**Evaluation and development of animal breeding in Ireland**

**Moorepark Research Centre**

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# 1. SUMMARY

*The primary objectives of this study were: 1) to annually evaluate the pertinence of the Irish dairy cattle breeding index, the Economic Breeding Index (EBI) and where necessary modify, 2) to evaluate the potential of do-it-yourself milk recording as an alternative to current supervised methods of milk recording, and 3) to estimate the level and rate of accumulation of inbreeding in Irish dairy and beef cattle, to quantify its effects on traits of economic importance, and to develop remedial measures to minimise the future accumulation of inbreeding in Ireland.*

Revisions of the EBI were undertaken throughout this study both as the addition of new traits as well as the calculation of respective economic values. Cumulative discounted genetic expression were derived and these were used with the economic values to optimally weight traits with differential in their timing and frequency of expression. Over the years, the emphasis on production within the EBI has decreased with the genetic response in calving interval expected to be favourable. Milk recording using DIY with only one sample taken for analysis of milk composition is a viable alternative to supervised milk recording. Inbreeding in the Irish Holstein-Friesian population is increasing at a rate of 0.10% per year which is similar to most other countries. However, inbreeding depression in milk production is lower in Ireland than observed in most other Holstein-Frisian populations although the effect of inbreeding on fertility is greatest in Ireland. A primiparous animal, 12.5% inbred (i.e., following the mating of non-inbred half sibs), is expected to have reduced milk, fat and protein yield of 61.8 kg, 5.3 kg and 1.2 kg, respectively, reduced fat and protein concentration of 0.05% and 0.01%, respectively, and increased somatic cell score (i.e. natural log of somatic cell count divided by 1,000) by 0.03. The 12.5% inbred animal was also expected to have a 2% greater incidence of dystocia, a 1% greater incidence of stillbirth, an increase in calving interval of 8.8 d, an increase in age at first calving of 2.5 d and a reduced survival to second lactation of 4 percentage units.

# 2. INTRODUCTION

Sustainable increases in profitability through genetic selection is dependent on many factors including a breeding goal with pertinent traits and accurate economic weights, ample phenotypic data to aid accurate estimation of genetic differences among animals, and a world class breeding program to ensure the most genetically superior animals are used in commercial herds while simultaneously maintaining genetic diversity. This study addresses each of these issues.

The Economic Breeding Index (EBI) was officially launched to the dairy industry in February 2001 by the Irish Cattle Breeding Federation. The EBI replaced the relative breeding index (RBI) which was a relative breeding goal made up of milk yield, fat yield, protein yield and protein percent. Continual updating of any total merit index is vital to ensure both the traits and economic weights in the total merit index are pertinent to when progeny from animals selected on the index start producing.

Cumulative discounted expressions (CDEs) are vital in the derivation of economic weights within breeding objectives. They account for differential rates and timing of expression of traits as well as accounting for the transfer of germplasm across sub-populations. This transfer of germplasm across sub-populations (e.g., dairy populations to beef populations or vice versa) occurs internationally although is rarely accounted for within breeding objectives. In Ireland, a large proportion of dams in beef herds originate within the national dairy herd. Despite this, prior to 2005 the expected beef performance of the descendants of a dairy sire was ignored within the national dairy breeding objective.

The level of milk recording in Ireland is low relative to most other major milk producing countries (ICAR, 2002), thereby hindering genetic progress

within the national dairy herd. Possible reasons for this low participation in milk recording in Ireland include the cost and inconvenience of the current official milk recording service. One possible option to help minimise these disadvantages is to encourage farmers to undertake the milk recording themselves and possibly reduce the necessity to take milk samples for composition analyses at both the morning and evening milking.

Inbreeding is defined as the probability that two alleles at any locus are 'identical by descent' and occurs when related individuals are mated. Inbreeding produces inbred animals and the degree to which an animal is inbred is measured by its inbreeding coefficient. Concerns over increased rates of accumulation of inbreeding are mounting, attributable mainly to the known deleterious effects of inbreeding depression. Inbreeding depression refers to the reduction in mean phenotypic performance as a result of inbreeding.

The objective of most commercial livestock breeding programmes is to maximise genetic gain for a particular breeding objective. However, it is now recognised that this goal must not be sought at the expense of losing genetic diversity, which can impact on long term genetic gain. Long term control of inbreeding will rely on minimising the genetic relationships both among the population of young test bulls and between the population of young test bulls and the future breeding female population. To date, no systematic approach has been taken in Ireland when selecting young test sires for progeny testing and subsequent widespread use in the national population. Although this approach has been sufficient to date, selection on genetic merit alone might not result in maximum genetic response over a longer time horizon. Selection decisions made now will influence the future relatedness with the Irish cattle population and an accumulation of inbreeding in the population will reduce the genetic variance resulting in reduced long-term response to selection.

*The primary objectives of this study were: 1) to annually evaluate the pertinence of the Irish dairy cattle breeding index, the Economic Breeding Index (EBI) and where necessary modify, 2) to evaluate the potential of do-it-yourself milk recording as an alternative to current supervised methods of milk recording, and 3) to estimate the level and rate of accumulation of inbreeding in Irish dairy and beef cattle, to quantify it effects on traits of economic importance, and to develop remedial measures to minimise the future accumulation of inbreeding in Ireland.*

## 3. CUMULATIVE DISCOUNTED GENETIC EXPRESSIONS

The aim of the current task was to derive generic equations, using transition probability matrices, to track the flow of genes across alternative production systems and to apply the equations to a representative Irish production system.

### 3.1 Materials and Methods

This task extends the discounted genetic expressions approach outlined by Amer et al. (2001) to a situation where descendants of specific animals are mated to more than one breed.

*3.1.1 Lifetime Survivability and Transition Matrices.*

A vector $\mathbf{a}^\alpha$ was calculated for each breed type ($\alpha$) to represent the probability of a cow surviving to and calving at age $i$, given it was alive at age $i$=1. A vector ($\mathbf{d}^\alpha$) describing the probability of a cow not surviving to $i$ years of age, was also calculated for each breed type from the respective $\mathbf{a}^\alpha$ vector. A vector $\mathbf{f}^\alpha$ was created to describe the number of calves born (including stillbirths) per cow at $i$

years of age allowing for the probability of multiple births but also for the possibility of barren cows remaining in the herd without producing a calf.

Let $\mathbf{D}^{\alpha}$ be an $h$ by $h$ transition matrix with columns of survival probabilities of breed $\alpha$ times the probability of producing a calf, lagged by one row for each new birth year. The variable $h$ represents the planning horizon, in years, from the birth of the self-replacing female. In the present study $h$ was set to twenty years. Thus, the $(i,j)^{th}$ element of each $\mathbf{D}^{\alpha}$ matrix was specified as follows:

$$D_{i,j}^{\alpha} = \begin{cases} a_{i-j}^{\alpha} \circ f_{i-j}^{\alpha} & \text{for } j < \text{afc}^{\alpha} + i - 1 \text{ and } i - j \leq c \\ 0 & \text{otherwise} \end{cases}$$

where $\circ$ represents the Hadamard product of the respective vectors, $afc^{a}$ denotes age at first calving for breed type $\alpha$ and $c$ represents the age culling threshold.

Matrices for cull cow expressions ($\mathbf{G}^{\alpha}$) and replacement heifer expressions ($\mathbf{H}^{\alpha}$) were calculated as:

$$G_{i,j}^{\alpha} = \begin{cases} d_{i-j}^{\alpha} & \text{for } j < \text{afc}^{\alpha} + i - 1 \text{ and } i - j \leq c + 1 \\ 0 & \text{otherwise} \end{cases}$$

$$H_{i,j}^{\alpha} = \begin{cases} 1 & \text{for } i = j + \text{afc}^{\alpha} - 1 \\ 0 & \text{otherwise} \end{cases}$$

*3.1.2 First Appearance of a Cow's Genes over Successive Generations.*

An $h$ by 1 vector ($\mathbf{g}_{k}^{\alpha}$) describing first appearances of genes in generation $k$=1 to $m$ of a cow of breed $\alpha$ that calves at least once were calculated as:

$$\mathbf{g}_k^\alpha = \begin{cases} [1,0,\ldots,0]' & \text{for } k = 1 \\ \dfrac{1}{2} \cdot \omega^{\alpha R} \cdot \mathbf{D}^\alpha \cdot \mathbf{g}_{k-1}^\alpha & \text{for } k = 2\ldots m \end{cases}$$

where *m* is the number of generations for which the flow of genes were tracked; in the present study *m* was set to twelve. Aggregate yearly first appearances of genes accumulated over the *m* generations were calculated as the sum of the $\mathbf{g}^\alpha$ vectors:

### 3.1.3 Multiple Expression of a Cow's Genes.

The **D**, **G**, and **H** matrices are used to multiply first appearances of a cow's genes to the actual expressions throughout her life and the lives of her self-replacing female descendants. A discounting vector (**q**) was created which is used throughout the calculations to discount the expressions back to a given time period. The vector **q** accounts for a lag of one year (i.e., row) in the **D**, **G**, and **H** matrices and discounts back to the time of birth of the animal accruing from the original mating.

The $i^{th}$ element of the discounting vector was defined as:

$$q_i = \left( \frac{1}{1+r} \right)^{i-1}$$

where *r* is a discounting factor.

### 3.1.3. Trait Categories.

Cumulative discounted expressions in integrated cattle populations need to account for the probabilities of cow and calf trait expressions occurring through

alternative pathways. Depending on the prevailing circumstances animal breeders may be interested in the CDE following the initial mating of either a breed A male or a breed B male with a breed A female. Separate vectors and matrices may be derived for each (cross)breed.

In the present study, six main trait categories were defined. These included annual traits (e.g., reproductive efficiency, lactation), replacement heifer traits (e.g., live weight at first calving), cull cow traits (e.g., carcass weight at culling), birth traits (e.g., birth live weight), yearling traits (e.g., yearling live weight) and slaughter traits (e.g., carcass conformation). The vectors and matrices previously defined were used to build equations for predicting CDEs for the six trait categories.

*3.1.4 Case study (Ireland).*

This case study represents the Irish system of cattle farming where a strong relationship exists between dairy (Breed A) and beef (Breed B) enterprises. A large proportion of dairy farms either supply animals to or operate a beef enterprise. Initial parameters required for the calculations were obtained from national data. An additional vector summarising the proportion of self-replacing dairy females of different ages mated to beef males was created based on national data. In a situation of complete market failure the benefits to the dairy farmer of generating superior crossbred replacement females for the beef herd are not realised through premium prices. Sensitivity analyses were performed by altering the various input parameters including the degree of market failure and recalculating the CDEs.

## 3.2 Results and Discussion

The CDE for each of the six trait categories following an initial mating between either a dairy male (Breed A) or a beef male (Breed B) with a dairy female are summarised in Table 1. A contributing factor to the difference in CDE between annual and replacement heifer traits is because heifer replacement traits are only expressed once per lifetime. Cumulative discounted expressions of cull cow traits are in turn lower than the CDE for replacement heifer traits because a cow is only culled once, while only a proportion actually exhibit the trait. Additionally culling occurs after a time delay and so cull cow expressions are discounted accordingly. Poorer cow longevity and/or lower cow mortality reduced the relative difference between the CDE for replacement heifer and cull cow traits.

The difference between the CDE for birth traits and yearling/slaughter traits arises because females destined to become replacements were not counted as expressing yearling or slaughter traits. Greater discounting and mortality also contribute to the difference in CDE between birth and yearling/slaughter traits. Differences in the CDE for yearling and slaughter traits reflect mortality from yearling to slaughter and higher discounting to age at slaughter.

**Table 1.** *Cumulative discounted expressions for annual, replacement heifer, cull cow, birth, yearling and slaughter traits.*

|  | Initial breed mating | |
| --- | --- | --- |
| Trait | A x A | B x A |
| Annual | 0.89 | 0.24 |
| Replacement heifer | 0.28 | 0.06 |
| Cull cow | 0.19 | 0.04 |
| Birth | 1.05 | 0.66 |
| Yearling | 0.66 | 0.45 |
| Slaughter | 0.59 | 0.41 |

It is important to realise that some annual traits may be economically relevant in dairy enterprises but not in beef enterprises, and vice versa. For example, the genetic merit of a dairy sire in Ireland for lactation milk yield will be irrelevant to a beef farmer; hence the expressions of these traits in beef herds should not be included in the CDE of a dairy sire for lactation milk yield.

Assuming that shortly after birth crossbred (AB) females destined to become replacement females (in Ireland this represents 12% of AB progeny) enter a beef herd, then less than 13% of the total CDE for all trait categories (using current input parameters) are expressed in the beef herd when the initial mating is between a dairy male and a dairy female. However, a number of the purebred dairy expressions for yearling and slaughter traits may also occur in the beef herds since a large proportion of surplus purebred and crossbred dairy progeny in Ireland will be finished in beef herds.

When no crossbred progeny enter beef herds the intensity of market failure is irrelevant. Under complete market failure the CDE of a dairy sire's genes for birth traits when mated to a dairy female decreased as the proportion of crossbred females entering the beef herd increased. The opposite was true when no market failure existed. Market failure does not exist if a farmer operates both a dairy and beef enterprise or a dairy farmer has a reputation for producing superior crossbred replacement females. For example, an Irish beef farmer may actively seek crossbred females from dams with favorable beef characteristics. However, in the majority of countries the full economic benefits of crossbred animals and their descendants are rarely realised by the generating farmer. This questions the (full) inclusion of such expressions in the CDE of the original sire. Nevertheless, the fundamental aim of all national breeding organisations should be to maximise genetic gain and profitability across all cattle. Thus, a national breeding organisation may choose to ignore market failure thereby servicing the entire cattle industry as a whole.

The CDE of a beef sire for all traits when mated to a dairy female were lower than for a dairy sire mated to a dairy female because of the low proportion of resulting progeny that enter the beef herd as beef replacements. Based on the parameters used in the present study, the CDE of yearling/slaughter trait genes of a beef sire are greater than the discounted expressions of annual cow traits of the sire. The difference between birth and yearling/slaughter traits was low because very few self-replacing female replacements were sourced from this breed type.

## 4. DEVELOPMENT OF THE ECONOMIC BREEDING INDEX

The objective of this task was to annually review the pertinence of the EBI to future dairy production systems in Ireland and to use all available data and knowledge of the future economic and social climate to ensure the EBI was applicable to Irish dairy farmers. The economic breeding index (EBI) has undergone many changes during this project in relation to the genetic evaluation statistical models, the traits and their economic weights.

### 4.1 Developments in 2004

Economic values for the milk production and fertility traits are derived using the Moorepark bioeconomic model (Shalloo et al., 2004). In 2004 the economic values were updated. Following analyses of the implications of the Fischler proposals, the Food and Agricultural Policy Research Institute Ireland partnership (FAPRI-Ireland) predicted a fall in milk price from 28 cents/kg to 22.2 cents/kg under the Fischler proposals (FAPRI, 2003). Male calf value of €102 and a cull cow value of €270 were also predicted (FAPRI, 2003); the previous male calf and cull cow value were €190 and €381, respectively.

In line with a fall in milk price, quota purchasing cost was reduced in the bioeconomic model from 9.8 cents/litre to 4.8 cents/litre. Quota purchase price was assumed to be €1/gallon and the money was assumed to be borrowed over 5 years at 4% interest. The estimated cost included the interest and capital repayments. Also the cost of rearing a replacement heifer was revised in the EBI for 2004 to be €1,319. Processing costs were also updated in the bioeconomic model with total reductions set to 6.332 euro cents/kg of which 4 euro cents was processing costs. In 2004, revised lactation curves based on national data were also included in the bioeconomic model. The impact of all changes in the EBI are detailed in Table 5.

**4.2 Developments in 2005**

In 2005 calving performance and beef performance traits were included in the EBI. Calving performance traits included direct calving difficulty, maternal calving difficulty, direct gestation length, and direct calving mortality. Beef performance traits included cull cow weight, and progeny carcass weight, carcass conformation and carcass fat score. Economic values were calculated for each of these traits which were subsequently multiplied by the appropriate cumulative discounted genetic expression to obtain the economic weight.

The economic costs of dystocia include increased stockman labour hours, veterinary fees, an increased probability of calf and cow mortality and reduced subsequent cow performance (both production and reproductive). For the purpose of inclusion in the EBI, the economic value for calving difficulty was defined based on an underlying liability scale within subclasses of sex of calf by age of dam (parity 1, 2, ≥3) with the phenotypic values assumed to follow a normal distribution (Meijering, 1980). The phenotypic value of an animal (on the underlying scale) relative to the thresholds will determine the category of assistance required by the animal. The categories of assistance considered were:

1) no assistance; 2) slight assistance, 3) severe assistance, 4) veterinary assistance (excluding caesarean section), and 5) caesarean section.

**Table 2.** *Full economic value of a 1% change in the proportion of cows requiring severe calving assistance or worse in a dairy herd.*

| Item | Caesarean | Veterinary assistance | Severe assistance | Slight assistance | Herd average cost |
|---|---|---|---|---|---|
| Stockman hours | 6 | 4 | 4 | 1 | |
| Stockman cost (€) per hour | 13 | 13 | 13 | 13 | |
| Veterinary costs (€) | 160 | 40 | 0 | 0 | |
| Probability of a dead cow | 0.05 | 0.025 | 0.025 | 0 | |
| Cost of a dead cow (€) | 1319 | 1319 | 1319 | 1319 | |
| Reduced reproductive success | 0.25 | 0.1 | 0.05 | 0 | |
| Barren cow costs (€) | 1026 | 1026 | 1026 | 1026 | |
| Lost milk (litres) | 600 | 150 | 50 | 0 | |
| Cost of lost milk (€) | 0.17 | 0.17 | 0.17 | 0.17 | |
| Calving cost relative to no assistance | 662 | 253 | 145 | 13 | |
| Percentage of calvings with 6% difficult | 0.97 | 2.51 | 2.52 | 20.28 | 20.82 |
| Percentage of calvings with 7% difficult | 1.19 | 2.94 | 2.86 | 21.91 | 24.30 |
| Economic effect (€) per cow of 1% change | | | | | -3.25 |

Because the EBI is a multiple trait breeding index that includes milk yield, fat yield, protein yield, calving interval and survival (Veerkamp *et al.*, 2002) it was necessary to derive two distinct economic values for calving difficulty. All costs associated with changes in calving difficulty were included in one estimate (full economic value; Table 2) and all costs, excluding those associated with reduced milk production and fertility/survival, were included in the second estimate (reduced economic value; Table 3) to avoid double-counting. It was also

proposed to include calf mortality in the EBI. Therefore the cost of calf mortality associated with calving difficulty was not included in the economic value for calving difficulty.

**Table 3.** *Reduced economic value of a 1% change in the proportion of cows requiring severe calving assistance or worse in a dairy herd.*

| Item | Caesarean | Veterinary assistance | Severe assistance | Slight assistance | Herd average cost |
|---|---|---|---|---|---|
| Stockman hours | 6 | 4 | 4 | 1 | |
| Stockman cost (€) per hour | 13 | 13 | 13 | 13 | |
| Veterinary costs (€) | 160 | 40 | 0 | 0 | |
| Calving cost relative to no assistance | 238 | 92 | 52 | 13 | |
| Percentage of calvings with 6% difficult | 0.97 | 2.51 | 2.52 | 20.28 | 10.32 |
| Percentage of calvings with 7% difficult | 1.19 | 2.94 | 2.86 | 21.91 | 11.86 |
| Economic effect (€) per cow of 1% change | | | | | -1.31 |

Assuming gestation length is independent of calving to conception interval then each one day increase in gestation length is synonymous with a corresponding one day increase in calving interval. The economic value for calving interval currently included in the EBI is -€7.09/day. Thus, the economic value for gestation length is -€7.09/day.

The economic value for calf mortality is the opportunity cost of the calf (i.e., the price obtainable for a newborn calf). Male calf value and female calf value were assumed to be €102 and €315, respectively in accordance with prices included in the bio-economic model based on FAPRI projections (FAPRI, 2003). In 2003, 57% of stillbirths in Ireland were males. The weighted average value of a

black and white calf was therefore assumed to be €193.59. Hence, the economic value per percentage increase in calf mortality is -€1.94.

The economic value for cow carcass weight is a function of three separate factors. The revenue from increased carcass size, the cost of increased maintenance of the cow and the cost of the increased energy demands of the cow as a growing nulliparous female.

The revenue attainable from a cull cow carcass is a function of the average carcass price per kg. However, animals slaughtered at a carcass weight of less than 272 kg are heavily penalised; it is assumed that they receive half the average cull cow price. Thus, as carcass weight increases the carcass value increases by the average carcass price per kg for each incremental kg increase in carcass weight. However, the proportion of cows with a carcass weight of greater than 272 kg also increases thereby increasing the average carcass price per kg across the population. Using the national distribution of cull cow carcass weights an average increase in carcass weight by 1kg, will increase the proportion of cows with a carcass weight >272 kg by 0.7 percentage units. The weighted average price of O3's was €1.61 /kg carcass weight. Thus, the economic benefits of a kg increase in carcass weight is €3.00.

The bio-economic model (Shalloo et al., 2004) includes a variable for cow live-weight as well as grass growth rate patterns; this facilitated the calculation of maintenance cost per incremental kg increase in live-weight. The maintenance cost per lactation for each incremental kg increase in liveweight was €0.167/year. Assuming a 45% kill out percentage this equates to €0.371/kg carcass weight (i.e., €0.167/0.45).

In order for the cow to attain the heavier weight she also requires an additional amount of energy as a growing female. Every additional 1 kg increase in liveweight requires an additional 4.5 UFL of energy throughout the growing

process (Jarrige, 1989). We can estimate the amount of this energy that comes from grazed grass, grass silage and concentrate. We can then convert this to kg of dry matter required and from there we can cost the additional energy required. Assuming a kill out percentage of 45%, the growing cost to increase carcass weight by 1kg is €0.88 (i.e., €0.398/0.45). Each of the three components of cow live-weight are expressed at different frequencies over different time horizons.

The economic value for calf carcass weight is the price attainable per kg carcass less the cost of increased dry matter intake associated with the increase. A projected future base carcass price of €2.40 was assumed. A projected price differential to O4L was assumed to be -€0.12 (Farmers Journal, 18th December 2004). Thus, the projected carcass price for a typical O4L steer is €2.28/kg carcass weight. The cost for each extra kg increase in carcass weight was calculated to be €1.06. Thus, the economic value for carcass weight is €2.28 - €1.06 = €1.22/kg.

The economic values applied to carcass conformation score and fat score were based on the relationships between carcass conformation and fat score and carcass cut weights. Data on carcasses of animals where both carcass conformation and cut weights have been measured were used to estimate the relationships between carcass conformation and fat score (recoded to a 15 point scale) and cut weights. The resulting (phenotypic) coefficients were used to derive economic values for carcass conformation and fat score. The economic value for carcass conformation and fat score were €5.24 and -€8.19, respectively

### 4.3  Developments in 2006

In 2006, a health subindex was added to the EBI including the traits somatic cell count and lameness. This increased the number of traits in the EBI from 13 to 15. Furthermore EBI's were made official for alternative breed sires on a common base. Due to a paucity of data on lameness and mastitis several assumptions had to be made when deriving economic values for these traits.

When deriving the economic value for lameness we wanted to investigate the marginal cost associated with shifting the mean of the underlying distribution. It is convenient that the height of the normal distribution at the truncation point giving the appropriate incidence gives us the expected change in incidence per unit change on the underlying scale. This is identical to taking the first derivative of a profit function which incorporates the incidence probability as a function of the mean of the underlying trait. The value of the distribution function at the truncation point then gets multiplied by the economic cost of an occurrence. This method is easily expanded to multiple categories of incidence (i.e. separate incidences of farmer treatment and veterinary treatment) with the products of probability changes and incidence costs summed over incidence categories to derive the economic value of a unit incremental change in the mean of the underlying distribution. Because there is a clear relationship between the underlying mean and the combined probability over all incidence categories, the units of the economic value can be translated to have units of the incidence rate of all cases of lameness (i.e. with a mean of 15%). This is done by dividing the underlying scale economic value by the expected change in the combined probability over all incidence categories per unit change in the underlying scale. The required value can be taken as the height of the underlying standard normally distributed trait at the truncation threshold which gives a 15% incidence. Hence, the economic value per incidence of any lameness accounting for both veterinary treated and farmer treatment costs was calculated as €53.83/case. When the same calculations are repeated but ignoring the farmer treatment costs, the economic value of any lameness was reduced to a value of €32.43/case.

Hence, the index weight on locomotion is calculated as:

€53.83 * 0.147 * 0.144 = €1.13/standardised locomotion score

The figure €53.83 represents the economic value for lameness per new case, 0.147 is the genetic regression of lameness on locomotion and 0.144 is the standard deviation of the PTAs of the base bulls for locomotion which is used to standardise the published locomotion scores between ±3.

The effect of an incremental change in the mean of the underlying normal distribution on the area under the curve between the thresholds mild and severe mastitis and between the threshold for severe mastitis and infinity were derived using the same methodology as described above for lameness. The change was multiplied by the respective costs and summed to give the economic value. This was re-scaled to an incidence rate based on the overall incidence of mastitis (i.e., 25%). The economic value for per case of mastitis was calculated as €71.84. A genetic correlation of 0.70 was assumed between SCS and mastitis which is the average across most studies that have investigated such (for review see Mrode and Swanson, 1996). Based on this correlation and the assumed incidence of 25% mastitis, it was possible to estimate the genetic regression of mastitis on SCS as:

$$b = r \cdot \frac{\sigma_{Mastitis}}{\sigma_{SCS}}$$

where $r$ is the genetic correlation, $\sigma_{Mastitis}$ is the genetic standard deviation of mastitis and $\sigma_{SCS}$ is the genetic standard deviation of SCS. The estimated genetic regression coefficient of mastitis on SCS was 0.167.

Hence, the index weight on SCS is calculated as:

€71.84 * 0.167 = €11.99 / unit SCS

The figure €71.84 represents the economic value for mastitis and 0.167 is the genetic regression of clinical mastitis incidence on SCS. Clinical mastitis incidence is an annual trait and thus has a cumulative discounted expression of one; hence the economic value equals the economic weight.

Somatic cell count also has an economic value in its own right because of its effect on milk price paid to the farmer. In Ireland, tiered pricing operates based on the monthly arithmetic mean of the bulk tank SCC. A shift in the distribution of the national herd SCS was modelled across each month of the year by obtaining the first derivate of the integral for each month separately. Although investigation of national SCC data revealed that the variance of a log-normal distribution of SCC changes with the mean, the variance of the normally distribution SCS did not, thereby justifying using the first derivative of the integral as an estimate of a incremental change. The economic effect on milk price based on the change in proportion of herds within each of the SCC bands was estimated on a monthly basis. The monthly effects on milk price were weighted by the milk supply pattern of a spring calving herd and were summed to give the weighted annual effect on milk price. The sum was multiplied by 6000 which is the average cow yield assumed in the bioeconomic model; this is the economic value. The economic value per unit $log_e$SCC (i.e. SCS) was €44.75 when assuming the Dairygold band pricing system and €42.23 when assuming the Glanbia band payment system. Hence, the average economic value of €43.49 per unit change in SCS is proposed.

## 4.4. Developments in 2007

Up to 2007, the limiting factor in the bioeconomic model was set to be milk quota. However, in 2007, the assumption was that milk quota would no longer be the limiting factor at farm level from 2013 and possibly then the next limiting factor would be land for most farms. Therefore the economic values were calculated from the bioeconomic model assuming that land was the limiting factor at farm level. In 2007, the Irish Dairy Board (IDB) paid a fat to protein ratio of 1.9 to 1 which was very similar to ratio in EU markets. However with support

for fat reducing within the EU budget the ratio of protein to fat was expected to increase to closer to 2.6:1 when quota was not the limiting factor.

The availability of additional carcass cut yield data facilitated more accurate quantification of the EUROP classification scoring system within carcass cut yield. Furthermore, a survey of veterinary charges undertaken by the Irish Farmers Journal provided a better estimate of veterinary charges associated with calving difficulty in Ireland. Median price of a caesarean increased from €160 to €204 while the median price to attend a calving increased from €40 to €70. A knackery charge to remove a dead calf of €20 was also imposed and the economic weight on gestation length was altered in line with changes in the economic value for calving interval as outlined below.

### 4. 5 Developments in 2008

A considerable increase in milk price paid was observed in international markets in 2007 and it was envisaged that this greater than expected milk price was anticipated to remain for several years. Therefore, in 2007 it was decided to undertake research in the impact of increasing milk price in the bioeconomic model as well as updating the costs of production. FAPRI projected a short-term and long-term milk price of 30 c/l and 26c/l, respectively while the OECD predicting a milk price of 28 c/l. It was the view of the dairy industry to implement the milk price of 30 c/l. This impacted on the economic values of milk yield, fat yield, protein yield, calving interval and survival. The impact of land being the limiting constraint as well as increased feed costs on cull cow live-weight was also investigated. The cost of growing an animal to an extra kg live-weight increased from €0.398 to €0.743 while the annual cost per extra kg live-weight increased from €0.167 to €0.295. Changing milk price also affected the economic weight on direct calving difficulty, lameness and somatic cell count as

well as the economic weight on gestation length through its effect on the economic weight on calving interval.

## 4.6 Impact of changes in EBI

A summary of the index weighting factors in the RBI and the different EBI's is given in Table 5. The economic weights on most traits within the EBI have increased with time in line with inflation although large increases in the absolute economic value for calving interval have been observed due mainly to changes in the bioeconomic model most notably the inclusion of milk production lactation profiles derived from national data for each month of calving. The heritability of each index was calculated as follows:

$$h^2 = \frac{\sum_{i=1}^{15}(ew_i^2 \cdot \sigma_{a_i}^2)}{\sum_{i=1}^{15}(ew_i^2 \cdot \sigma_{p_i}^2)}$$

where $ew_i$ is the economic weight on trait $i$ in the breeding goal, $\sigma_{a_i}^2$ is the additive genetic variance of trait $i$ and $\sigma_{p_i}^2$ is the phenotypic variance of trait $i$.

The heritability of RBI, EBI2001, EBI2004, EBI2005, EBI2006, EBI2007 and EBI2008, was 0.350, 0.113, 0.072, 0.074, 0.079, 0.061 and 0.066, respectively. The decrease in heritability of the breeding goal over time is due to the increased emphasis on low heritability traits such as calving interval and survival.

*4.6.1 Correlations between sire proofs*

A total of 2,710 AI sires with a reliability for milk yield of at least 70% were used to determine, using correlation analyses, the effect of changes in the EBI over the years on the ranking of sires. The correlations among sire RBI and the various EBI's is detailed in Table 4. The low correlation between the RBI and EBI (in particular the most recent EBIs) is due to increased emphasis on calving interval which is unfavourably correlated with milk production, the only traits included in the RBI.

**Table 4.** *Correlations between sire proofs (n=2710) for RBI and the various EBIs over the years*

| Index | RBI | EBI2000 | EBI2004 | EBI2005 | EBI2006 | EBI2007 |
|-------|-----|---------|---------|---------|---------|---------|
| EBI2000 | 0.87 | | | | | |
| EBI2004 | 0.59 | 0.86 | | | | |
| EBI2005 | 0.58 | 0.59 | 0.85 | | | |
| EBI2006 | 0.51 | 0.79 | 0.95 | 0.98 | | |
| EBI2007 | 0.13 | 0.48 | 0.82 | 0.85 | 0.90 | |
| EBI2008 | 0.35 | 0.66 | 0.92 | 0.94 | 0.97 | 0.97 |

*4.6.2 Impact of change in breeding goal on response to selection and relative emphasis*

Genetic and phenotypic (co)variance matrixes with categories of traits evaluated together in a multi-trait analysis were obtained from the respective parameters included in the genetic evaluations. Genetic correlations between traits not evaluated together were estimated from correlations between EBVs of sires of moderate to high reliability. The P, G and C matrixes required for analysis using selection index theory were derived from the respective genetic and phenotypic parameters assuming a progeny group size of 100 for all traits. Traits included in the breeding goal were identical to those included in the selection index and only a single trait for calving interval and survival (parameters were based on the average across lactations) were used. These

matrices were also used to derive the weighting factors as well as the standard deviation of the breeding goal and selection index.

An annual response to selection of 0.22 standard deviations of the selection index was assumed. The response to selection in the individual traits is summarised in Table 6. The standard deviation of the breeding goal was 25, 69, 83, 90, 96, 116 and 129 for the RBI, EBI2001, EBI2004, EBI2005, EBI2006, EBI2007 and EBI2008, respectively; the respective standard deviations of the index (assuming a progeny group size of 100) was 24, 60, 66, 76, 82, 95 and 106. EBIs are on a PTA basis so these standard deviations must be divided by 2. The response to selection based on the responses per trait from selection on each breeding goal and the economic values of the EBI in 2008 assuming 0.22 standard deviations per annum are €10.81, €15.39, €19.79, €22.15, €22.51, €23.02 and €23.33 for the RBI, EBI2001, EBI2004, EBI2005, EBI2006, EBI2007 and EBI2008, respectively.

The top 100 AI sires (of at least 70% reliability for milk production; n=2710) were ranked on each index separately and their mean predicted transmitting abilities calculated; the results are summarised in Table 7.

The response to selection in fat and protein yield with the EBI is lower than selection on the RBI due mainly to the large emphasis on calving interval which is unfavourably correlated with fat and protein yield. The mean genetic merit of the top 100 sires for fat and protein yield for the EBI2008 is half that of the top 100 sires on RBI; however, what is important to remember is that genetic evaluations for milk production in Ireland are based on a standardised 305-day lactation and therefore does not account for a potentially shorter lactation length (and thus a potentially lower yield) of cows calving later in the year under a seasonal calving system which is not currently reflected in the sire's genetic merit for milk production. One could argue that the deficit in difference in genetic merit could be met, if not surpassed, by longer lactation lengths of a more fertile

population following selection on the EBI. The RBI was expected to increase (i.e., unfavourable) calving interval in the population by 0.46 days/year which is in contrast to the expected reduction (i.e., favourable) decline of -0.83 days/year with selection on the EBI2008; the effect is even greater when looking at the top 100 sires ranked on EBI2008. Furthermore, the greater increase in functional survival with selection on the EBI will result in a more mature herd which may subsequently result in greater herd yield for the same number of cows, as well as facilitating herd expansion. The RBI was selecting towards larger cows while the most recent EBIs are selecting towards smaller cows. The inclusion of fertility in the EBI is likely to minimise any effect of selection for lower cow weight on lower body condition score.

The response to selection from selection on the current EBI for the traits included in the EBI were almost all in the favourable direction with the exception of calf mortality, progeny carcass fat score and locomotion score (Table 6) all of which have a low relative emphasis in the EBI (Table 8; Figure 1).

**Table 5.** *Summary of the economic weighting factors on the different traits for the RBI and EBI's*

| Index / trait[†] | Const. | MILK kg | FAT kg | PROT kg | PROT % | CIV | SUR | DCD | MCD | GEST | MORT | CWT | CCONF | CFAT | CULL | LOCO | SCS |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| RBI | 100 | -0.014 | 0.36 | 1.64 | 74 | | | | | | | | | | | | |
| EBI2001 | | -0.08 | 0.86 | 5.7 | | -2.07 | 11.4 | | | | | | | | | | |
| EBI2004 | | -0.08 | 1.5 | 5.22 | | -7.09 | 10.77 | | | | | | | | | | |
| EBI2005 | | -0.076 | 1.5 | 5.22 | | -7.09 | 10.77 | -2.96 | -1.48 | -4.47 | -2.58 | 0.92 | 3.93 | -6.14 | 0.04 | | |
| EBI2006 | | -0.084 | 1.55 | 5.27 | | -7.17 | 10.8 | -2.96 | -1.48 | -4.52 | -2.58 | 1.38 | 5.99 | -4.49 | 0.04 | 1.13 | -55.48 |
| EBI2007 | | -0.085 | 0.96 | 5.36 | | -10.87 | 10.51 | -3.26 | -1.73 | -6.85 | -2.85 | 1.38 | 10.32 | -11.71 | 0.04 | 1.13 | -55.48 |
| EBI2008 | | -0.09 | 1.26 | 6.91 | | -11.97 | 11.17 | -3.65 | -1.73 | -7.54 | -2.85 | 1.38 | 10.32 | -11.71 | -0.5 | 1.13 | -57.21 |

[†]RBI = relative breeding index; EBI2001= economic breeding index in 2001; EBI2004= economic breeding index in 2004; EBI2005= economic breeding index in 2005; EBI2006= economic breeding index in 2006; EBI2007= economic breeding index in 2007; EBI2008= economic breeding index in 2008; MILK kg = milk yield; Fat kg = fat yield; PROT kg = protein yield; PROT% protein percent; CIV = calving interval; SUR = survival; DCD = direct calving difficulty; MCD = maternal calving difficulty; GEST = gestation length; MORT = calf mortality; CWT = progeny carcass weight; CCONF = progeny carcass conformation; CFAT = progeny carcass fat score; CULL = cull cow carcass weight; LOCO = locomotion score; SCS = somatic cell score.

**Table 6.** *Response to selection for the different traits from selection on the RBI or different EBI*

| Index / trait[†] | MILK kg | FAT kg | PROT kg | CIV | SUR | DCD | MCD | GEST | MORT | CWT | CCONF | CFAT | CULL | LOCO | SCS |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| RBI | 42.8 | 2.8 | 2.4 | 0.46 | 0.03 | 0.01 | 0.00 | -0.05 | -0.04 | 0.9 | -0.07 | -0.01 | 0.83 | 0.01 | -0.06 |
| EBI2000 | 31.7 | 2.4 | 2.2 | 0.13 | 0.13 | -0.04 | -0.02 | -0.04 | -0.03 | 0.7 | -0.06 | 0.00 | 0.48 | 0.00 | -0.05 |
| EBI2004 | -2.9 | 1.6 | 1.3 | -0.51 | 0.16 | -0.09 | -0.07 | -0.03 | 0.00 | 0.2 | -0.02 | 0.02 | -0.12 | 0.00 | -0.07 |
| EBI2005 | -0.2 | 1.5 | 1.2 | -0.50 | 0.17 | -0.19 | -0.16 | -0.05 | 0.04 | 1.4 | 0.03 | 0.01 | 0.16 | 0.00 | -0.09 |
| EBI2006 | -5.2 | 1.2 | 1.0 | -0.53 | 0.18 | -0.18 | -0.15 | -0.04 | 0.04 | 1.9 | 0.05 | 0.01 | 0.32 | -0.01 | -0.07 |
| EBI2007 | -29.1 | 0.1 | 0.2 | -0.92 | 0.19 | -0.23 | -0.19 | -0.02 | 0.07 | 1.4 | 0.09 | 0.02 | -0.19 | -0.01 | -0.07 |
| EBI2008 | -20.0 | 0.5 | 0.6 | -0.83 | 0.19 | -0.23 | -0.19 | -0.03 | 0.07 | 1.2 | 0.06 | 0.02 | -0.36 | -0.01 | -0.08 |

[†]For abbreviations see Table 24

**Table 7.** *Mean predicted transmitting ability for a range of traits of the top 100 sires ranked on each index separately*

| Trait | RBI | EBI2001 | EBI2004 | EBI2005 | EBI2006 | EBI2007 | EBI2008 |
|---|---|---|---|---|---|---|---|
| Milk yield | 258 | 261 | 138 | 170 | 121 | -51 | 79 |
| Fat yield | 15 | 14 | 11 | 12 | 11 | 2 | 7 |
| Protein yield | 13 | 12 | 8 | 9 | 8 | 1 | 6 |
| Fat % | 0.1 | 0.08 | 0.11 | 0.11 | 0.12 | 0.09 | 0.08 |
| Protein % | 0.09 | 0.07 | 0.07 | 0.07 | 0.07 | 0.06 | 0.06 |
| Calving interval | 0.9 | -0.59 | -2.66 | -2.18 | -2.61 | -5.29 | -3.85 |
| Survival | -0.28 | 0.72 | 1.31 | 1.13 | 1.21 | 1.8 | 1.57 |
| Direct calving difficulty | 0.07 | -0.33 | -0.5 | -0.93 | -0.91 | -1 | -1.08 |
| Maternal calving difficulty | 0 | 0.02 | 0.09 | 0.16 | 0.18 | 0.34 | 0.28 |
| Gestation | -0.12 | -0.34 | -0.34 | -0.56 | -0.49 | -0.6 | -0.7 |
| Calf mortality | 0.08 | -0.08 | -0.03 | -0.16 | -0.12 | -0.06 | -0.11 |
| Cull cow carcass weight | 0.33 | -1.82 | -3.54 | -2.08 | -1.84 | -3.68 | -4.3 |
| Progeny carcass weight | 1.4 | 0.6 | -0.6 | 1 | 1.4 | -0.2 | -0.6 |
| Progeny carcass conformation | 0.06 | 0.1 | 0.18 | 0.16 | 0.2 | 0.35 | 0.26 |
| Progeny carcass fat | 0.05 | 0.07 | 0.11 | 0.09 | 0.08 | 0.14 | 0.14 |
| Locomotion | -0.37 | -0.28 | -0.24 | -0.27 | -0.24 | -0.15 | -0.2 |
| Somatic cell count | 0.04 | 0.04 | 0.04 | 0.04 | 0.01 | 0 | 0.02 |
| Overall type | -0.59 | -0.87 | -1.29 | -1.13 | -1.23 | -2.01 | -1.56 |
| Overall mammary | -0.51 | -0.7 | -1.08 | -0.93 | -0.97 | -1.6 | -1.25 |
| Overall feet & legs | -0.4 | -0.32 | -0.41 | -0.44 | -0.51 | -0.78 | -0.57 |
| Dairy composite | -0.28 | -0.49 | -0.84 | -0.77 | -1.06 | -2.18 | -1.37 |
| Body composite | -0.24 | -0.54 | -0.81 | -0.75 | -0.97 | -1.84 | -1.24 |

**Table 8.** *Change in relative emphasis for each trait calculated using the method of Van Raden, (2002).*

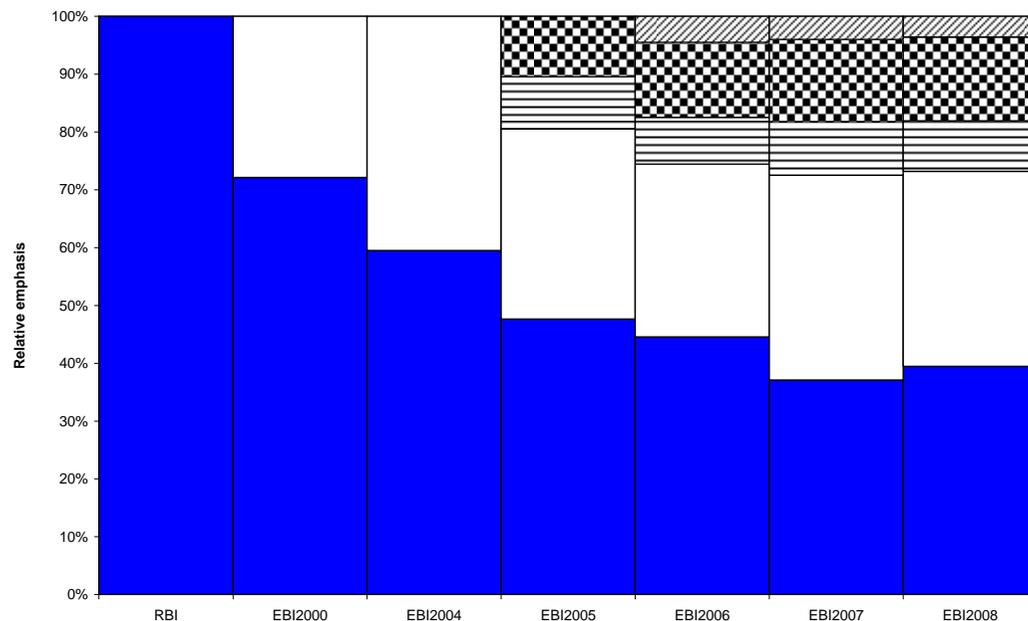| Index / trait[†] | MILK kg | FAT kg | PROT kg | PROT % | CIV | SUR | DCD | MCD | GEST | MORT | CWT | CCONF | CFAT | CULL | LOCO | SCS |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| RBI | 15% | 14% | 50% | 20% | | | | | | | | | | | | |
| EBI2000 | 21% | 8% | 43% | | 10% | 18% | | | | | | | | | | |
| EBI2004 | 17% | 12% | 31% | | 27% | 14% | | | | | | | | | | |
| EBI2005 | 13% | 10% | 25% | | 22% | 11% | 3% | 1% | 4% | 1% | 7% | 1% | 2% | | | |
| EBI2006 | 13% | 9% | 23% | | 20% | 10% | 3% | 1% | 3% | 1% | 10% | 2% | 1% | 0% | 1% | 4% |
| EBI2007 | 11% | 5% | 21% | | 27% | 9% | 3% | 1% | 5% | 1% | 9% | 3% | 2% | 0% | 1% | 3% |
| EBI2008 | 11% | 6% | 23% | | 26% | 8% | 2% | 1% | 4% | 1% | 8% | 3% | 2% | 2% | 1% | 3% |

[†]For abbreviations see Table 24



**Figure 1.** *Change in relative emphasis for each subindex calculated using the method of Van Raden, (2002). Dark shaded=milk production; white=fertility &s survival; horizontal lines = calving performance; checked = beef performance; diagonal = health.*

# 5. DO-IT-YOURSELF MILK RECORDING

The objective of this task was to quantify the feasibility of DIY milk recording as a viable alternative to supervised milk recording in Ireland.

## 5.1. Materials and Methods

### 5.1.1 Raw data

Milk weights and milk samples were collected across 23 DIY herds in Southern Ireland for both AM and PM at roughly four-weekly intervals. Data from the 23 DIY herds were extracted from the ICBF database on the 12th August 2004. The initial, unedited data set consisted of 7,945 part-day observations from 1,581 cows across 23 herds. In total, 68 herd-testdays were included in the data set; the number of part-day observations per herd-testday varied from 10 to 576. Part-day milk yield varied from 0.8 kg to 46.7 kg. Part-day fat, protein and lactose percentage varied from 1.5-7.58%, 2.19-5.12%, and 3.31-5.44%, respectively. Somatic cell count varied from 7 to 9928 cells/ml; the SCC of nine records was 9999 which is the maximum cell count possible in the IRIS database. In total 118 composition results were missing while 111 SCC results were missing. Missing analyses were observed for 35 herd-testdays across 19 herds; the number of samples missing per herd-testday varied from 1 to 9 with one herd-testday having 38 samples missing.

### 5.1..2 Data editing

Only consecutive non-zero PM-AM (or AM-PM) samples per cow-testday were retained. Parities greater than two were grouped together. Days in milk were grouped into seven classes, each of 50 days interval from 0 to 300 and a final class for >300 days. Following editing 3,850 records (includes both AM and PM records as one record) from 1,565 cows across 23 herds on 68 different herd-testdays were available for inclusion in the analysis. Milking interval was defined as the difference, in minutes, between morning and evening milking for each cow-testday.

*5.1.3 Data analysis*

The procedures adopted in the present study were similar to those reported by Berry et al. (2005). A linear multiple regression model, fitted in SAS (SAS, 2004) to predict actual 24-hour yield from AM and/or PM samples was as follows:

$$Y_{ijk} = [b_0 + b_1(MI) + b_2(Milk)_i + b_3 (Fat)_i + b_4 (Protein)_i ]_k + e_{ijk}$$

Where:

$Y_{ijk}$ = 24-hour yield (milk, fat or protein yield)

$MI$ = herd milking interval from AM to PM (milking interval from PM-AM is directly related so was not included in the model)

$(Milk)_i$ = milk yield on the ith milking of the day

$(Fat)_i$ = fat yield on the ith milking of the day

$(Protein)_i$ = protein yield on the ith milking of the day

$e_{ijk}$ = random residual effect

An additional independent predictor variable of SCC on the ith milking was included in the prediction model for SCC only. Regression analyses were carried out within subclasses *k* to account for the heterogeneous means and variances of the different subclasses. In total 21 subclasses were created based on stage of lactation (0-49, 50-99, 100-149, 150-199, 200-249, 259-299, ≥300) by parity (1, 2, ≥3). The prediction equations were initially derived from 75% of the data randomly chosen from the data set using PROC SURVEYSELECT (SAS, 2004). The number of records per subclass varied from 18 to 411 in the sub-dataset; the average number of records per subclass was 138.

*5.1.4 Tests for comparing alternative milk recording schemes*

Prediction equations derived from 75% of the data were applied to the remaining 25% of the data. The comparison between predicted and actual 24-hour

yield involved estimating the bias between the different measures (i.e., the average difference between the actual yield and predicted yield) and the variance of the difference between the measures (mean square error). The average bias was computed as the mean of the difference following subtraction of actual 24-hour yield from predicted 24-hour yield.

Correlations between actual and predicted yields were estimated and the 25% and 75% quartiles were also estimated. Correlation analyses were also used to evaluate the independence of the residuals whereby a correlation of zero indicates total randomness of the error.

The accuracy of predicting 24-hour yield was also investigated as:

Accuracy = $(\sigma^2 \text{actual} / (\sigma^2 \text{actual} + \sigma^2 \text{difference}))$
where:
$\sigma^2 \text{actual}$ = variance of the actual yield,
$\sigma^2 \text{difference}$ = variance of the difference between the actual yield and the predicted yield

Prediction of actual SCC *per se* may not be as important as identifying samples of high (i.e., >200,000 SCC/ml) somatic cell count. Therefore, the sensitivity and specificity of predicted 24-hour SCC at identifying samples with a true daily SCC >200,000 cells/ml was investigated within the data. Sensitivity was calculated as the proportion of daily SCC >200,000 that had an predicted SCC >200,000, and specificity was calculated as the proportion of daily SCC <200,000 that had an predicted SCC of <200,000 cells/ml. Precision was defined as the proportion of correct (positives or negatives) diagnoses made from the AM/PM samples from all samples tested.

## 5.2. Results and Discussion

*5.2.1 Data*

The mean and standard deviation for milk yield, and composition in the edited data set are summarised in Table 9. In total, 1,031 records (27% of the data set) had a daily SCC >200,000. The ratio of AM SCC to PM SCC varied from 0.012 to 181.25 thereby indicating considerable diurnal variation. The ratios of AM to PM milk yield varied from 0.21 to 10.7; the average was 1.4. The large ratio (10.7) was an outlier and occurred when one cow produced 16 kg milk in the morning and 1.5 kg milk in the evening; compositions were similar for the AM and PM samples. It appears that the 16-kg milk weight was manually inputted. Correlations between AM yield, PM yield and true daily yield were similar to those previously reported from research data (Berry et al., 2005). Thus, the results are in line with expectations suggesting accurate recording and milk sampling using DIY procedures.

**Table 9.** *Average and standard deviation (SD) or milk production variables in the edited data set.*

|       |         | Milk (kg) | Fat (%) | Protein (%) | SCC (cells/ml) |
|-------|---------|-----------|---------|-------------|----------------|
| AM    | Average | 15.5      | 3.25    | 3.32        | 258            |
|       | SD      | 4.97      | 0.65    | 0.31        | 699            |
| PM    | Average | 11.5      | 4.05    | 3.37        | 354            |
|       | SD      | 4.13      | 0.75    | 0.32        | 841            |
| Daily | Average | 26.9      | 3.59    | 3.34        | 296            |
|       | SD      | 8.59      | 0.57    | 0.30        | 714            |

Correlations between AM SCC, PM SCC and true daily SCC are summarised in Table 10. The correlations in Table 10 indicate that AM SCC or PM SCC closely resemble daily SCC. The Spearman correlations reflect the similarly in how cows rank for SCC based on either AM, PM or daily SCC; this criteria will be most influential in culling decisions rather than SCC level *per se*. The results demonstrate, that even without prediction equations either AM or PM SCC ranks cows very

similar to if both AM and PM samples were analysed separately and weighted by their respective milk yield.

The sensitivity, specificity, and precision of the AM sample as an indicator of daily SCC >200,000 was 82%, 99% and 95% respectively; the corresponding variables for the PM sample were 95%, 93% and 95%. The accuracy of predicting daily SCC from only using AM SCC or PM SCC (i.e., no prediction equations used) was 0.92 and 0.85, respectively. This substantiates previous remarks that even without prediction equations either AM or PM SCC are a good indicator of daily SCC.

**Table 10.** *Pearson (above diagonal) and Spearman (below diagonal) correlations between AM SCC, PM SCC and true daily SCC.*

|      | AM   | PM   | DAY  |
|------|------|------|------|
| AM   |      | 0.80 | 0.96 |
| PM   | 0.86 |      | 0.94 |
| DAY  | 0.96 | 0.95 |      |

*5.2.2 Prediction of daily yields with either an AM or PM sample*

The ability of the prediction equations to estimate daily milk, fat, and protein yield from either AM or PM samples is summarised in Table 11. There was a tendency for daily yield predicted from the AM sample to be an underestimate of true daily yield; the opposite was true for daily yield predicted from PM samples. This may have implications for prediction of 305-day yield and may suggest the superiority of an alternate AM-PM scheme. Berry et al. (2005) reported that an alternate AM-PM milk record schemes predicted actual 305-day yield more accurately than a recording scheme based on all AM or all PM records.

**Table 11.** *Accuracy, correlation between predicted daily yields and actual daily yields, mean square error (MSE), mean, 25% percentile (Q1), and 75% percentile (Q3) of the residuals from predicting 24-hour milk, fat and protein yield from either an AM or PM sample in an independent data set.*

|  |  | Accuracy | Correlation | MSE | Mean | Q1 | Q3 |
|---|---|---|---|---|---|---|---|
| AM | Milk | 0.93 | 0.96 | 5.88 | -0.16 | 1.20 | -1.48 |
|  | Fat | 0.84 | 0.90 | 0.018 | -0.010 | 0.069 | -0.077 |
|  | Protein | 0.92 | 0.95 | 0.006 | -0.005 | 0.038 | -0.047 |
|  | SCC | 0.91 | 0.95 | 84747 | -5.2 | 46.5 | -19.2 |
| PM | Milk | 0.88 | 0.93 | 9.98 | 0.056 | 1.69 | -1.52 |
|  | Fat | 0.83 | 0.87 | 0.019 | 0.005 | 0.085 | -0.071 |
|  | Protein | 0.87 | 0.92 | 0.011 | 0.002 | 0.055 | -0.050 |
|  | SCC | 0.88 | 0.93 | 115257 | -3.14 | 41.3 | -22.1 |

Examination of the quartiles reveals that 50% of the predicted milk yields were within ±1.7 kg of the actual milk yield; this represents an error of 6% of the mean. The sensitivity, specificity, and precision of daily SCC predicted from AM samples was 96%, 92% and 94% respectively; the corresponding variables for the PM sample were 93%, 92% and 93%. The high mean square error associated with SCC was attributable mainly to a few larger individual SCC. When AM SCC was restricted to be less than 9,999,999 cells/ml the mean square error was reduced by 10,000; the mean square error halved when AM SCC >5 million were removed from the analysis.

Accuracy of predicting 24-hour SCC was reduced through the use of the prediction equations compared to using the AM sample itself; however, the sensitivity was increased through the use of the prediction equations. Accuracy of predicting 24-hour SCC was increased through the use of the prediction equations compared to using the PM sample alone; however, the sensitivity, specificity and precision was reduced through the use of the prediction equations. Similarly, the

correlations between predicted daily SCC and actual daily SCC were lower than correlations between AM/PM SCC and daily SCC.

Absolute correlations between residuals and predicted yields were less than 0.10 for milk, fat and protein yield; the majority were not significantly (P>0.05) different from zero. This suggests randomness of the error. The residual correlation for SCC varied from 0.10 to 0.14 and were significantly different from zero; however, such correlations were strongly influenced by testday records with exceptionally high SCC.

Graphical examination of the relationship between the residual and month of calving revealed no trend. Correlations between the residuals with month of calving were generally not significantly different from zero indicating no systematic linear bias across months of calving.

*5.2.3 Prediction of daily yield using two consecutive milk weights but only one composition*

An additional scenario was investigated whereby two milk weights (both AM and PM) were available but with either an AM or PM milk composition. The accuracy of prediction of daily milk, fat, and protein yield from two consecutive milk weights and either an AM or PM composition is summarised in Table 12. Daily milk yield was not predicted in this scenario as the true measure would be physically recorded.

In agreement with Schaeffer *et al.* (2000) the accuracy of predicting 24-hour fat and protein yield increased when both milk weights were available for inclusion in the prediction equation; the mean square error of the variance also decreased across both studies. The accuracy of predicting 24-hour protein yield was 1.00 and 0.99 from AM or PM samples, respectively; Schaeffer *et al.* (2000) also reported an accuracy of 0.995 and 0.99, respectively. The accuracy of predicting 24-hour fat yield from AM (0.93) or PM (0.90) samples was in agreement with Schaeffer *et al.* (2000) who reported accuracies of 0.93 and 0.92, respectively.

**Table 12.** *Accuracy, correlation between predicted yields and actual yields, mean square error (MSE), mean, 25% percentile (Q1), and 75% percentile (Q3) of the residuals from predicting 24-hour fat and protein yield from both AM and PM milk weights but either an AM or PM composition sample.*

|    |         | Accuracy | Correlation | MSE | Mean | Q1 | Q3 |
|----|---------|----------|-------------|-----|------|----|----|
| AM | Fat     | 0.93 | 0.96 | 0.007 | -0.004 | 0.044 | -0.046 |
|    | Protein | 1.00 | 1.00 | 0.000 | 0.001 | 0.010 | -0.009 |
|    | SCC     | 0.91 | 0.95 | 83181 | -5.76 | 48 | -19 |
| PM | Fat     | 0.90 | 0.95 | 0.010 | 0.003 | 0.058 | -0.054 |
|    | Protein | 0.99 | 1.00 | 0.001 | 0.001 | 0.013 | -0.012 |
|    | SCC     | 0.88 | 0.93 | 115180 | -3 | 46 | -26 |

From the derived daily fat and protein yields, fat and protein percentages were calculated and compared to actual daily fat and protein percentages. For daily fat percentage 50% of the predicted records were within ±0.2% of actual records; the corresponding figure was ±0.04% for protein percentage.

The rank correlation within test-day (with a minimum of 20 cows per test-day) between fat yield predicted from AM or PM samples and true fat yield varied from 0.83 to 0.97 and from 0.83 to 0.96, respectively; 14 herd-test days were included in the analysis. The rank correlation within test-day (with a minimum of 20 cows per test-day) between daily protein yield predicted from AM or PM samples and true protein yield varied from 0.98 to 1.00 and from 0.97 to 0.99, respectively. Therefore, the ranking of cows for predicted daily fat and protein yield on any given test day was very similar to cow rankings based on actual 24-hour fat and protein yields.

The sensitivity, specificity, and precision of identifying daily SCC >200,000 using an AM sample incorporated within a prediction equation (with two milk weights) was 95%, 91% and 93% respectively; the corresponding variables for the PM sample were 94%, 92% and 93%. This was very similar to previous results where only one milk weight was included in the prediction equation.

However, farmers may only be interested in identifying the cows with the highest SCC. The rank correlation within the 14 herd-testdays between predicted 24-hour SCC from AM samples and actual 24-hour SCC varied from 0.83 to 0.97. The rank correlation within herd-testdays between predicted 24-hour SCC from PM samples and actual 24-hour SCC varied from 0.76 to 0.97.

Absolute correlations between residuals and predicted fat and protein yield were not significantly ($P>0.05$) different from zero indicating total randomness of the error. Residual correlations for SCC were 0.10 and 0.14 but were strongly influenced by test day records with exceptionally high SCC.

Graphical examination of the relationship between the residuals and month of calving revealed no trend. Correlations between the residuals with month of calving were generally not significantly different from zero indicating no systematic linear bias across months of calving.

### 5.2.4 Prediction equations for national use

Given these favourable results reported herein, prediction equations were re-derived using the whole (100%) data set. Correlations between previously derived solutions (75% of the data) and solutions from the whole data set were all greater than 0.98 for fat and protein yield. The correlation between previous and current solutions for AM SCC was 0.62; the corresponding correlation for PM SCC was 0.49. The correlations became stronger when the data was restricted to include only SCC records below a pre-defined threshold. This suggests that the prediction equations for SCC are not robust and question their usefulness in predicting daily SCC since AM/PM compositions themselves are a good indicator of daily SCC. However, the reduced accuracy of predicting SCC is not surprising given the considerable variation in SCC between two consecutive records.

To investigate this further average lactation SCC was calculated for true daily SCC, AM SCC alone (i.e., no use of prediction equations), PM SCC alone, daily SCC

predicted using the prediction equations incorporating an AM sample, and daily SCC predicted using the prediction equations incorporating a PM sample. Pearson correlations between average lactation SCC (cows with at least 4 tests) derived from AM SCC alone, PM SCC alone, daily SCC predicted using the prediction equations incorporating an AM sample, and daily SCC predicted using the prediction equations incorporating a PM sample with true daily SCC were 0.99, 0.98, 0.99 and 0.98 respectively; the corresponding Spearman rank correlations were 0.94, 0.92, 0.96 and 0.94. Pearson correlations between average lactation SCC (cows with at least 1 test) derived from AM SCC alone, PM SCC alone, daily SCC predicted using the prediction equations incorporating an AM sample, and daily SCC predicted using the prediction equations incorporating a PM sample with daily SCC were 0.98, 0.97, 0.98 and 0.97 respectively; the corresponding Spearman rank correlations were 0.96, 0.94, 0.96 and 0.95. Thus, little benefit exists in predicting daily SCC using prediction equations.

# 6. INBREEDING LEVELS AND INBREDEING DEPRESSION

The objective of this task was to quantify the level and rate of change in inbreeding in the Irish Holstein-Friesian population and the populations of Irish Charolais, Angus, Limousin, Hereford and Simmental and to quantify the effect of inbreeding on economically important traits within those breeds.

## 6.1 Materials and methods

Pedigree information on up to 9 million animals was obtained from the Irish Cattle Breeding Federation database. Data on breed fraction, recorded in increments of 1/32, were available for most animals. Information on Holstein-Friesian cattle and the five largest beef breeds, the Charolais, Limousin, Simmental, Hereford, and Angus, was extracted. Pedigree information was traced back to 1950 for Holstein-Friesian animals and back to 1960 for the beef cattle Founder animals (animals with unknown parents) were assumed to be unrelated and have an inbreeding coefficient

of zero. The software package Pedig (Boichard, 2002) was used to analyse the pedigree of each of the cattle populations.

*Pedigree Completeness.* Depth of pedigree known was calculated for all purebred populations. Pedigree depth in the present study was measured in complete generation equivalents (**CGE**). A CGE refers to the degree of pedigree information for an animal. It was computed as $\sum_{i=1}^{n_j} \dfrac{1}{2^{g_{ij}}}$, where $n_j$ = number of ancestors of animal $j$, and $g_{ij}$ is the number of generations between individual $j$ and its ancestor $i$ (Sorensen et al., 2005).

*Inbreeding Coefficients.* Inbreeding coefficients (F) were calculated using the Meuwissen and Luo (1992) algorithm. Following the calculation of the inbreeding coefficients for all animals, the annual mean inbreeding of only the purebred animals was extracted. Annual rate of inbreeding was estimated by fitting a linear regression using PROC REG (SAS, 2006) through the time period from 1994 to 2004. Animals were also classed according to their level of inbreeding and were assigned one of five groups: F=0, 0<F≤6.25, 6.25<F≤12.5, 12.5<F≤25, or F>25. Furthermore, the level of inbreeding for inbred animals (i.e., animals with F>0) by year of birth was determined.

*Generation Intervals.* A generation interval is defined as the average age of parents when their progeny, upon becoming parents themselves Generation intervals were calculated along the four selection pathways; sire to male offspring, sire to female offspring, dam to male offspring, and dam to female offspring. Average generation interval, weighted by the number of animals within each pathway was subsequently calculated.

*Effective Population Size.* The effective population size ($N_e$) is defined as the number of breeding animals that would lead to the actual increase in inbreeding if they contributed equally to the next generation (Wright, 1923). It was calculated for

purebred animals only as: $N_e = \dfrac{1}{2\Delta F_y * L}$ , where $\Delta F_y$ is the annual rate of inbreeding

in the population and L is the generation interval (Hill, 1972).

*6.1.1 Estimation of inbreeding depression*

The effect of inbreeding on a series of performance traits in the Holstein-Friesian and beef populations was determined. Inbreeding was included in a linear mixed model as either a class variable or a continuous variable where higher order polynomials of the latter was also tested in the model as an indicator of non-linear inbreeding depression. The effects of dam inbreeding and calf inbreeding on calving related traits were analysed separately. Fixed effects included in the model, where applicable, were contemporary group, age nested within parity, days in milk as well as a random permanent environmental effect, and sire. Where the dependent variable was calving performance sex of calf was included in the model as a fixed effect and maternal grandsire was included as a random effect. When the dependent variable was linear type score, herd-visit and stage of lactation was also included in fixed effects.

**6.2 Results and Discussion**

Complete generation equivalents by year of birth are illustrated in Figure 2 for the six breeds. All breeds followed the same trend of pedigree completeness, increasing over time; however, the absolute levels varied. In 2004, Herefords had the deepest pedigree with a CGE of greater than 6. Simmentals had the shallowest pedigree of all the beef breeds with pedigree completeness less than 4 CGEs. Of the purebred. The Holstein-Friesian had information on 5 CGEs in 2004, yet only 48% of animals had full information on their dam and sire.
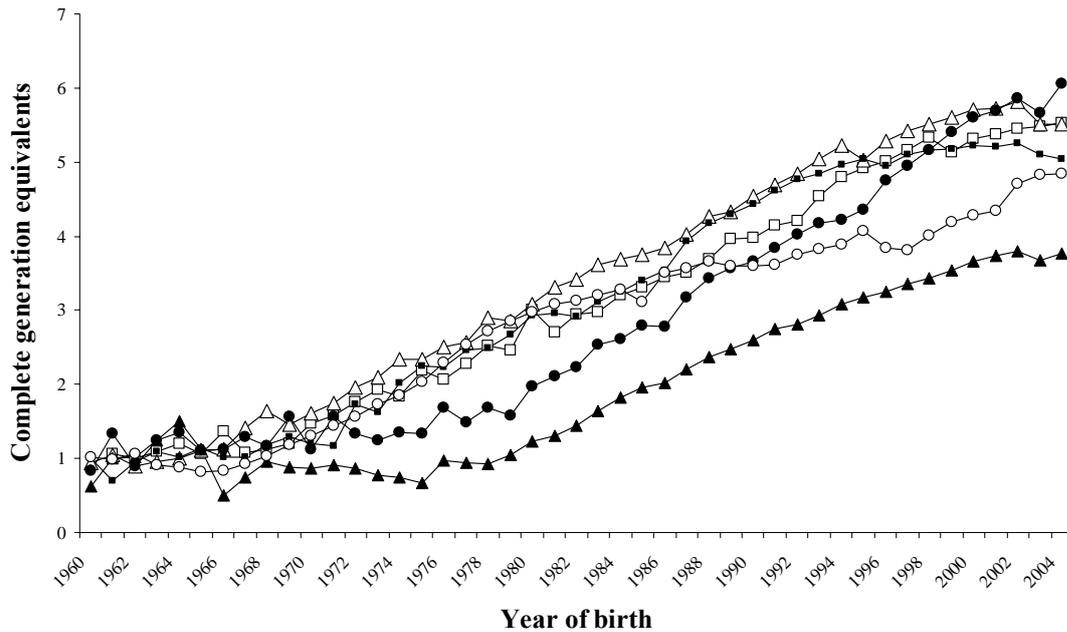
**Figure 2.** *Pedigree completeness for the Charolais (-Δ-), Limousin (-■-), Hereford (-●-), Angus (- -), Simmental (-▲-), and Holstein-Friesian (-○-) breeds across year of birth*

Mean annual inbreeding by year of birth is shown in Figure 3 for purebred beef animals and Holstein-Friesians born between 1975 and 2004. The Hereford breed had the highest recorded level at 2.19% in 2004, rising consistently at 0.13% per annum between 1994 and 2004. The Holstein-Friesian breed had an average inbreeding coefficient of 1.49% in 2004, also increasing by 0.12% per annum. The level of inbreeding in the Holstein-Friesian in 2004 is lower than that of both the purebred Holstein (2.15%) and Friesian (1.61%) populations in 2004. Inbreeding level within the Simmental population has also been rising, with an annual increase of 0.06% (P<0.001), reaching an inbreeding level of 1.35% in 2004. Level of inbreeding in the Angus population was 1.31% in 2004 and has been decreasing at a rate of -0.02% (P<0.05). Inbreeding level in the Limousin and Charolais populations was 0.57% and 0.54% in 2004, respectively, and has remained relatively stable over the past decade.
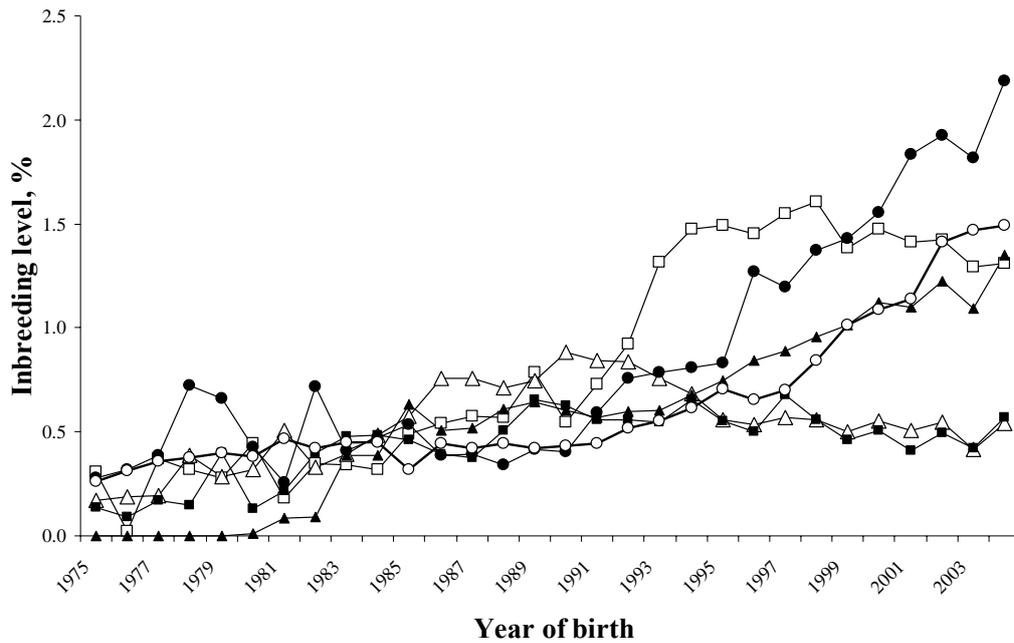
**Figure 3.** *Trend in level of inbreeding for the Charolais (-Δ-), Limousin (-■-), Hereford (-●-),*

*Angus (- -), Simmental (-▲-), and Holstein-Friesian (-○-) breeds across year of birth*

Generation intervals across the alternative selection pathways have generally been increasing over time, although at a declining rate. The average age of parents of progeny born in 2004 was 6.17, 6.71, 6.54, 6.03, 6.09, and 6.66 yr for Charolais, Limousin, Simmental, Hereford, Angus, and Holstein-Friesian, respectively. Based on the reported rate of increase in inbreeding and generation intervals, the effective population size for the Hereford, Simmental, and Holstein-Friesian breeds was calculated as 64, 127, and 75, respectively. As the effective population size is calculated using the rate of increase in inbreeding per generation, no effective population size could be estimated for the Charolais, Limousin, and Angus where negative inbreeding changes occurred.

The cumulative marginal genetic contributions of the top 100 contributing ancestors to the females born in 2004 are shown in Figure 4. The cumulative marginal genetic contributions of the top 100 ancestors in the Simmental and Angus breeds accounted for 87% of the genes of purebred females born in 2004 for these two breeds, whereas it accounted for 81, 78, 77, and 72% of the genes of purebred females

born in 2004 for the Hereford, Limousin, Charolais, and Holstein-Friesian populations, respectively.
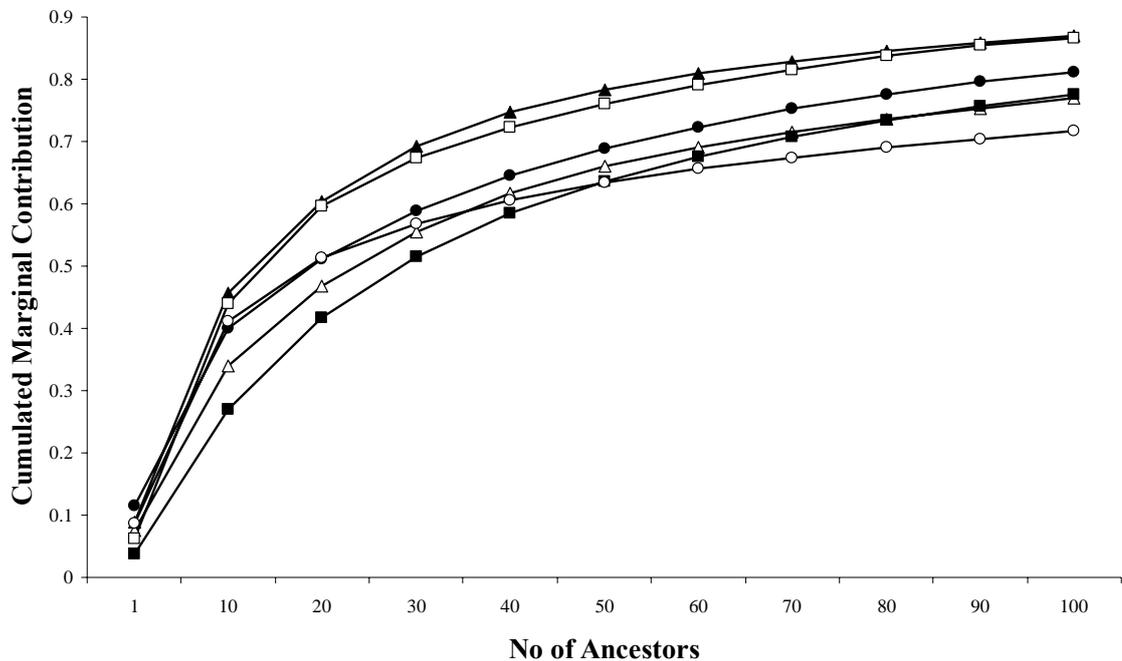
**Figure 4.** *Cumulative marginal contribution for the purebred populations of Charolais (-Δ-), Limousin (-■-), Hereford (-●-), Angus (- -), and Simmental (-▲-), and of Holstein-Friesian (-○-) up to 100 ancestors*

*6.2.1 Inbreeding depression in dairy cattle*

Tables 13 and 14 summarise the effect of inbreeding on milk production and SCS (i.e., $\log_e$SCC). All yield traits decreased ($P<0.01$) with inbreeding. When inbreeding was treated as a continuous variable, its effect on milk yield was non-linear, with a greater negative impact at higher inbreeding levels. Inbreeding also had a non-linear effect on milk protein concentration; low levels of inbreeding resulted in a decrease in protein concentration while, higher levels of inbreeding (>18%) resulted in a rise in protein concentration.

**Table 13.** *Model solutions (SE in parenthesis) for the effect of inbreeding on milk, fat and protein yield (kg), milk fat and protein concentration (%\*10³) and somatic cell score (SCS units; \*10²)*

| | Milk yield | Fat yield[1] | Fat %[2] | Protein yield[2] | Protein % | SCS[2] |
|---|---|---|---|---|---|---|
| Inbreeding as a continuous variable | | | | | | |
| Linear | 0.03 (2.56) | -0.4(0.06) | - | - | -1.6(0.52) | - |
| Quadratic | -0.4(0.15) | - | - | - | 0.1(0.03) | - |
| Inbreeding as a class variable | | | | | | |
| 0<F≤6.25 | 6.8(16.74) | 1.9(0.67) | 24.3(7.39) | 0.2(0.51) | 2.0(3.44) | 7.6(1.41) |
| 6.25<F≤12.5 | -47.5(21.98) | -0.9(0.88) | 15.3(9.66) | -1.9(0.68) | -0.1(4.50) | 10.8(1.85) |
| 12.5<F≤25 | -160.9(43.12) | -6.0(1.72) | 5.9(18.89) | -4.8(1.32) | 15.1(8.80) | 2.4(3.65) |
| F>25 | -172.5(67.70) | -4.8(2.70) | 50.6(29.51) | -5.9(2.08) | 7.9(13.75) | 14.6(5.74) |

[1]No significant quadratic effect of inbreeding on fat yield was observed when inbreeding was treated as a continuous variable thus only the linear solution is provided

[2]The effect of inbreeding when treated as a continuous variable, on fat concentration, protein yield and SCS differed significantly across parities and therefore effects are included in Table 14.

**Table 14.** *Model solutions (SE included in parenthesis) for the effect of inbreeding when interacting with parity on protein yield (kg), fat concentration (%\*10³) and somatic cell score (SCS units; \*10²) and the statistical significance of the interactions*

| | Protein yield | Fat concentration | SCS |
|---|---|---|---|
| P-value | 0.005 | 0.039 | <0.001 |
| Parity 1 | -0.1(0.06) | -3.8(0.76) | 0.2(0.16) |
| Parity 2 | -0.3(0.06) | -2.0(0.83) | 0.9(0.19) |
| Parity 3 | -0.4(0.08) | -1.8(0.96) | 1.0(0.22) |
| Parity 4 | -0.4(0.09) | -0.2(1.17) | 1.2(0.27) |
| Parity 5 | -0.4(0.12) | 0.2(1.51) | 1.5(0.35) |

The effect of inbreeding on protein yield and milk fat concentration differed ($P<0.05$) across parities (Table 14). The negative impact of inbreeding on protein yield was greater in multiparous animals. However, a reverse trend was observed with milk fat concentration in that the negative impact was greater in younger animals, although mean fat concentration was also greatest in first parity animals.

The deleterious effect of inbreeding on milk production, although in agreement with previous literature was generally less than most previously reported estimates (Wiggans et al., 1995; Smith et al., 1998; Croquet et al., 2006), although low estimates of inbreeding depression on 305-d milk yield (-9.8 kg) have also been reported in Jersey cattle (Miglior et al., 1992). Inbreeding may however be considered relative to production (Fuerst and Sölkner, 1994); average 305-d yield for animals in the present study was 7,099 kg compared to the 8,794 kg mature equivalent for US Holsteins reported by Smith et al. (1998). Furthermore, rates of accumulation of inbreeding are likely to impact inbreeding depression. Falconer and Mackey (1996) stated that a rapid rise in inbreeding will result in greater inbreeding depression. The rate of increase in inbreeding in Irish Holsteins is 0.10% per annum (Mc Parland et al., 2007) which is slower than the increase of 0.15% per annum estimated from fitting a linear regression to annual inbreeding levels in the US across the same time period (Animal Improvement Programs Laboratory, 2007). Additionally, the non-linear effect of inbreeding on milk production in the present study indicates that the effect of inbreeding is dependent on the levels compared. For example, the marginal decrease in 305-d milk yield by increasing inbreeding from 25 to 26% was 20 kg, which is more consistent with previous estimates (Casanova et al., 1992; Croquet et al., 2006).

Inbreeding increased SCS in the present study, the effect being greater in older animals (Table 14). Inbreeding depression for SCS equated to an increase in SCC of 23,000 cells/mL above the mean for a fifth lactation animal 12.5% inbred. The inbreeding depression associated with a 12.5% inbred animal represented 2.6% of the mean and 2.5% of the additive genetic standard deviation. Several studies have attempted to quantify the effect of inbreeding on SCS and have either found no significant effect (Smith et al., 1998; Thompson et al., 2000; Gulisija et al., 2007) or reported low levels of inbreeding depression for SCS (Miglior et al., 1995; Biffani et al., 2002; Mrode et al., 2004). Miglior et al. (1995) reported a linear increase of 0.012 SCS units in lactation average SCS per 1% inbreeding in primiparous Canadian Holsteins; however, SCS reported by Miglior et al. (1995) was transformed using the logarithm to the base two. The effect of inbreeding on SCS in the present study was

linear which is at odds with the significant non-linear effect of inbreeding on SCS in primiparous Danish Holsteins (Sørensen et al., 2006). As SCS is an indicator of mastitis (Mrode and Swanson, 1996) results from the current study suggest that inbreeding may also increase the incidence of mastitis; no information on clinical mastitis was available in the current study. However, Sørensen et al. (2006) using data on clinical mastitis did report a higher incidence of clinical mastitis in inbred animals.

The effect of dam inbreeding and calf inbreeding were studied separately since both maternal and fetal effects may influence calving performance (Adamec et al., 2006). The effect of dam inbreeding on dystocia in the present study did not differ by parity or sex of calf. Dystocia increased with level of dam inbreeding up to 25% at which point it reversed ($P<0.001$), possibly due to inbred dams producing smaller calves. Another reason may be that fetuses from highly inbred dams, where calving difficulty may have been expected, may have died in utero or aborted prior to full term and therefore did not receive a score for dystocia. The increased risk of dystocia in moderately inbred animals observed in the present study may be due to smaller dam size at calving; Young et al. (1969) reported lower live-weights at 2 yrs of age in inbred animals. Adamec et al. (2006) also reported small effects of inbreeding on calving difficulty, justifying the slight effect of inbreeding depression to potentially undersized calves being born from inbred dams; however, Adamec et al. (2006) defined calving dystocia as calvings with more than a "slight problem".

Calf inbreeding did not affect ($P>0.05$) dystocia in the present study, although the trend was towards a reduction in dystocia with increased calf inbreeding which may also be due to inbred calves being potentially smaller in size. Young et al. (1969) reported lower calf birth weights of 0.11 kg per unit increase in inbreeding.

Dam inbreeding resulted in a greater incidence of stillbirths of 0.06% (SE=0.02%) per 1% increase in inbreeding, which is within the range of inbreeding depression reported by Adamec et al. (2006) in US Holsteins; the effect did not differ significantly across dam parity or calf sex in the present study. However, the effect of

calf inbreeding on stillbirth incidence in the present study was parity dependant ($P$<0.01) but was consistent across both sexes. Stillbirth incidence increased with calf inbreeding in primiparous animals at a rate of 0.2% (SE=0.04%) per 1% increase in inbreeding, while the effect of inbreeding on multiparous animals was lower and not significantly different from zero. The greater effect of calf inbreeding on stillbirths in primiparous animals is in somewhat agreement with Adamec et al. (2006) who reported a greater effect of dam inbreeding on stillbirths in primiparous animals.

Inbreeding had an unfavourable linear effect ($P$<0.01) on age at first calving, calving interval and survival to second lactation. From these results it may be determined that a cow 12.5% inbred (born following the mating of non-inbred half-siblings) is expected to have, on average, a longer calving interval of 8.8 d, be 2.5 d older at first calving and have a 4% lower survival to second lactation. The inbreeding depression experienced by a cow with inbreeding of 12.5% (following the mating of non-inbred half-sibs) was 0.36%, 2.09%, and 4.35% of the mean for age at first calving, calving interval and survival, respectively. When expressed as a proportion of the additive genetic standard deviation of the respective traits inbreeding depression equated to 1.2 to 1.6% for these traits; the corresponding values for milk, fat and protein yield was 3.6 to 8.1% of the additive genetic standard deviation and 15.6 to 21.9% of the additive genetic standard deviation for milk concentration. This therefore suggests that the level of inbreeding depression is greater in the milk production traits, which is at odds with expectations that inbreeding depression is greater in traits associated with fitness and survival (Falconer and Mackey, 1996). Nevertheless, milk production may be considered a "fitness" trait since it is the primary energy source for the growth of a calf.

Smith et al. (1998) corroborating results from the present study reported reduced days of productive life (-5.96 days / % inbreeding) and greater calving interval (0.31 days / % inbreeding) and age at first calving (0.55 days / % inbreeding) in inbred animals. Furthermore, Biffani et al. (2002) and Wall et al. (2005) in Italian and UK Holsteins, respectively, also reported lower unfavourable effects of inbreeding on calving interval than reported in this study while Hoeschele (1991)

and Biffani et al. (2002) reported an increase in days open (a trait strongly correlated to calving interval) of 0.13 days and 0.31 days / % inbreeding, respectively. Further agreeing with the present study, Sewalem et al. (2006) reported an increased risk of being culled as level of inbreeding increased. The lack of any significant non-linear effects in the present study disagrees with Thompson et al. (2000) and Biffani et al. (2002) both of which reported a non-linear effect of inbreeding on age at first calving with only inbreeding levels greater than 10% and 16%, respectively having an unfavourable effect on age at first calving.

*6.2.4 Inbreeding depression in beef*

Inbred beef animals had lower carcass weight and less carcass fat, the effects of inbreeding ranging from a reduction in carcass weight of -0.87 kg (Charolais) to -1.90 kg (Hereford) per 1% increase in inbreeding, the effects being more pronounced in the British beef breeds. Inbred Charolais and Hereford animals were younger at slaughter by 3 and 5 days, respectively, per percent increase in inbreeding, while the effect of inbreeding on age at slaughter differed significantly with animal gender in the Limousin and Angus breeds, with heifers only having reduced time to slaughter by 5 and 7 days, respectively per percent increase in inbreeding. Continental animals were more affected by inbreeding for live muscling and skeletal conformational measurements than the British breeds; inbred animals were smaller and narrower with poorer developed muscle. Calf inbreeding significantly affected peri-natal mortality in Charolais, Simmental and Hereford animals. The effects were dependent upon dam parity and calf sex, however where significant the association was always unfavorable. Dam inbreeding significantly affected peri-natal mortality in Limousin and Hereford animals, however effects differed by parity in Limousins. Inbred first parity Angus dams had greater incidence of dystocia.

## 7. DEVELOPMENT OF A SYSTEM OF CONTRACT MATINGS FOR IRELAND

The objective of this task was to test and put in place the logistics for generating contract matings between elite sires and dams that would maximise the rate of genetic gain while constraining the accumulation of inbreeding

### 7.1 Materials and Methods

Using current Irish population cattle statistics, the maximum feasible number of young test sires that could be progeny tested was derived. The number of candidate parents required to generate these young test sires was calculated. Consideration was given to potential bulls lost from the system because of sex ratio, perinatal mortality, pre-weaning mortality, bull infertility and loss of daughters to unrecorded herds. Calculations showed that 1,000 contract matings should be generated.

The top 500 AI sires ranked on EBI with semen available in Ireland were considered as potential candidates sires. Following consultation with the Irish dairy industry, it was decided that the sires should be predominantly Holstein-Friesian with at least three full generations of pedigree known. In addition, sires were required to have a predicted transmitting ability (PTA) for both the mammary composite and feet and legs composite of at least -2, PTA for calving interval of less than two days and a PTA for survival of greater than -1%. A total of 61 potential sires of sires were selected for the contract matings. Furthermore, it was decided in consultation with the industry that the contract matings generated should be from a maximum of 30 different sires.

Elite dams were defined as being both genetically and phenotypically superior. Although phenotypic performance is largely affected by management and random noise (i.e., 1-$h^2$), cognisance must be taken of their phenotypic performance to ensure acceptance by most Irish farmers and breeding companies. To ensure phenotypically sound cows were selected, milk recorded animals only were selected and minimum and maximum threshold values were set for the economically

important traits, following consultation with the industry. Cow performance had to fall within the thresholds set for all traits and only cows that had calved at least once were considered. Thresholds decided upon included that all completed lactations (not in progress at the time of data extraction) had to be ≥ 100 days in length and have a 305-day predicted milk yield of ≥ 4,000kg with a protein percent of ≥ 3.3%. Cows were required to have an average calving interval of 400 days and no calving interval between parity 1 and parity 5 was to exceed 500 days. In addition cows must have calved for the first time between 22 and 38 months of age, have calved in the last 12 months prior to data extraction and were to be no greater than ninth lactation. Where classified by Holstein-Friesian official classifiers, cows had to have both a feet and legs composite and a mammary composite of ≥ 70 points for any classification.

Restrictions were also placed on cow genetic merit. Only cows of ≥ 78% Holstein-Friesian genetics with at least two complete generations of pedigree known were considered. The weighting on the cow's parental information included in her PTA for milk production was to be no greater than 65%, with a PTA for both fat and protein yield of ≥ -2.5kg. Three sires, Galtee Merci, Newhouse Sjoerd and Collins Royal Hugo are particularly prominent in the pedigree of Irish Holstein-Friesians and the young test sires currently in layoff. The daughters and granddaughters of these sires were removed. Finally, all cows were required to have positive milk and fertility sub-indices values of the EBI and have an EBI of ≥ €90. Of the 408,375 living milk recorded cows in Ireland, 8,748 remained. Restrictions on pedigree information and their most recent calving date were the main reasons why potential candidates were removed from the list.

A customised economic index was derived for each cow hereafter known as the Customised Index (CUI), using the economic weights for the 2008 EBI for milk production (but at a lower milk price of 28c/l), fertility and survival, calving performance and health. The economic weights in the beef performance sub index were set to zero with the exception of cull cow weight. In addition, a genetic evaluation for calving interval and survival was undertaken in PEST (Neumaier and Groeneveld, 1998) using the data, models and genetic and residual (co)variances

currently used in the Irish national genetic evaluations with the exception that the genetic co-variance between milk yield and calving interval employed in the multi-trait analysis was set to zero. This was done because cow estimated breeding values for calving interval are influenced by their milk yield due to the higher heritability of milk yield and its genetic correlation within calving interval and the objective of this study was to identify cows that did not conform to the norm where higher genetic potential for milk production is associated with inferior genetic merit for calving interval. Cows were subsequently ranked on the CUI and only the top 150 daughters per sire and top 150 grand-daughters per maternal grandsire were retained; a total of 4,568 cows remained. The top 3,000 of these cows ranked on their CUI were retained for contract mating.

### 7.1.1 Contract mating

Every possible combination of mating between the candidate sires ($n = 61$) and dams ($n = 3,000$) was undertaken to generate 183,000 "phantom" progeny. For each phantom calf, an inbreeding coefficient ($F$, Meuwissen and Luo, 1992) and co-ancestry with the breeding female population (R-value) was computed. Breeding females were defined as all Holstein-Friesian females with at least two complete generations of pedigree, and also included virgin Holstein-Friesian heifers and developing Holstein-Friesian foetuses (no distinction was made for the sex of the developing foetus). An EBI was calculated for the phantom progeny; likewise milk and fertility sub-indices were calculated for each phantom progeny. The ratio of milk sub index value to the fertility sub index value of the phantom progeny was restricted to be between 3:1 and 1:3.

The minimum and maximum number of matings per sire of sires was decided upon by sire analysts. The thresholds were based on the representation of germlines in the population, presence in the pedigree of young test sires currently in lay-off and the availability of semen. Each dam was allocated a maximum of one mating. Constraints on the maximum number of matings per sire and per dam were used for linear programming and sequential methods only, while the constraint on dam matings only was applied to the random method.

### 7.1.2 Methods tested

Two alternative methods of selection were tested. Linear programming (LP) optimises a linear objective function subject to linear equality and inequality constraints and has been suggested as a tool to select breeding stock in a production unit in a non-random way under constraints (Jansen and Wilton, 1984). The LP approach was undertaken in the present study using PROC LP (SAS Institute Inc., Cary, NC).

The RAN method selects a random sample of the population. Using PROC SURVEYSELECT (SAS Institute Inc., Cary, NC), 1,000 matings were selected randomly from the population. Mean performance of these randomly selected progeny was computed and the entire procedure iterated 1,000 times. The current method of selecting matings in Ireland is similar to the RAN method, in that little consideration is given to the combination of bull dams and bull sires used. Therefore the RAN method of selection was used only as a control for the purpose of the study.

Phantom progeny EBI and R-values were standardised with a standard deviation of 1. Three different objectives were defined: 1) a positive value on EBI and negative value on R-value with 100 times more emphasis on EBI, 2) a positive value on EBI and negative value on R-value with 100 times more emphasis on R-value, and 3) a dual objective of maximising EBI while simultaneously minimising R-value. In the latter objective, a positive value was always placed on EBI and a negative value placed on R-value. The relative weightings on each were altered ranging from equal emphasis on both to 10 times more emphasis on either EBI or R-value. In this analysis twice as much emphasis was put on EBI relative to the R-value.

For both mating methods and objectives, 1,000 matings were selected. Mean performance of the selected matings were compared across selection methods in terms of EBI, R-value, milk and fertility sub-index values and average inbreeding of the groups. The average within-group relationship for each group of 1,000 phantom progeny (with the exception of the group selected by RAN) was also computed.

## 7.2 Results and Discussion

Controlling the accumulation of inbreeding, whilst minimising the impact on genetic gain within dairy cattle populations has become an important factor in the designing of breeding programmes. This study has compared a system of contract mating (LP) with a control (RAN) in the Irish population of Holstein Friesians. Important factors considered were the genetic and phenotypic merit of potential bull dams and genetic merit of the bull sires, as well as the genetic merit and inbreeding coefficients of the first generation of offspring produced from the new breeding programme and the average co-ancestry between the offspring and the future population of breeding females.

**Table 15.** *Summary of the performance of the 61 bulls selected as potential bull sires[1]*

| Trait | Mean | SD | Minimum | Maximum |
|---|---|---|---|---|
| EBI (€) | 134 | 26 | 102 | 262 |
| Milk sub index (€) | 57 | 24 | -9 | 114 |
| Fertility sub index (€) | 64 | 23 | 13 | 131 |
| Calving difficulty sub index (€) | 19 | 9 | -7 | 44 |
| Beef sub index (€) | -7 | 6 | -25 | 11 |
| Health sub index (€) | 1 | 6 | -10 | 15 |
| PTA milk | 211.26 | 165.27 | -177.00 | 599.20 |
| PTA fat | 9.69 | 6.05 | -5.00 | 22.50 |
| PTA protein | 9.27 | 4.02 | -1.50 | 20.30 |
| PTA calving Interval | -3.11 | 1.49 | -6.25 | 0.33 |
| PTA survival | 2.41 | 1.22 | 0.01 | 6.26 |

[1]PTA=predicted transmitting ability

### 7.2.1. Genetic merit of candidate sires

Table 15 summarises the performance of the 61 candidate sires chosen by sire analysts as potential sires of sires. The EBI and sub-index performance of the 61 sires was superior to the national average (ICBF, 2008). Sire age ranged from 6 years to 16 years.

### 7.2.2. *Performance of candidate dams*

Table 16 describes the genetic merit of the top 3,000 potential candidate dams as ranked by the CUI Index after implementation of the various editing criteria. The mean EBI of the cows was €119, considerably higher than the national average of €47 in 2007 (ICBF, 2008). In addition, the sub-index performance of these cows was also superior to the national average. The 3,000 potential dams were from 467 different sires. The selection criteria adopted in the present study identified cows that had acceptable performance in all genetic and phenotypic criteria specified, with some phenotypically and genetically excellent cows identified. Thus the initiative to identify genetically excellent cows with satisfactory proven performance for milk, fertility and conformation was successful. However a considerable amount of cows were discarded during the editing process. The main editing criterion causing the greatest loss of potential candidate dams was the restriction on pedigree information. Because it is a legal requirement to record the dam of each animal born since 1996, this loss of data was due to a lack of sire recording. It must be impressed upon Irish farmers the importance of accurately recording pedigree information to increase the number of potential bull dams available for selection.

**Table 16.** Genetic merit of the 3,000 cows selected as potential bull dams[1]

| Trait | Mean | SD | Minimum | Maximum |
|---|---|---|---|---|
| EBI (€) | 119 | 17 | 90 | 195 |
| Milk sub index (€) | 58 | 24 | 0 | 142 |
| Fertility sub index (€) | 51 | 22 | 0 | 125 |
| Calving difficulty sub index (€) | 13 | 5 | -11 | 28 |
| Beef sub index (€) | -9 | 7 | -35 | 17 |
| Health sub index (€) | -1 | 3 | -14 | 10 |
| PTA Milk | 130.2 | 147.2 | -337.0 | 661.0 |
| PTA Fat | 8.9 | 5.3 | -2.5 | 29.0 |
| PTA Protein | 8.5 | 4.5 | -2.5 | 22.5 |
| PTA Calving Interval | -2.9 | 1.5 | -8.3 | 2.3 |
| PTA Survival | 1.3 | 0.6 | -0.5 | 3.8 |

[1]PTA=predicted transmitting ability

### 7.2.3 Comparison of methods

For the LP selection method, the 3 alternative objectives were maximised and the resulting average EBI, R-value and inbreeding coefficient of the "phantom progeny" from the selected top 1,000 matings are summarised in Table 17. Average EBI, R-value and inbreeding coefficients of the groups selected by LP were better than RAN in achieving the set objectives. When the objective changed from maximising EBI to minimising R-value, the average EBI of the resulting phantom progeny was lower across all selection methods. This demonstrates how the alternative objectives conflict in their aims and highlights the need to combine these individual objectives into a multiple or dual selection objective.

**Table 17.** *Average EBI (€), R-value (%) and inbreeding coefficient (F, %) of phantom progeny from the top 1,000 matings as selected by linear programming (LP), random selection (RAN) across the 3 objectives.*

| Objective & parameter | LP | RAN |
|---|---|---|
| Maximise EBI | | |
| EBI | 149 | 127 |
| R-Value | 1.39 | 1.34 |
| $F$ | 1.19 | 1.48 |
| Minimise R-value | | |
| EBI | 125 | 127 |
| R-Value | 0.55 | 1.34 |
| $F$ | 0.4 | 1.48 |
| Maximise sum | | |
| EBI | 145 | 127 |
| R-Value | 0.93 | 1.34 |
| $F$ | 0.69 | 1.48 |

The co-ancestry among the phantom progeny selected (i.e. within group co-ancestry) using the LP method was 1.93% (SD=0.45%). When the objective was to maximise EBI using the LP method, the average R-value of the group selected was 1.39% (Table 17), which is lower than the level of inbreeding of 1.5% in Irish Holstein-Friesian females in 2004. The average EBI for the group was €149. As the mean EBI for the group selected by the LP method when maximising the dual

objective was €145, genetic gain will be lost, albeit small, through the incorporation of minimising R-values in the population into the breeding programme.

## 8. CONCLUSIONS AND IMPLICATIONS

- Economic weights within the EBI have been revised on a continuing basis to reflect future expected changes in market prices and costs of production. Over the duration of this project the relative emphasis on milk production within the EBI has decreased but the expected response in fertility has reverse to now be favourable

- Do-it-yourself milk recording, with two milk weights and one milk composition taken is a viable alternative to supervised milk recording in Ireland

- The annual rate of increase in inbreeding over the past decade was 0.13% in the Hereford, 0.06% in the Simmental, and 0.10% in the Holstein-Friesian breeds. Inbreeding in the Limosin, Charolais and Angus remained relatively constant over the past decade. Herefords had the highest mean inbreeding in 2004 at 2.19%, whereas Charolais had the lowest at 0.54%. Effective population size was estimated for the Hereford, Simmental, and Holstein-Friesian only, as 64, 127, and 75, respectively.

- A primiparous animal, 12.5% inbred (i.e., following the mating of non-inbred half sibs), is expected to have reduced milk, fat and protein yield of 61.8 kg, 5.3 kg and 1.2 kg, respectively, reduced fat and protein concentration of 0.05% and 0.01%, respectively, and increased somatic cell score (i.e. natural log of somatic cell count divided by 1,000) by 0.03. The 12.5% inbred animal was also expected to have a 2% greater incidence of dystocia, a 1% greater incidence of stillbirth, an increase in calving interval of 8.8 d, an increase in age at first calving of 2.5 d and a reduced survival to second lactation of 4 percentage units.

- The option of contract mating to simultaneously maximise genetic merit and reduce co-ancestry within the population of Irish Holstein-Friesians through the use of linear programming is a viable and practical method of selecting potential young test sires

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