrary day later in lactation ratios of yields, i.e. rate of decline. Yields at these particular day can be derived from the parameters that describe the shape of the lactation curve of individual cows. Wood's, Wilmink's and Legendre polynomials are the most common models used. Using Wood's model, Schaeffer and Jamrozik (1996), defined persistency as the difference in yields between 60D and 280D estimated based on lactation curve parameters and deviated from cow class standard that the cow belongs to and multiplied by 110. The authors report that this measure of persistency is free of the absolute yield of the cow unlike ratios of yields hence, is less correlated with yield. Almost the same methodology was adopted by Pryce, et al. (2010) wherein in two of the lactation persistency measures they used was to take the difference in yield between 39D and 235 (for P1) and 54D and 274 (for P2). P1 approximates the day of peak yield whereas P2 approximates the initiation of decline after

peak. The third measure of persistency, P3, used the methodology of best prediction as described by VanRaden (2006)

$$\sum_{d=5}^{300} (D_d - D_0)(\mu_d - \mu_0)$$

where D is a vector whose elements represent yield at day D of lactation, D_0 is the tipping point so that the covariance between P3 and milk yield is uncorrelated, $D_0 = \frac{dV1}{1'V1}$, matrix V accounts for the changing phenotypic standard deviations and covariance across lactations. Tipping point was determined to be at 128D, 146D, 135D and 155D for milk, fat, protein and SCS, respectively. Verbyla and Verbyla (2009) described the use of natural cubic smoothing spline and allowed for the day of peak yield to vary among individuals. The difference between peak yield and yield at the end of lactation (305D) was taken. Togashi and Lin (2006a) used eigenvectors derived from the random regression coefficient matrix. Cole and Null (2009) mentioned that use of eigenvectors has no biological meaning. The same authors used best prediction (BP) as described by VanRaden. Earlier work derived factors or parameters related to the lactation curve. Macciotta et al. (2004) used factor analysis to extract factors representing measures for the increasing rate of yield at the initiation of lactation and the decreasing rate of yield after the peak. The two factors were calculated as a linear combination of TD records with relative weights derived from the correlation structure of the original data. The two factors, however, were highly correlated with total milk yield. The various measures of persistency described thus far all take into consideration that these measures should be least correlated with milk yield. Given two cows with the same yield, the more persistent cow will have a lower and later peak that declines more slowly after peak production. This cow is expected to have less health problems and may become pregnant earlier after calving.

There has not been any work reported on determining lactation persistency measures in buffaloes and estimates of genetic parameters even though average buffalo cows have low persistency.

Lactation persistency may very well be an important trait in dairy buffalo population in the Philippines primarily due to two reasons. First, it will be very difficult for the local dairy farmer to keep a high-yielding cow that has high peak yield and maintains a positive energy balance during the first 100 days of lactation given that cows are kept under a low-input management system. Second reason is that dairy buffaloes have inherently poor reproduction and under this situation, lactation persistency is important. While the tipping point and day for peak yield has been determined in dairy cattle, these figures may not be applicable to buffaloes and need to be estimated separately.

2.5 Derivation of selection indices for multiple traits

Current genetic evaluation models in place in dairy cattle and other large ruminants now involve multiple traits. If there are several traits to be considered in ranking animals, selection becomes complicated and in order to optimize responses for individual traits under consideration, the use of selection indices may be necessary. A good example is if we consider the milk production trait group, i.e., milk yield, milk fat yield, milk protein yield, milk fat percentage, and milk protein percentage. Within the group, genetic correlations have to be taken into account. It is known that milk yield is favourably correlated with milk fat and milk protein yield, such that selection for one trait will have an expected increase in the other two traits without putting selection pressure on the latter two traits (Strabel & Jamrozik, 2006). At the same time, milk fat percentage and milk protein percentage will go down due to the negative correlation of the two traits to milk yield (Wilcox et al., 2003). Thus, there is a need to balance the selection of these traits depending on the market need. Selection for production traits alone was reported to have an undesirable effect on fertility and functional traits (Nielsen & Christensen, 2005). The quest for breeding for high-yielding cows may have contributed to the decline in fertility traits in dairy cattle (Esslemont & Kossaibati, 2001). In reality, productivity of an animal does not rely on production traits alone. Fitness, fertility and other traits contribute to overall productivity of an animal. It is desirable that traits that can be measured and can contribute to the productivity of an animal be

selected to hasten genetic improvement. Current practice in dairy cattle breeding programs is the use of total merit indices and balanced breeding goals (Nielsen & Christensen, 2005). Traits reportedly included in selection indices other than milk were fertility traits (Lindhé, 2001), functional traits (Pryce et al., 2007), growth and carcass traits (Wolfova et al., 2007).

Genetic progress could be maximized in economic terms if selection is based on index selection. Beard (1987) defined selection index as the sum of the breeding values for traits of economic importance, weighed according to their relative economic value that addresses a breeding objective. Thus, setting up of a selection index requires that the breeding objective is known as this will determine the direction of improvement and traits that need to be improved. Traits to be included in the selection index should be those that can be measured/quantified, can be improved (heritable) and these should have economic value or are correlated with breeding objective traits. There are, however, some breeding objective traits that have economic values that are difficult to derive but are otherwise important (Nielsen & Christensen, 2005) and should be included in the selection process by some other means. Perhaps an example of a trait that dairy farmers consider important but may not have exact economic value is the “likeability” factor of their cows. There are also other traits that are difficult to measure. If these are correlated with other traits that can be measured, then improvement can still be achieved, though indirectly. Thus, the traits that are to be included in the selection index may not necessarily be the same as the ones identified in the breeding objective but should be able to contribute to the breeding objective. Combining all these breeding objective traits for ranking an animal is termed aggregate genotype, where breeding value of an animal is multiplied by the economic weight for each particular trait (Gibson, 2010).

$$A = v_1g_1 + v_2g_2 + v_3g_3 + \dots$$

Where A (sometimes referred to as H) is the aggregate genotype, v_1, v_2, v_3 are the economic weights and g_1, g_2, g_3 are the breeding values for traits 1, 2, 3, respectively.

Economic weights are calculated as difference between income and cost for every one unit increase in trait at the farm level. To be able to derive economic weights, two methods are given. The first one is a production model wherein income and expenses that are related to the traits are taken into account. This is usually by way of simulating a farm condition where activities and probable items of expenditures and income are listed (Pryce et al., 2007). Expenses include cost of feed, rearing cost, medications and veterinary fees, opportunity cost due to too long days open or other fertility problems, among others. Income can be by way of sale of product, sale of breeder animals and culls, among others. Assumptions on average production parameters are known or calculated in order to derive a realistic estimate of economic weight of traits of interest. For the development of bio-economic model for the Boran cattle of Kenya (Rewe et al., 2006a), the profit per herd per year was expressed as a function of traits in the breeding objective

$$Profit = \sum_{i=1}^m [n_i(R_i - C_i)X_i]$$

where:

m = the number of traits in the profit model

n = the number of expressions for traits X_i

R = the value of revenue per unit for traits X_i

C = the cost per unit for traits X_i

The revenue per cow per year is the sum of revenue/value from steers/heifers/cow and other direct products from the cow. The costs on the other hand were derived using the following equation:

$$C = (CM_s + CH_s + CF_s + CM_h + CH_h + CF_h + CM_c + CH_c + CF_c) + \text{fixed costs}$$

where s, h and c correspond to steers, heifers and cows, respectively, and M, H and F correspond to marketing, husbandry and feeding activities, respectively. Apart from costs incurred by the producer, including those attributable to equipment, machines and farm structures (fixed costs), all other costs are

variable costs because they are influenced by the level of herd production (Rewe et al, 2006a). Economic values were calculated by the same authors in another study (Rewe et al., 2006b) using the formula:

$$EV = \frac{\Delta R - \Delta C}{\Delta t}$$

where EV is the economic value, ΔR is the change in revenue, ΔC is the change in costs and Δt is the marginal change in trait.

The other means of deriving economic weight is by way of modelling a profit function. One study defined marginal economic value as the partial derivative of the profit function with respect to a trait (Wolfova et al, 2007).

$$ev_i = \left. \frac{\partial profit}{\partial TV_i} \right|_{TV_i = TV_{lav}}$$

where *profit* is the profit per cow and year, TV_i is the value of the given trait and TV_{lav} is the trait mean in the population. Variations in derivation of economic weights are reported in different papers depending on the definition of the trait (Perez-Cabal et al., 2006), production system and market condition. Response obtained varied depending on the weight applied to suit particular market condition. Still, Nielsen et al. (2005) was able to demonstrate the derivation of non-market value (NV) breeding goal and its inclusion into a selection index in dairy cattle.

Predicted response per round of selection is calculated using economic values derived from the farm production model or modelling a profit function. The economic values are used as weighing factors to derive the selection index coefficients (Rewe *et al.*, 2006b; van der Werf, 2010):

$$\mathbf{b} = \mathbf{P}^{-1}\mathbf{G}\mathbf{v}$$

where \mathbf{b} is a vector containing the coefficients of the index traits that are solutions for optimal weights of the index traits; \mathbf{P} is the phenotypic variance-covariance matrix of the observations for characters in

the selection index; **G** is the genetic variance-covariance matrix between measured the characters in the index and the breeding values for traits in the breeding objective; **v** is a vector of economic values for the traits in the breeding objective. Response per round of selection per trait is:

$$R = ib'G_i/\sigma_I$$

where *i* is selection intensity; σ_I is the standard deviation of the selection index ($\sigma_I = \sqrt{b'Pb}$); **b**, **P** and **G** are the same as above. Response to breeding objective traits can be manipulated by increasing or decreasing economic values or varying the information sources depending on which trait are given more emphasis in selection. Most indices reported for dairy cattle put greater emphasis on milk protein and milk fat yield (Spelman & Garrick, 1997) with milk protein more than double in weight than that of milk fat. Milk protein, which is important in cheese making, has far greater economic value such that milk yield is often given a negative weight in selection indices. Fertility traits, such as days-open, involuntary culling rate and first service to conception interval (Vargas-Leitón & Cuevas-Abrego, 2009), were also reported to have unfavourable correlations with milk yield. Berry et al. (2003) reported similar findings on pregnant 63d after the start of breeding season, pregnant to first service. A positive but unfavourable genetic correlation of milk yield with the number of services per cow and the interval from first service to conception was also reported by Berry et al. (2003). The unfavourable correlations of milk production and fertility traits may result in genetic progress for one trait and deterioration of the other traits. However, careful manipulation of weights makes possible selection in opposite direction. This is the desired gains approach. Though the response may be less than that of single-trait selection, significant progress can nevertheless be achieved (Pryce et al, 2007) for all traits.

In dairy buffaloes, selection indices reported also involved a combination of milk production, fertility, functional and sometimes growth traits. The most common is a combination of milk production traits (milk, fat, protein yield, lactation length) together with fertility traits, such as calving interval and

age at first calving (Kumar et al., 2008; Gandhi & Joshi, 2004). Correlations between production and fertility traits reported in dairy buffaloes were negative, similar to those reported in dairy cattle. Various indices were reported with different responses depending on the various combination of economic weights or combination of traits. Profit is maximal when selection for milk components is made under a system where mozzarella cheese is included in the fluid milk market (Seno et al. 2006). Selection indices that include milk yield, milk fat and protein percentage together with fertility or fitness traits have not been reported in dairy buffaloes even though selection for increased milk yield may result in deterioration in milk fat and protein percentage. The inclusion of fertility traits in the breeding program for dairy buffaloes is very important not primarily due to the anticipated deterioration in fertility traits due to selection for milk production traits but because dairy buffaloes have inherently poor reproductive performance. Problems include late attainment of puberty, long days to first post-partum service, low AI conception rate and long calving interval (Barile, 2005). Genetic parameters for milk yield, milk fat percentage, milk protein percentage and somatic cell count have been reported in buffaloes (Aspilcueta-Borquis et al., 2010a). However, fertility traits are often not included in multi-trait analyses.

2.6 Conclusions

The recent advances in computing technology has made possible the analysis of large data set using more complex models in dairy cattle involving more traits. This provided an opportunity for animal breeders to have better or more accurate estimates of animal performance and predictions of genetic merit. Such models involving more production traits are only now being explored by researchers working on genetic evaluation of dairy buffaloes. Almost all published work on dairy buffaloes regarding milk recording, genetic evaluation and breeding strategies were based on methods used in dairy cattle.

Despite having several methods for 305D yield calculation, projecting short lactations and standardizing to a single length prior to genetic evaluation using multiple trait prediction or best

prediction has not been done. These two methods are especially suitable for use in situations where irregular or missing test days are often encountered. More recent methods for genetic evaluation of production traits, such as the random regression model have yet to be adopted in the breeding program of dairy buffaloes in countries with dairy buffalo populations, except Brazil. Other traits in support of milk production, such as persistency and fertility, have yet to be included in selection in the local breeding program. Furthermore, the use of multi-trait selection index involving production and fertility traits are yet to be implemented in the breeding program for most buffalo-rearing countries including the Philippines. Currently, the only trait being selected on is milk yield. Methods that were used in dairy cattle could be applied in developing genetic evaluation system for Philippine dairy buffaloes to improve milk yield, milk component traits, and persistency of lactation.

Chapter III

Predicting lactation yields in dairy buffaloes by interpolation and multiple trait prediction

Ester B. Flores ¹, Brian P. Kinghorn and Julius van der Werf

School of Environmental and Rural Sciences, University of New England Armidale NSW Australia

Published in *Livestock Science* (2013) 15:97–107

¹ Corresponding author: Ester B. Flores, Homestead Bldg. 28 School of Environmental and Rural Sciences, University of New England Armidale NSW 2351 Australia. Email: eflores@une.edu.au, esterflrs@yahoo.com Tel.: +61 2 6773 2155

Chapter IV

The genetic analyses of milk yield and milk component traits using of test day and 305D lactation records of Philippine dairy buffaloes and the consequence of long term selection for milk yield on fat and protein percentage

Ester B. Flores¹ and Julius van der Werf

School of Environmental and Rural Sciences, University of New England, Armidale NSW Australia

Prepared for the Livestock Science Journal

¹ Corresponding author: Ester B. Flores, Homestead Bldg. 28 School of Environmental and Rural Sciences, University of New England Armidale NSW 2351 Australia. Email: eflores@une.edu.au Tel.: +61 2 6773 2155

Chapter V

Random regression test day models to estimate genetic parameters for milk yield and milk components in Philippine dairy buffaloes

Ester B. Flores ¹ and Julius van der Werf

School of Environmental and Rural Sciences, University of New England, Armidale NSW Australia

Prepared for the Journal of Animal Breeding and Genetics

¹ Corresponding author: Ester B. Flores, Homestead Bldg. 28 School of Environmental and Rural Sciences, University of New England Armidale NSW 2351 Australia. Email: eflores@myune.edu.au; esterflrs@yahoo.com Tel.: +61 2 6773 2155

Chapter VI

Optimizing response to selection on milk production and lactation persistency of first parity Philippine dairy buffaloes by random regression analysis

Ester B. Flores¹ and Julius van der Werf

School of Environmental and Rural Sciences, University of New England Armidale NSW Australia

Prepared for the Journal of Animal Breeding and Genetics

¹ Corresponding author: Ester B. Flores, Homestead Bldg. 28 School of Environmental and Rural Sciences, University of New England Armidale NSW 2351 Australia. Email: eflores@myune.edu.au; esterflrs@yahoo.com Tel.: +61 2 6773 2155

Chapter VII

General Discussion and Conclusions

7.1 General Discussion

7.1.1 The suitability of test day and 305D lactation records for genetic evaluation. The availability of performance records is essential to any genetic evaluation system. The recording system must not be difficult to implement and standardized across different herds. Among dairy farms in developed countries, monthly or even daily records of milk yield are easily obtainable using technology for both recording and animal identification. Such a situation is not present in the various dairy buffalo cooperatives in the Philippines. Due to the difficulty in regularly recording milk and milk solids from cows in dairy cooperatives, these cows are not included in the genetic evaluation program. The use of multiple trait prediction (MTP-Wil) in Chapter III can help in addressing the difficulties in monthly test day recording. It can handle irregular intervals between tests as well as short/on-going lactations. With a slight compromise in accuracy, decreasing the number of official tests to 6 times per lactation might help to reduce the cost and logistical constraints to record cows from the dairy cooperatives making it easier to implement a recording system. These performance records could be analysed and provide information about management and genetic merit of cows and bulls for selection purposes. For genetic evaluation, test day records could be used directly or 305D lactation records could be used as well, both of which could come from multiple trait prediction (MTP-Wil) method. By increasing the number of animals that could be evaluated, selection intensity will be increased and so might be the rate of genetic gain. Furthermore, increasing the number of cows included in genetic evaluation means the accuracy of selection is also improved.

For genetic evaluation, the need to standardize records to a uniform length is necessary per reports of previous studies in dairy cattle. But, as yield prediction of cows with short lactations are less

accurate, this must be reflected in genetic evaluation of cows by assigning appropriate weights to these lactation records. The reporting of lactation yields for each cow with MTP-Wil method provides an accuracy relative to the diagonal elements of the $(X'R-1X + G-1)^{-1}$ matrix for parameter A of 11 evenly spaced test days (relative accuracy) and could be used as appropriate weights for records used in genetic evaluation. The use of 305D lactation records for genetic evaluation in Chapter IV indicated that for both single- and multi-trait analyses, standard error of the estimate of heritability was large due to relatively small number of records available for parameter estimation. Providing more information per cow for analysis using test day records is thus necessary to decrease standard error. There was a substantial difference in heritability estimates between the first and second parity when 305D lactation records were used. Furthermore, unlike in first parity where there was consistency in estimates between the use of 305D and test day records, this was not apparent in second parity records; there was a substantial difference in heritabilities estimated between the use of 305D and test day records. Hence, in the meantime it would be more suitable to evaluate cows' performance based on first parity 305D or test day records only. It is expected that there would not be any substantial re-ranking of cows with the shift to MTP-Wil for 305D yield calculation as it has been shown that production yields predicted from MTP-Wil were very similar to TIM.

7.1.2 Suitable random regression test day model for use in genetic evaluation. In chapter III, the use of test day records in a repeatability model for parameter estimation resulted low estimates of heritability and small standard error of heritability. A better model might be with the use of random regressions. The MTP-Wil method for yield prediction is actually a random regression model (RRM) applied at the phenotypic level. For genetic evaluation in this study, an almost similar random regression test day model was used. For first parity cows, lactation yields can be predicted using RRM; but for older cows that are not included in genetic evaluation, lactation yields can be predicted for management purposes using MTP-Wil, complementing RRM. The use of lower order function ($k=3$) for fitting the fixed

and genetic and permanent effects in a random regression test day model in this study was shown to be adequate for Philippine dairy buffaloes. Extreme values at the edges of lactation trajectory that were reported in previous studies using higher order Legendre polynomials were not evident and the heritabilities estimated were well within the range of reported studies on dairy buffaloes. The use of random regression test day model resulted in higher estimates of heritability relative to the use of repeatability test day model where test day records within lactation are considered repeated measures of the same trait.

With a random regression model, selection on EBVs at specific days in lactation rather than on EBVs for 305D yield is an option. By selection on canonical variates Z_1 , Z_2 and Z_3 which have equivalence to selection on EBVs at specific days in milk, the need for a separate set of appropriate weights for short/on-going lactations that are used for genetic evaluation is no longer needed. There might be slight re-ranking with the shift to random regression test day models due to the difference in performance records analysed (305D vs. TD records) and difference in heritability estimates used.

7.1.3 The consequence of selection for higher milk yield on fat and protein concentration.

Multi-trait selection of 305D lactation measure for MY, FY and PY will result in correlated increase in yield per round of selection for all three traits. However, as the increase was higher for MY compared with FY and PY, continuous selection for the three traits will decrease fat and protein concentration. This was due to moderately high negative genetic correlation of MY with Fat% and Prot%. In order to prevent or minimize the reduction in Fat% and Prot%, milk, fat and protein yield response will have to be compromised. Selection for higher milk yield will also invariably increase peak yield. This is evidenced by the high correlation between total milk yield and yield at DIM60 and DIM90. This could lead to further deterioration of persistency. Dissociating the response to the three traits as well as higher total yield and peak yield with 305D lactation model might be limited. With RRM, there might be an opportunity to select at later days when correlations between traits are less. Response per round of selection on total

lactation EBV by multi-trait RRM indicated that relative to base values for MY, FY and PY, the percentage increase for MY was 20.3%, whereas for FY and PY, these were 12.7% and 18.4%; hence, there would still be a deterioration in Fat% and Prot%. However, the percentage increase for each trait was higher relative to selection on 305D lactation yield even though the difference in responses between MY and FY or PY remained the same using 305D lactation model and RRM. There will still be a net decrease therefore in Fat% and Prot% after long-term continuous selection even though total yields will increase. An advantage of using multi-trait RRM for selection is that the deterioration in fat and concentration is less which could be due to slightly lower genetic correlations among the three traits compared with 305D lactation model. In RRM. At the current situation, increasing the productivity and yields for fat and protein is more important than concentration.

7.1.4 Balancing the response to selection on milk production, milk components and lactation persistency. While persistency could also be selected simultaneously with milk yield using various definition of persistency, such as ratio of peak yield with yield at some particular day later in lactation, calculating economic value for persistency is difficult. With RRM in this study, selection on the second and third canonical variates could potentially change the shape of the lactation curve for better persistency, and this change in shape can be quantified using economic values for milk yields on a daily basis. Among the different selection indices presented in Table 6.2, MFP3 index was the most preferred. This is because at this point, the dairy buffalo population needs to first increase yield for better production efficiency. The moderate genetic correlation between MY at peak lactation and CI indicates the adverse effect on fertility due to high peak yield, as a correlated response due to selection for higher milk yield might be less than the effect of selection for persistency on calving interval. The MFP3 index gives maximum total yield response without sacrificing persistency, which could lengthen lactation period. For dairy buffaloes, both are needed to increase efficiency of production. It has been shown that calving interval is greater with later lactation stages indicating that calving interval increases with longer

lactation. The second canonical variate Z_2 , related to lactation persistency is highly correlated with calving interval. Indirectly, it suggests that selection for persistency will increase calving interval and that calving interval may not be the best measure to use for selection on fertility. There is an opportunity to improve fertility using measures in early lactation, such as days to first post-calving estrus or days to first post-calving conception. This could be done in future studies.

7.2 Summary and Conclusions

The use of test day records for lactation yield prediction in dairy cooperatives and institutional herds using MTP-Wil method could be implemented with ease and practicality. It can handle missing test days and irregular test day intervals better than the test interval method. The same records could also be used for genetic evaluation directly based on test day records such that the number of recorded cows in the breeding program could be expanded into the dairy cooperatives. Analysis of multi-trait 305D lactation model gave slightly higher heritability estimates and reduced standard errors compared with single-trait analysis. Heritability estimates obtained from analysis of first parity records were moderately low for MY, FY, and PY at 0.15, 0.14 and 0.15, respectively. For analysis of 2nd parity records, estimates were higher at 0.37, 0.35 and 0.36 for MY, FY and PY, respectively. Using selection index, maximum response to multi-trait selection based on first parity records was 101.8 kg, 6.0 kg, and 3.8 kg per round of selection for MY, PY and PY, respectively. For analysis of 2nd parity records, maximum response per round of selection was: 239.4 kg, 15.4 kg and 9.1 kg for MY, FY and PY, respectively. Results indicated deterioration in fat and protein concentration despite an overall increase in fat and protein yields after several rounds of selection based on yield traits because of the negative genetic correlation of Fat% and Prot% with MY. While maximum genetic response from selection on first parity yield traits was lower, the deterioration in Fat% and Prot% was also less compared with the response from selection on 2nd parity yield traits. Furthermore, multi-trait selection on yield traits minimized the deterioration in Fat% and Prot% compared with single trait selection.

Analysis of test day records directly using a repeatability test day model gave slightly lower estimates of genetic parameters compared with analysis of 305 lactation records. Similarly, the estimates of heritability from analysis of first parity test day records were lower than those estimated from second parity test day records with regards to milk yield. On the other hand, estimates derived from both parities were almost similar with regards to fat and protein yield. However, accuracy was lower with second parity estimates. A random regression test day model that utilize the Wilmink's function to fit the fixed and random additive genetic effects and a 2nd order Legendre polynomial function to fit permanent environment effects was used for analysis of first parity test day records to estimate heritabilities and genetic correlations for different days in lactation, within and across traits. The same model was used for MY and FY. However, for PY, 1st order Legendre polynomial was used to fit permanent environment effects. For Fat% and Prot%, Wilmink's function was used to fit fixed, random additive and permanent environment effects. Heritabilities estimated by multi-trait RRM at different days in lactation ranged from 0.21 – 0.37, 0.14 – 0.27, 0.19 – 0.28, 0.20 – 0.30, 0.12 – 0.36 for MY, FY, PY, Fat% and Prot%, respectively. Genetic correlations of FY and PY with MY were high but, slightly less than those estimated by 305D lactation model. Correlations were highest at mid-lactation for FY while it was at peak lactation for PY. Similarly for genetic correlations of Fat% and Prot% with MY, values were slightly less negative than those estimated by 305D lactation model, especially in early lactation period.

Eigenvalue decomposition by principal component analysis enabled selection on canonical variates related to the first three leading eigenvalues of the genetic covariance matrix. The Eigenfunctions plotted across the lactation period for MY and FY had similar pattern although the scale was lower for the latter trait. Furthermore, the percentage of genetic variance explained by the 2nd eigenvalue was almost the same for MY and FY. The pattern for the eigenfunction for PY was also similar to FY, but the 2nd and 3rd eigenfunctions were very slightly different from FY. For all three traits (MY,FY,PY), selection on the 2nd and 3rd canonical variates resulted in more response in the 3rd trimester

of lactation relative to selection on total lactation, thus, better persistency. Selection measures that result in more persistency also resulted in a reduction in response for total lactation yield due to concomitant reduction in response at peak lactation period. Optimized weights applied to Z_2 and Z_3 allowed for only a slight reduction in response to lactation yields without deteriorating persistency for all three traits. The optimum weights applied to the canonical variates for MY and FY were similar as the two traits had the same eigenfunctions across the lactation period.

Multi-trait random regression analysis of MY, FY and PY records indicated higher response to selection relative to single-trait analysis. As the three traits were highly correlated with each other and the eigenfunctions across the lactation period were almost similar, a single set of weights applied to Z_1 , Z_2 and Z_3 was feasible, resulting in more persistency without compromising response to production relative to selection on total lactation. Bivariate analysis between MY and CI indicated moderate genetic correlation between the two traits. The correlation actually increased gradually from 0.25 at the beginning to 0.47 towards the end of lactation. This suggests that longer lactations are more correlated with calving interval. More specifically, the large part of the correlation observed between MY and CI might be due to Z_2 , the canonical variate related to genetic basis for lactation persistency. Genetic correlation of CI with Z_2 was estimated at 0.87 while that of Z_1 and Z_3 were -0.27 and -0.22, respectively. Selection for persistency will also increase lactation length and indirectly, increase calving interval.

Optimum response to milk production (MY, FY, PY) and persistency is possible by selection on canonical variates Z_1 , Z_2 and Z_3 in the MFP3 index. This is equivalent to selection on $EBV_{DIM90} - 1.52EBV_{DIM160} + 4.55EBV_{DIM240}$ of buffaloes included in the breeding program. It addresses the issues laid out in Chapter I of the need to have a genetic evaluation system for milk and milk components; minimizing the deterioration in fat and protein concentration as a consequence of increasing milk yield; increasing lactation length indirectly by selection on persistency. As the local data set expands in the future, multi-trait RRM involving multi-parity test day records should be used in genetic parameter

estimation. In the meantime, EBVs from 2nd parity 305D lactation records could be included in ranking genetic merit of Philippine dairy buffaloes.

In future studies, other measures of fertility should be explored for possible inclusion in selection, especially those that are measured early in lactation before or during peak production, such as days-to-first-service.

Chapter VIII

Consolidated Reference List

- AIPL. (2010). Description of national genetic evaluation system. *USDA ARS*. Retrieved from http://aipl.arsusda.gov/reference/Form_GE_Yield_1008.pdf
- Alexiev, A. (1998). Buffalo breeding in Europe *The Water Buffalo* (pp. 72-88). Sofia: St. Kliment Ohridski University Press.
- Ali, T. E., & Schaeffer, L. R. (1987). Accounting for covariances among test day milk yields in dairy cows. *Canadian Journal of Animal Science*, 67, 637-644.
- Aspilcueta-Borquis, R., Araujo Neto, F., Baldi, F., Bignardi, A., Albuquerque, L., & Tonhati, H. (2010a). Genetic Parameters for buffalo milk yield and milk quality traits using Bayesian inference. *Journal of Dairy Science*, 93 (95), 2195-2201.
- Aspilcueta-Borquis, R. R., Sesana, R. C., Berrocal, M. H. M., Seno, L. O., Bignardi, A. B., El Faro, L., Albuquerque, L. G., de Camargo, G. M. F., & Tonhati, H. (2010b). Genetic parameters for milk, fat and protein yields in Murrah buffaloes (*Bubalus bubalis* Artiodactyla, Bovidae). *Genetics and Molecular Biology*, 33(1), 71-77.
- Aspilcueta-Borquis, R. R., Bignardi, A. B., de Seno, L., de Camargo, G. M. F., Muñoz-Berrocal, M. H., de Albuquerque, L. G., Di Palo, R., & Tonhati, H. (2010c) Genetic parameters for milk test day analyzed by test-day models in Murrah buffaloes in Brazil. *Italian Journal of Animal Science*, 9:e34, 179-182.
- Aspilcueta-Borquis, R. R., Baldi, F., Araujo Neto, F. R., Albuquerque, L. G., Munoz-Berrocal, M., & Tonhati, H. (2012a). Genetic parameters of total milk yield and factors describing the shape of lactation curve in dairy buffaloes. *Journal of Dairy Research*, 79(1), 60-65.

- Aspilcueta-Borquis, R. R., Araujo Neto, F. R., Baldi, F., Santos, D. J., Albuquerque, L. G., & Tonhati, H. (2012b). Genetic parameters for test-day yield of milk, fat and protein in buffaloes estimated by random regression models. *Journal of Dairy Research*, 79(3), 272-279.
- Baldi, F., Marianna, M., Laureano, M., Gordo, D., Bignardi, A., Aspilcueta-Borquis, R., Albuquerque, L. G., & Tonhati, H., 2011. Effect of lactation length adjustment procedures on genetic parameter estimates for buffalo milk yield. *Genetics and Molecular Biology*, 34, 62-67.
- Barile, V. L. (2005). Improving reproductive efficiency in female buffaloes. *Livestock Production Science*, 92:183-194.
- BAS. (2011a). *Performance of Philippine Agriculture*. Retrieved January 10, 2011, from Bureau of Agricultural Statistics: <http://www.bas.gov.ph>
- BAS. (2011b). *Livestock population survey: Preliminary report*. Quezon City: Bureau of Agricultural Statistics: <http://www.bas.gov.ph>
- Beard, K. T. (1987). Efficiency of index selection for dairy cattle using economic weights for major milk constituents. *Australian Journal of Agricultural Research*, 38, 2673-2684.
- Berry, D., Buckley, F., Dillon, P., Evans, R., Rath, M., & Veerkamp, R. (2003). Genetic relationships among body condition score, body weight, milk yield, and fertility in dairy cows. *Journal of Dairy Science*, 86:2193–2204.
- Bhat, P. N., Kumar, R., & Garg, R. C. (1981). Note on comparative efficiency of various lactation curve functions in Haryana cattle. *Indian Journal of Animal Science*, 51, 102.
- Bilal, G., & Khan, M. S. (2009). Use of test-day milk yield for genetic evaluation in dairy cattle: A review. *Pakistan Veterinary Journal*, 29(21), 34-41.
- Bondoc, O. L. (1998). Biodiversity of Livestock and Poultry Genetic Resources in the Philippines. Los Baños: IAS-CA/UPLB and PCARRD/DOST. 141 pp.

- Bondoc, O. L., & Bantoc, A. C. M. (1996). Assessment of the genetic and economic impacts of artificial insemination (AI) on the cattle and carabao breeding programs of the Philippines. Terminal report DOST-PCARRD Project No. 89-540-21. Los Baños, Laguna: PCARRD.
- Catillo, G., Macciotta, N. P., Carretta, A., & Cappio-Borlino, A. (2002). Effects of age and calving season on lactation curves of milk production traits in Italian water buffaloes. *Journal of Dairy Science*, 85, 1298-1306.
- Catillo, G., Mioli, B., & Napolitano, F. (2001). Estimation of genetic parameters of some productive and reproductive traits in Italian buffalo. *Asian-Australasian Journal of Animal Sciences*, 14 (6), 747-753.
- Cilek, S., & Tekin, M. E. (2006). Calculation of adjustment factors for standardizing lactations to mature age and 305-day and estimation of heritability and repeatability of standardized milk yield of Simmental cattle reared on Kazova State Farm. *Turkish Journal of Veterinary and Animal Sciences*, 30, 283-289.
- Cobby, J. M., & Le Du, Y. L. P. (1978). On fitting curves to lactation data. *Animal Production*, 26, 127-133.
- Cole, J. B., & Null, D. J. (2009). Genetic evaluation of lactation persistency for five breeds of dairy cattle. *Journal of Dairy Science*, 92(5), 2248-2258.
- Cole, J. B., & VanRaden, P. M. (2006). Genetic evaluation and best prediction of lactation persistency. *Journal of Dairy Science*, 89, 2722-2728.
- Congleton, W. R., & Everett, R. W. (1980a). Application of the incomplete gamma function to predict cumulative milk production. *Journal of Dairy Science*, 63, 109-119.
- Congleton, W. R., & Everett, R. W. (1980b). Error and bias in using the incomplete Gamma function to describe lactation curves. *Journal of Dairy Science*, 63, 101-108.
- de Jong, G. (2001). *Selection for cow fertility in the Netherlands*. Paper presented at the Recording and Evaluation of Fertility Traits in UK dairy cattle, Edinburgh.

- Druet, T., Jaffrezic, F., Boichard, D., & Ducrocq, V. (2003). Modeling lactation curves and estimation of genetic parameters for first lactation test-day records of French Holstein cows. *Journal of Dairy Science*, 86, 2480-2490.
- Elzo, M. A. (2001). Discussion on the Current Situation of Animal Genetic Improvement and Its Prospects for the Future: Invited seminar, University of Chile, Santiago, Chile.
- Esslemont, R. J., & Kossaibati, M. A. (2001). *Economics of fertility in dairy cows*. Paper presented at the Recording and Evaluation of Fertility Traits in UK dairy cattle, Edinburgh.
- Everett, R. W., Taylor, J. F., & Hammond, K. (1982). Mixed model estimation of age and month of calving adjustment factors for milk and butterfat yields. *Australian Journal of Agricultural Research*, 33, 731-741.
- Ferris, T. A., Mao, I. L., & Anderson, C. R. (1983). Selecting for Lactation Curve and Milk Yield in Dairy Cattle. *Journal of Dairy Science*, 68, 1438-1448.
- Flores, E. B. (2003). The lactation curve of dairy buffaloes. M.S. Thesis. Fayetteville, Arkansas: University of Arkansas.
- Flores, E. B., Kinghorn, B. P., & van der Werf, J. H. J. (2011). *Breeding objectives and breeding strategies for Philippine dairy buffaloes*. Paper presented at the 19th AAABG conference, University of Western Australia, 19-21 July 2011.
- Flores, E. B., Kinghorn, B. P., & van der Werf, J. H. J. (2013a). Predicting lactation yields in dairy buffaloes by interpolation and multiple trait prediction. *Livestock Science*, 151(2-3), 97-107.
- Flores, E. B., Kinghorn, B. P., & van der Werf, J. (2013b) *Genetic parameters for milk yield and milk component traits estimated from test day and 305D lactation records of Philippine dairy buffaloes*. In: Proceedings of the 10th World Buffalo Congress. Phuket, Thailand, 6-8 May 2013.
- Foster, D. P., Stine, R. A., & Waterman, R. P. (1998). *Business Analysis Using Regression: A Casebook*. New York, NY: Springer-Verlag.

- France, J., & Dhanoa, M. S. (1984). Short note on estimating lactation yield. *Journal of Agricultural Science*, 103, 245-247.
- Gandhi, R. S. (2003). Ranking of Murrah buffaloes by multi-trait criteria of selection. *Indian journal of Animal Sciences*, 73(1), 83-86.
- Garcia, S. C., & Holmes, C. W. (2001). Lactation curves of autumn and spring-calved cows in pasture-based dairy systems. *Livestock Production Science*, 68, 189-203.
- Geetha, E., Chakravarty, A. K., & Vinaya Kumar, K. (2006). Genetic persistency of first lactation milk yield estimated using random regression model for Indian Murrah buffaloes. *Asian-Australian Journal of Animal Science*, 19 (12), 1696-1701.
- Gianola, D., & Fernando, R. L. (1986). Bayesian methods in animal breeding theory. *Journal of Dairy Science*, 63, 217-244.
- Gibson, J. P. (2010). Breeding objectives. In D. E. Cottle, *Gene 422/522 Genetic Evaluation and Breeding Program Design - Course Notes* (pp. 3-7 ch. 13). Armidale: School of Environmental and Rural Science, University of New England.
- Gilmour, A. R., Gogel, B. J., Cullis, B. R., & Thompson, R. (2009). *ASREML User Guide Release 3.0*. Hemel Hempstead, HP1 1ES, UK: VSN International Ltd.
- Guo, Z., Lund, M., Madsen, P., Korsgaard, I., & Jensen, J. (2002). Genetic parameter estimation for milk yield over multiple parities and various lengths of lactation in Danish Jerseys by random regression models. *Journal of Dairy Science*, 85, 1596 - 1606.
- Hagiya, K., Atagi, Y., Kawahara, T., Gotho, Y., Suzuki, M., Shirai, T., & Astumi, T. (2004). The comparison of three methods for predicting whole lactation records from test day records of Holstein cows. *Nihon Chikusan Gakkaiho*, 75(73), 345-351.

- Haile-Mariam, M., Bowman, P. J., & Goddard, M. E. (2003). Genetic and environmental relationship among calving interval, survival, persistency of milk yield and somatic cell count in dairy cattle. *Livestock Production Science*, 80(3), 189-200.
- Harder, B., Bennewitz, J., Hinrichs, D., & Kalm, E. (2006). Genetic parameters for health traits and their relationship to different persistency traits in German Holstein dairy cattle. *Journal of Dairy Science*, 89, 3202-3212.
- Hayes, J.F., & Hill, W.G. (1981) Modification of estimates of parameters in the construction of genetic selection indices ('bending'). *Biometrics*. 37, 483-493.
- Henderson, C. R. (1974). General flexibility of linear model techniques for sire evaluation. *Journal of Dairy Science*, 57(8), 963 - 972.
- ICAR. (2010). ICAR rules, standards and guidelines for dairy production recording *International Agreement of Recording Practices* (pp. Section 2: 23). Riga, Latvia: International Committee on Animal Recording.
- Jamrozik, J., & Schaeffer, L. R. (1997). Estimates of genetic parameters for a test day model with random regressions for yield traits of first lactation Holsteins. *Journal of Dairy Science*, 80(4), 762-770.
- Jamrozik, J., Schaeffer, L.R., & Dekkers, J. C. M. (1997). Genetic evaluation of dairy cattle using test day yields and random regression model. *Journal of Dairy Science*, 80, 1217-1226.
- Jensen, J. (2001). Genetic evaluation of Dairy cattle using test-day models. *Journal of Dairy Science*, 84, 2803-2812.
- Kellogg, D. W., Urquhart, N. S., & Ortega, A. J. (1977). Estimating Holstein lactation curves with a gamma curve. *Journal of Dairy Science*, 60, 1308-1315.
- Keown, J. F., Empet, N. B., Everett, R. W., & Wadell, L. H. (1986). Lactation curves. *Journal of Dairy Science*, 69, 767-781.

- Keown, J., & Everett, R. (1985). Age-month adjustment factors for milk, fat and protein yields in Holstein cattle. *Journal of Dairy Science*, 68, 2664-2669.
- Khan, M., Hyder, A., Bajwa, I., Rehman, M., & Hassan, F. (2005). Prediction of lactation yield from last-record day and average daily yield in Nili-Ravi buffaloes. *Pakistan Veterinary Journal*, 25(4), 175-178.
- Khan, M. S., & Shook, G. E. (1996). Effects of age on milk yield: Time trends and method of adjustment. *Journal of Dairy Science*, 79, 1057-1064.
- King, G. J., & Miller, R. H. (1965). The National Cooperative Dairy Herd Improvement Program Handbook no. 278 Washington DC, USA: Agricultural Research Service Department of Agriculture.
- Kinghorn, B. P. (2010). Breeding program design principles. In D. E. Cottle, *Gene 422/522 Genetic Evaluation and Breeding Program Design - Course notes* (pp. 1-11 ch. 15). Armidale: School of Environmental and Rural Science, University of New England.
- Kirkpatrick, M., Lofsvold, D., & Bulmer, M. (1990). Analysis of the inheritance, selection and evolution of growth trajectories. *Genetics*, 124(4), 979-993.
- Koçak, Ö., & Ekiz, B. (2008). Comparison of different lactation curve models in Holstein cows raised on a farm in the south-eastern Anatolia region. *Archive Tierzucht*, 51(4), 329-337.
- Kumar, S., Yadav, M., & Prasad, R. (2008). Multi-trait selection for genetic improvement in Indian buffaloes. *Buffalo Bulletin*, 27(1), 154-160.
- Lindhé, B. (2001). *Genetic evaluations for fertility - Experience from Scandinavia*. Paper presented at the Recording and Evaluation of Fertility Traits in UK Dairy Cattle, Edinburgh.
- Liu, Z., Jaitner, J., Reinhardt, F., Pasman, E., Rensing, S., & Reents, R. (2008). Genetic evaluation of fertility traits of dairy cattle using a multiple-trait animal model. *Journal of Dairy Science*, 91, 4333 - 4343.

- López-Romero, P., & Carabaño, M. J. (2003). Comparing alternative random regression models to analyse first lactation daily milk yield data in Holstein–Friesian cattle. *Livestock Production Science*, 82, 81-96.
- Macciotta, N. P. P., Vicario, D., & Di Mauro, C. (2004). A multivariate approach to modelling shapes of individual lactation curves in cattle. *Journal of Dairy Science*, 87, 1092-1098.
- Mamuad, F., Venturina, H., Aquino, D., Lorenzo, N., Mamuad, V., & Cuaresma, R. (1981). Milk production performance of island born buffaloes under Central Luzon conditions. *Philippine Journal of Veterinary and Animal Sciences*, 17, 1-2.
- Metry, G. H., Mourad, K. A., Wilk, J. C., & McDaniel, B. T. (1994). Lactation curves for first lactation Egyptian buffalo. *Journal of Dairy Science*, 77, 1306-314.
- Meuwissen, T. H. E., & Luo, Z. (1992). Computing inbreeding coefficients in large populations. *Genetics Selection and Evolution*, 24, 305-313.
- Meyer, K. (2005). Random regression analyses using B-splines to model growth of Australian Angus cattle. *Genetics Selection and Evolution*, 37(5), 473-500.
- Meyer, K. (1985) Maximum likelihood estimation of variance components for a multivariate mixed model with equal design matrices. *Biometrics*, 41, 153-165.
- Miglior, F., de Roos, S., Liu, Z., Mathevon, M., Rosati, A., Schaeffer, L. R., VanRaden, P. M., 2002. ICAR Working Group on lactation calculation methods: review and update of guidelines for milk recording. Proc. 33rd ICAR Meeting EAAP Pub. pp. 227-232.
- Miller, R., Pearson, R., Fohrman, M., & Creegan, M. (1972). Methods of projecting complete lactation production from part-lactation yield. *Journal of Dairy Science*, 55 (11), 1602-1606.
- Mostert, B., Theron, H., & Kanfer, F. (2001). The effect of calving season and age at calving on production traits of South African dairy cattle. *South African Journal of Animal Science*, 31(3), 205-213.

- Mrode, R. A. (1996). *Linear Models for the Prediction of Animal Breeding Values*. Oxon: CAB International.
- Muir, B. L., Fatehi, J., & Schaeffer, L. R. (2004). Genetic relationships between persistency and reproductive performance in first lactation Canadian Holsteins. *Journal of Dairy Science*, 87, 3029-3037.
- Naranchulum, G., Ohmiya, H., Masuda, Y., & Hagiya, K., 2011. Selecting the desirable method for predicting 305-day lactation yields in Mongolia. *Animal Science Journal*, 82, 383–389.
- Nelder, J. A. (1966). Inverse polynomials, a useful group of multifactor response functions. *Biometrics*, 22, 128-141.
- Nielsen, H. M., Christensen, L. G., & Groen, A. F. (2005). Derivation of sustainable breeding goals for dairy cattle using selection index theory. *Journal of Dairy Science*, 88, 1882-1890.
- Norberg, E., Madsen, P., & Pedersen, J. (2009). A multi-trait genetic analysis of protein yield, udder health, and fertility in first lactation Danish Holstein, Danish Red, and Danish Jersey using an animal model. *Acta Agriculturae Scand Section A*, 59, 197-203.
- Norman, H., Dickinson, F., & Wright, J. (1985). Merit of extending completed records of less than 305 days. *Journal of Dairy Science*, 68, 2646-2654.
- Olori, V. E., Brotherstone, S., Hill, W. G., & McGuirk, B. J. (1999). Fit of standard models of the lactation curve to weekly records of milk production of cows in a single herd. *Livestock Production Science*, 58, 55-63.
- Olori, V., & Galesloot, P., (2011). *Projection of partial lactation records and calculation of 305D yields in the Republic of Ireland*. Retrieved September 9, 2011, from cgiar.org.
http://agtr.ilri.cgiar.org/library/docs/Interbull/Bulletn22_files/Docs/OLORI.pdf
- PCARRD. (1978). *Philippine Recommends for Carabao Production*. Manila: Philippine Council for Agriculture and Resources Research and Development.

- Perez-Cabal, M. A., Gonzalez Santillana, R., & Alenda, R. (2006). Mature body weight and profit selection in Spanish dairy cattle. *Livestock Science* 99, 257-266.
- Pryce, J. E., Haile-Mariam, M., Verbyla, K., Bowman, P. J., Goddard, M. E., & Hayes, B. J. (2010). Genetic markers for lactation persistency in primiparous Australian dairy cows. *Journal of Dairy Science*, 93, 2202-2214.
- Pryce, J. E., van der Werf, J. H. J., Haile-Mariam, M., Malcolm, B., & Goddard, M. (2007). *Updated index weights for Australian profit ranking in dairy cattle*. In: Proceedings of the 18th Conference of the Association for the Advancement of Animal Breeding and Genetics. Barosa Valley, South Australia, 18, 143-146.
- Ptak, E., Satoła, A., & Czaja, H. (2004). Prediction of 305-day lactation milk, fat and protein yields using Legendre Polynomials and test day yields from different parts of lactations. *Animal Science Papers and Reports*, 22 (22), 173-183.
- Quist, M. A., LeBlanc, S. J., Hand, K. J., Lazenby, D., Miglior, F., & Kelton, D. E., (2007). Agreement of predicted 305-day yields relative to actual 305-day milk weight yields. *Journal of Dairy Science*, 90, 4684-4692.
- Quaas, R. L., & Pollak, E. J. (1980). Mixed model methodology for farm and ranch beef cattle testing programs. *Journal of Animal Science*, 51(6), 1277-1287
- Ramos, A. A., Malhado, C. H. M., Carneiro, P. L. S., Gonçalves, H. C., & Azevedo, D. M. M. (2006). Phenotypic and genetic characterization of the milk yield and calving interval in buffalo of the Murrah breed. *Pesquisa Agropecuária Brasileira*, 41(8), 1261-1267
- Rewe, T. O., Indetie, D., Ojango, J. M. K., & Kahi, K. A. (2006a). Breeding objectives for the Boran breed in Kenya: Model development and application to pasture-based production system. *Animal Science Journal*, 77, 163-177.

- Rewe, T. O., Indetie, D., Ojango, J. M. K., & Kahi, A. K. (2006b). Economic values for production and functional traits and assessment of their influence on genetic improvement in the Boran cattle in Kenya. *Journal of Animal Breeding and Genetics*, 123, 23-36.
- Rosati, A., & Van Vleck, L. D. (2002). Estimation of genetic parameters for milk, fat, protein and mozzarella cheese production for the Italian river buffalo *Bubalus bubalis* population. *Livestock Production Science*, 74, 185-190.
- Ruiz, R., Oregui, L. M., & Herrero, M. (2000). Comparison of models for describing the lactation curve of Latxa sheep and an analysis of factors affecting milk yield. *Journal of Dairy Science*, 83, 2709-2719.
- Sarabia, A. S., Aquino, D. L., Flores, E. B., Abes, N. S., et al. (2009). Dairy buffalo production handbook. Science City of Muñoz, Nueva Ecija Philippines.
- SAS Institute. 2009. JMP 8.02. SAS Institute Inc. Cary, North Carolina, USA
- Sawalha, R., Keown, J., Kachman, S., & Van Vleck, L. D. (2005). Genetic evaluation of dairy cattle with test-day models with autoregressive covariance structures and 305-d model. *Journal of Dairy Science*, 88, 3346-3353.
- Schaeffer, L. R., & Dekkers, J. C. M. (1994) *Random regressions in animal models for test-day production in dairy cattle*. In: Proceedings of the 5th World Congress on Genetics Applied to Livestock Production. Guelph, Ontario, Canada. 7-12 August 1994 .
- Schaeffer, L. R., Jamrozik, J., Kistemaker, G., & Van Doormaal, B. (2000). Experience with a test-day Model. *Journal of Dairy Science*, 83, 1135-1144.
- Schaeffer, L. R., & Jamrozik, J. (1996). Multiple-trait prediction of lactation yields for dairy cows. *Journal of Dairy Science*, 79, 2044-2055.
- Scott, T. A., Yandell, B., Zepeda, L., Shaver, R., & Smith, T. (1996). Use of lactation curves for analysis of milk production data. *Journal of Dairy Science*, 79, 1885-1894.

- Seno, L. O., Cardoso, V. L., El Faro, L., Sesana, R. C., Aspilcueta-Borquis, R. R., de Camargo, G. M. F., & Tonhati, H. (2010). Genetic parameters for milk yield, age at first calving and interval between first and second calving in milk Murrah buffaloes. *Livestock Research for Rural Development*, Volume 22, Article #38. Retrieved November 27, 2013, from <http://www.lrrd.org/lrrd22/2/seno22038.htm>.
- Seno, L. O., Cardoso, V. L., & Tonhati, H. (2006). Responses to selection for milk traits in dairy buffaloes. *Genetics and Molecular Research*, 5 (4), 790-796.
- Sesana, R. C., Bignardi, A. B., Borquis, R. R., El Faro, L., Baldi, F., Albuquerque, L. G., & Tonhati, H. (2010). Random regression models to estimate genetic parameters for test-day milk yield in Brazilian Murrah buffaloes. *Journal of Animal Breeding and Genetics*, 127(5), 369-376.
- Sherchand, L. R. (1994). Modeling the lactation curve of Holstein cows. *PhD Dissertation*. Fayetteville, Arkansas, USA: University of Arkansas.
- Shook, G. E., Johnson, L. P., & Dickinson, F. N. (1980). Factors for improving accuracy of estimates of test-interval yield. *DHI Letters*, 56(4), 9-24.
- Spelman, R. J., & Garrick, D. J. (1997). Effect of live weight and differing economic values on responses to selection for milk, fat, protein, volume, and live weight. *Journal of Dairy Science*, 80, 2557-2562.
- Strabel, T., & Jamrozik, J. (2006). Genetic analysis of milk production traits of Polish Black and White cattle using large-scale random regression test-day models. *Journal of Dairy Science*, 89, 3152-3163.
- Swalve, H. H. (2000). Theoretical basis and computational methods for different test-day genetic evaluation methods. *Journal of Dairy Science*, 83, 1115-1124.
- Swalve, H. H., & Guo, Z. (1999). An illustration of lactation curves stratified by lactation yields within herd. *Archive Tierzucht*, 42, 515-515.

- Tarres, J., Liu, Z., Reinhardt, F., Reents, R., & Ducrocq, V. (2009). Binational evaluation of type traits from Germany and France with a single-trait MACE animal model. *Animal*, 3(7), 925-932.
- Thevamanoharan, K., Vandepitte, W., Mohiuddin, G., & Chaudhry, M. (2001). Animal model estimates of repeatability for various performance traits of Nili-Ravi buffaloes. *Pakistan Journal of Agricultural Science*, 38(3-4), 11-14.
- Tobias, O., Kosgey, I., & Kahi, A. (2010). Economic evaluation of breeding strategies for improvement of dairy cattle in Kenya. *Tropical Animal health and Production*, 42, 1081-1086.
- Togashi, K., & Lin, C. Y. (2004). Efficiency of different selection criteria for persistency and lactation milk yield. *Journal of Dairy Science*, 87(5), 1528-1535.
- Togashi, K., & Lin, C. Y. (2006). Selection for milk production and persistency using eigenvectors of random regression coefficient matrix. *Journal of Dairy Science*, 89, 4866-4873.
- Tonhati, H., Muñoz, M., Duarte, J., Reichert, R., Oliveira, J., & Lima, A. (2004). Estimates of correction factors for lactation length and genetic parameters for milk yield in buffaloes. *Arquivo Brasileiro de Medicina Veterinária e Zootecnia*, 56(2), 251-257.
- Tonhati, H., Vasconcellos, F. B., & Albuquerque, L. G. (2000). Genetic aspects of productive and reproductive traits in a Murrah buffalo herd in Sao Paulo, Brazil. *Journal of Animal Breeding and Genetics*, 117, 331-336.
- Tozer, P. R., & Huffaker, R. G. (1999). Mathematical equations to describe the lactation curves for Holstein-Friesian cows in New South Wales. *Australian Journal of Agricultural Research*, 50, 431-440.
- van den Berg, J. C. T. (1990). *Strategy for Dairy Development in the Tropics and Subtropics*. Wageningen: Centre for Agricultural Publishing and Documentation (Pudoc).
- van der Werf, J.H. J. (2002) *Optimizing selection along trajectories*. In: Proceedings of the 7th World Congress on Genetics Applied to Livestock Production, Montpellier, France. 19-23 August 2002.

- van der Werf, J. H. J., Goddard, M. E., & Meyer, K. (1998). The use of covariance functions and random regressions in test day models. *Journal of Dairy Science*, 81(12), 3300-3308.
- VanRaden, P. M. (1997). Lactation yields and accuracies computed from test day yields and (co)Variances by Best Prediction. *Journal of Dairy Science*, 80, 3015-3022.
- Vargas-Leitón, B., & Cuevas-Abrego, M. (2009). Stochastic model to estimate economic values of production and functional traits in dairy cattle. *Agrociencia*, 43, 881-893.
- Verbyla, K. L., & Verbyla, A. P. (2009). Estimated breeding values and association mapping for persistency and total milk yield using natural cubic smoothing splines. *Genetics Selection and Evolution*, 41:48 doi: 10.1186/1297-9686-41-48
- Villegas, V. L. (1958). *Livestock Production in the Philippines*. Manila: Agricultural Credit and Cooperative Financing Administration.
- Voelker, D. E. (1981). Dairy herd improvement associations. *Journal of Dairy Science*, 64, 1269-1277.
- Weigel, K., & Rekaya, R. (2000). Genetic parameters for reproductive traits of Holstein cattle in California and Minnesota. *Journal of Dairy Science*, 83, 1072-1080.
- Wiggans, G. R., & Dickinson, F. N. (1985). Standardization of NCDHIP dairy cattle lactation records. *National Cooperative Dairy herd Improvement Program handbook factsheet G2*.
- Wiggans, G. R., Misztal, I., & Van Vleck, L. D. (1988). Implementation of an animal model for genetic evaluation of dairy cattle in the United States. *Journal of Dairy Science*, 71(Suppl. 2), 54-69.
- Wilcox, C. J., Webb, D. W., & De Lorenza, M. A. (2003). Genetic Improvement of Dairy Cattle. *University of Florida IFAS document DS75*. Florida, USA: University of Florida Cooperative Extension Service.
- Wilmink, J. B. M. (1987a). Comparison of different methods of predicting 305-day milk yield using means calculated from within-herd lactation curves. *Livestock Production Science*, 17, 1-17.

- Wilmink, J. B. M. (1987b). Adjustment of lactation yield for age at calving in relation to level of production. *Livestock Production Science*, 16(14), 321-334.
- Wilmink, J. B. M. (1987c). Adjustment of test-day milk, fat and protein yield for age, season and stage of lactation. *Livestock production science*, 16(4), 335-348.
- Wilmink, J. B. M. (1988a). Effects of incomplete records on relations among cumulative yields in first lactation and on extension of part lactations. *Livestock Production Science*, 18 (1), 19-34.
- Wilmink, J. B. M. (1988b). Selection on fat and protein to maximise profit in dairy herds. *Livestock Production Science*, 20, 299-316.
- Wolfova, M., Wolf, J., Kvapilík, J., & Kica, J. (2007). Selection for profit in cattle: I. Economic weights for purebred dairy cattle in the Czech Republic. *Journal of Dairy Science*, 90, 2442–2455.
- Wood, P. D. P. (1967). Algebraic model of the lactation curve in cattle. *Nature*, 216, 164-165.