ABACUSBIO LIMITED

Implications of alternative breeding program structures for dairy cattle in Ireland:

AbacusBio cost benefit analysis

Final

Prepared for

The Irish Cattle Breeding Federation Ltd

By

Peter Amer

AbacusBio Limited

December 2010

AbacusBio Limited
PO Box 5585
Dunedin
New Zealand.

Phone: (03) 477 6375
Fax: (03) 477 6376
Email: pamer@abacusbio.co.nz
Website: www.abacusbio.com

Executive Summary

This cost benefit analysis follows up a report by McHugh et al. (2010) that identified a series of key factors that would lead to enhanced rates of genetic progress from progeny testing schemes. The McHugh report identified testing of young males in genomic schemes, maintaining high numbers of bulls mated, and genotyping of cows to train genomic predictions as potential key factors that could contribute to substantially faster and more sustainable rates of genetic improvement of dairy cattle in Ireland.

This report describes cost benefit methodology to evaluate a range of schemes and compared them with a conventional progeny test system.

Very high rates of return to investment in genetic improvement were identified, irrespective of the strategy employed. This is attributed to the permanent and cumulative nature of genetic improvement. Reliance on importation to deliver genetic progress for overall economic profitability in the pastoral based and highly seasonal dairy systems in Ireland has failed historically. Thus, investment in a breeding scheme beyond the current modest levels of progeny testing should lead to a very high rate of return in the order of 30 to 60 Euros returned for every 1 Euro invested depending on the share (i.e. 50 to 100%) of semen sales captured by the domestic scheme.

Assuming conservative prediction accuracies and in the absence of a highly co-ordinated system for identifying elite dams and contract matings, genomic schemes are expected to deliver benefits from genetic progress that are comparable to or higher than a conventional progeny testing scheme testing 100 sires, but at a substantially lower cost (i.e. costs are approximately one half).

Future improvements in genomic test accuracy would likely deliver substantially higher benefits. For example benefits increase by approximately 50% with an increase in genomic selection accuracy from 0.66 to 0.9.

Genomic breeding schemes can benefit from tactical exploitation of existing industry structure. In particular, targeting high merit herds for genotyping young bull calves substantially increases the benefits of genetic improvement. Systems whereby elite cows across a large number of herds are identified for recommended matings to elite bulls that will not intensify national levels of inbreeding have the potential to further increase genetic progress substantially.

With careful management, investment in genomic testing of cows for training genomic predictions should generate a very high rate of return on the investment required. For example, it is estimated that a €250,000 investment in cow genotyping could return an extra €20 Million per annum of benefits from genetic improvement in genomic selection schemes. In the future, genotyping of cows may well become routine with testing costs met by farmers who would benefit from more accurate replacement heifer selections. However, this will create analytical challenges, as only animals with favourable genotype results will finish up getting phenotypic information.

Bio-security risks need to be managed via application of extensive health testing protocols. Retaining previously used genomically selected bulls is likely to be more cost effective than increasing the size of the team of bulls in order to create a reserve pool of bulls to use in case a significant number become unavailable thought a disease outbreak.

Increasing the size of the team of genomically selected bulls is also likely to be a costly strategy for managing inbreeding. A more cost effective strategy would involve using optimised contributions algorithms to select the team of high merit bulls with a constraint on their degree of relationship amongst themselves, with the cow herd, and with previous teams of genomically selected and mated bulls. A system of targeted matings would increase the level of control over inbreeding by ensuring diversity among sires of sires. Furthermore, having the option to restrict the extent of matings of very popular bulls by their enforced removal from the active bull list would be a powerful and beneficial tool for managing inbreeding. However, it is likely that this option would only need to be exercised in a limited number of circumstances.

Nucleus herds containing screened in high merit cows could contribute moderate additional gains in genetic progress, while also contributing greatly to enhancing the profile of genetic improvement at a national level, the pioneering of novel phenotyping methods, and on-farm research.

Introduction

New genomic technologies offer potential to increase the contribution that genetic improvement makes to the profitability of the dairy farming industry in Ireland. Since the advent of ICBF over a decade ago, the rate of genetic progress in dairy farm profitability has been accelerating. This has been further enhanced recently with the release of genomic evaluation technologies.

Genomic evaluation technologies use large numbers of markers spread around the DNA to better predict which young cows and bulls have inherited useful genes for profit traits even before they or their daughters have herd performance records. The statistical techniques involved in genomic evaluation are complex, and still subject to a large amount of research and development.

Before the DNA markers can be useful for predictions in young animals, a reservoir of historical information is required to “train” the predictions. The genetic evaluation process links DNA of young selection candidates with the DNA of high performing ancestors (including bulls with high performing daughters), thus, sharing a lot of DNA with high performing individuals in the population, and not so much with low performing individual is a more accurate prediction of superior genetic merit in young bulls than when relying on pedigree information alone.

ICBF wish to develop a business case for industry investment in genetic improvement initiatives for dairy cattle. Results of simulation studies of genetic improvement strategies conducted specifically for Ireland (McHugh et al. 2010), and also for other countries are available. The study of McHugh et al. 2010 identified some key factors that lead to higher rates of genetic progress and lower rates of inbreeding in genomic selection schemes as follows:

- Increasing the numbers of male calves genotyped as potential selection candidates for widespread matings through AI increased the rate of genetic progress
- Increasing the number of bulls selected for widespread mating in genomic selection decreased the rate of accumulation of inbreeding
- Genotyping cows is a powerful and viable option for future training of genomic predictions

This document collates a set of parameters and assumptions provided by ICBF to develop the business case for industry investment in a new state of the art approach to genetic improvement. Deterministic prediction models are used to predict the increase in profitability of dairy farms in Ireland over time that is expected to directly result from the different breeding strategies. Other aspects of the strategies including how they might affect the balance of genetic progress in production versus functional traits, potential inbreeding risks, and opportunity to manage bio security risks are also considered.

Methodologies

Industry benefits from genetic progress

Rationale for approach

Literature studies including those undertaken specifically for the Irish dairy breeding context make predictions of steady state rates of genetic progress once new schemes have become bedded down and the perturbations associated with their introduction have been established. A number of these studies are reviewed in Appendix 1. They take two forms, firstly a deterministic form which uses Rendel and Robertson steady state prediction equations to quantify annual rate of genetic progress with the various strategies at a time point in the future. The second form use stochastic simulation, with a view to accounting explicitly for the impact of the breeding scheme design to build and maintain the accuracy of genomic predictions going forward in time.

For the purpose of a cost-benefit analysis, simulation studies that target steady state predictions have limitations. This is because of failure to identify considerable cost savings and/or short term genetic progress that might occur with one breeding strategy versus an alternative that results in the same long term steady state response. Genomic selection strategies that accelerate the availability of high merit bulls, versus establishment and/or scaling up of progeny test programs involves a substantial time lag before the steady state situation is achieved.

A new deterministic model has therefore been established with specific focus on modelling the transition from status quo to a new scheme for the purpose of carrying a cost benefit analysis.

Deterministic model

There are three separate steps as follows:

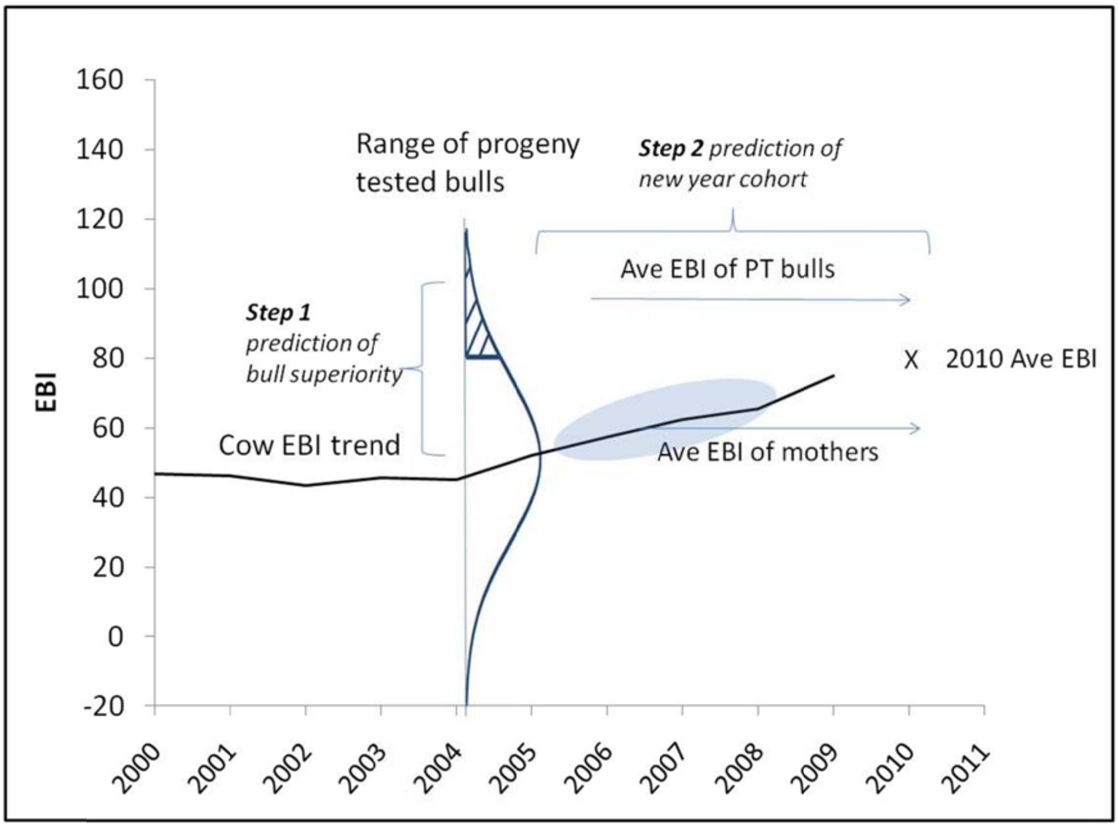
Step 1. Predict the genetic merit of future bull teams relative to bulls born in the same year (born 6 years earlier than main calf crop for PT bulls and born 3 years earlier than main calf crop for Genomic bulls). PT bulls are modelled using two stage selection theory, the first stage is based on parent average, second stage is on daughters. Genomic bulls are modelled assuming testing across a range of herds of different genetic merit. The genetic standard deviation of true EBI is about €125 on the EBV scale which becomes €62.5 on the daughter proof effect scale which is typically used for presentation and publication of bull proofs and cow genetic merit. In other words, if a bull has 10 euro higher EBI than another bull, his daughters will give about 10 euros more profit per lactation than the other bull.

Step 2. Model genetic trend in calves (and cows) at year of birth based on no selection among industry cows, so that each calf crop has genetic merit half way between merit of cows (based on typical age distribution of herd and historic genetic trend) and the selected bulls. Model details for predicting the genetic merit of selected bulls is considered in detail below. This is a cyclic model which allows current known genetic trend to be projected out into the future depending on the type and effectiveness of ongoing bull selection.

Step 3. Project future cow performance as a function of genetic merit of main crop bulls using gene flow models that extend genetic merit at time of mating and consequent birth of heifer calves destined to become replacements to the future time points when lactating cows express their genetic merit for EBI.

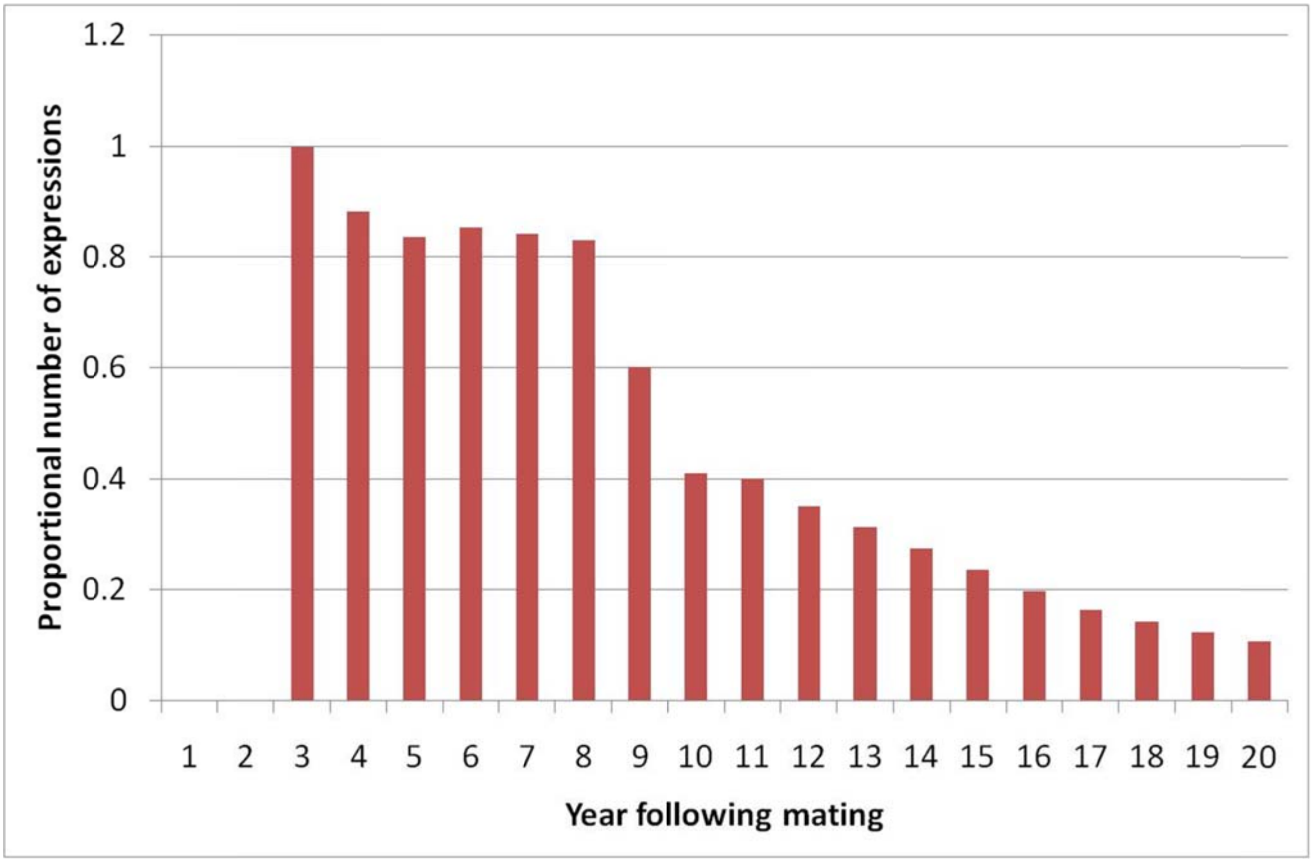
Figure 1 illustrates how steps 1 & 2 are integrated based on the superiority of selected bulls (in the illustrated example bulls are selected following progeny testing) predicted at step 1, and then combined with historic genetic trends in the cow population (step 2) to predict genetic merit in a new year cohort. Over time, predicted genetic trends form the foundations for the new year cohort prediction, but initially, the historic genetic trend forms the basis of predictions.

Figure 1. Example illustration for a progeny testing breeding program of integration of steps 1 & 2 to predict genetic merit for a new year cohort based on historic genetic trend



The units of the EBI are standardised to predict the genetic impact of a bulls genes per lactation of his daughters and female descendants. Genetic trend predicts the genetic merit for EBI of all animals by year of birth. Thus, the key purpose of step 3 is to translate genetic trend results into expected expressions of the cows' genes for EBI in the future. It is easiest to do this from the projected trend in the genetic merit of main crop bulls which is an indirect output of step 2. Figure 2 shows the projection of genetic expressions in future years of the genes of a bull from a specific mating.

Figure 2. Impact of a bulls genes on the expression (no decay due to discounting) of his genes for EBI via daughters and further descendents in the years following mating.



It is assumed that 21% of lactating cows are in their first lactation, and so when computing benefits across the industry, calculations need to be aggregated across the total number of cows mated in the year of superior mating, multiplied by 0.21, the replacement rate. Industry benefits from a higher level of genetic merit (EBI on daughter superiority scale) in a single crop of bulls results in all of the benefits being expressed in first lactation cows two years later, and a proportion of these survive to deliver benefits 3 years later. After 5 years, expressions are boosted by granddaughters, and granddaughter expressions continue to compensate for attrition of immediate daughters through until year 8. Expressions over subsequent years decline as expressions are halved each generation, and the expressions of genes from future crops of bulls become relatively more important. Benefits can be aggregated based on numbers of replacement females entering the national herd each year. The cow population in Ireland was assumed to be increasing by 30,000?? cows per year (i.e. 5%) from 1 million at present and then stabilising at 1.5 million cows in ten years time.

Further aggregation can be achieved by successively modelling improved year cohorts of bulls over time as output from step 2.

Benefit statistics

Each breeding scheme is modelled using the above approach. For each scheme, the superiority of the main crop cohort of bulls over all animals of the same birth year remains constant. This superiority (from step 1) is a function of selection accuracy, the standard deviation of index merit (units are Euro's of EBI improvement expressed on the breeding value scale as opposed to an EPD or daughter proof scale), and number of candidates tested. This superiority is translated into a projection of genetic trend over time (step 2) and then aggregated (step 3) to work out the overall benefit to dairy farmers in Ireland with genetic improvement from current levels. Benefits are counted from ten years of the genetic trend from the same breeding strategy, and all benefits that accumulate over a 20 year planning horizon are included but with a 7% annual discount rate. A baseline for comparison of schemes assumed that the EBI of sires used would remain static at €136 for the next twenty years. The present values (PV) of all schemes evaluated had the PV of this baseline situation with static EBI deducted to account for historic trend in EBI to the current time point.

The resulting PVs are also converted to an annualised basis (APV) by dividing by ten, the number of years of genetic improvement modelled. These annualised values allow for simple comparisons against annual costs of running the schemes. Annualised benefits are much greater than the benefits of one year of genetic trend counted over a single year. That is because genetic improvement is permanent and cumulative. Thus, the benefits of the first year of genetic progress actually get counted over 20 years (but with discounting). Acceleration in the rate of genetic progress through faster generation turnover also gets accounted for.

Alternative genetic progress schemes

Scheme 1. Conventional progeny test 50 bulls to select 30 bulls for widespread use for one year at 6 years of age

Scheme 2. Conventional progeny test 100 bulls to select 30 bulls for widespread use for one year at 6 years of age

Scheme 3. Scheme 1 but with genomic testing used to help identify the best bulls for progeny testing

Scheme 4. Scheme 2 but with genomic testing used to help identify the best bulls for progeny testing

Scheme 5. No formal progeny test – genomic selection of young bulls – 15 bulls selected from among 1000 chosen at random across Ireland for genomic testing

Scheme 6. No formal progeny test – genomic selection of young bulls – 30 bulls selected from among 1000 chosen at random across Ireland for genomic testing

Scheme 7. No formal progeny test - genomic selection of young bulls – **30** bulls selected from among 1000 genomic tested out of the top EBI herds in Ireland

Scheme 7a. No formal progeny test - genomic selection of young bulls – **60** bulls selected from among 1000 genomic tested out of the top EBI herds in Ireland

Scheme 7b. No formal progeny test - genomic selection of young bulls – **30** bulls selected from among 1000 genomic tested out of the top EBI herds in Ireland. Targeted matings are used to lift the genetic merit of the young bull candidates sourced.

Scheme 8. No formal progeny test - genomic selection of young bulls – 30 bulls selected from among 5000 genomic tested out of the top EBI herds in Ireland

Scheme 9. No formal progeny test - genomic selection of young bulls – 30 bulls selected from among 1000 genomic tested out of the top EBI herds in Ireland plus a further 200 genomic tested in nucleus herds containing assembled cows of very high genetic merit where there is extra recording

Scheme 10. No formal progeny test - genomic selection of young bulls – **30** bulls selected from among 5000 genomic tested out of the top EBI herds in Ireland plus a further 200 genomic tested in nucleus herds containing assembled cows of exceptional genetic merit where there is extra recording for economically very important traits

Scheme 10a. No formal progeny test - genomic selection of young bulls – **60** bulls selected from among 5000 genomic tested out of the top EBI herds in Ireland plus a further 200 genomic tested in nucleus herds containing assembled cows of exceptional genetic merit where there is extra recording for economically very important traits

Scheme 10b. No formal progeny test - genomic selection of young bulls – **60** bulls selected from among 5000 genomic tested out of the top EBI herds in Ireland plus a further 200 genomic tested in nucleus herds containing assembled cows of exceptional genetic merit where there is extra recording for economically very important traits. Targeted matings are used to lift the genetic merit of the young bull candidates sourced.

Because of uncertainty in the ability of 2 year old bulls to yield sufficient amounts of semen to be used widely at two years of age, the genomic selection scenarios modelled here have assumed widespread use of young bulls at three years of age following test matings at two years of age to check for calf deformities etc. Test matings from bulls at two years of age are possible because much smaller volumes of semen are required and the majority of test bulls are capable of generating the required amounts at a young age.

Two stage selection modelling for progeny test pre-selection

Progeny testing is made more efficient in practice by identifying genetically superior young bulls to enter the progeny test. Pre-selection information can take the form either of parent average genetic prediction of merit, or through genomic pre-selection. Two stage selection theory as described by Jopson et al. (2004) was implemented to derive selection intensity after the second stage of a two stage selection process. The key parameters are the proportions selected in each of stages 1 and 2, and the genetic correlation between stage 1 and stage 2 selection criteria. For example, if there are 1000 young bulls accessible for progeny testing with a normal spread of EBI values around the year cohort average, and 100 bulls are selected for progeny testing, and bulls chose for breeding taken from the best 30 bulls, then the selection proportions are 10% for stage 1 and 3% for stage 2. The correlation between stage 1 and stage 2 selection is computed as $r_{12} = \frac{b_1' P b_2}{\sqrt{b_1' P b_1 \cdot b_2' P b_2)}}$ where P is a variance covariance matrix for information sources available at selection stage 2 constructed using selection index theory (see below), and b_i is a set of selection index weights for selection stage i based on information sources available at that selection stage.

Selection index theory

Selection index theory was used to compute selection accuracy with combinations of information sources for prediction of EBI. Selection index weights are derived using

$$b = P^{-1}G$$

where

$$P = \begin{bmatrix} \dfrac{\dfrac{1+(n-1)r}{n} + (p-1).25h^2}{p} & .125h^2 & .25h^2 & .5\alpha h^2 \\ .125h^2 & \dfrac{1+(s-1).25}{s} & 0 & .25\alpha h^2 \\ .25h^2 & 0 & \dfrac{1+(d-1)r}{d} & .5\alpha h^2 \\ .5\alpha h^2 & .25\alpha h^2 & .5\alpha h^2 & h^2 \end{bmatrix},$$

a phenotypic variance covariance matrix for information sources and

$$G = \begin{bmatrix} .5h^2 \\ .25h^2 \\ .5h^2 \\ \alpha^2 h^2 \end{bmatrix},$$

is a genetic covariance matrix between information sources and true values for the trait being predicted. Variable n is the number of repeated records on p progeny of a selection candidate for a trait or index with a heritability of h^2 and a repeatability r. A single record on s paternal half sibs and d repeated records on the dam of the selection candidate are incorporated in the equations. The symbol α denotes the accuracy of a standalone genomic prediction of an animal's genetic merit.

Accuracy is computed as $r_{TI} = \sqrt{.5b_1 + .25b_2 + .5b_3 + b_4}$.

To understand how the selection index theory was applied, consider a situation where young bulls are preselected for progeny testing based on a combination of parent average (i.e. dams performance records from two repeated lactations and 100 paternal half sib daughters with one lactation each) and a genomic selection test with accuracy 0.6 defined as the correlation between the pure genomic prediction (Direct Genomic Value using Interbull terminology) and the true genetic merit of the animal for its EBI index. Parameters used to compute b1 were therefore n=1, p=0, s=100, d=2 and α=0.6. Stage 2 selection is based on the same information as stage 1 with the addition of 100 daughters with a single recorded lactation each. Thus, parameters used to compute b2 and P were n=1, p=100, s=100, d=2 and α=0.6.

Bull superiority with schemes incorporating progeny testing

Selection differentials (the mean for the trait or index of interest in non-standardised form of bulls selected for widespread use as a deviation from their contemporaries born in the same year) after both stages of selection have been completed are computed as

$$SD_{Bulls.PT} = i_{2st} \cdot r_{TI} \cdot \sigma_G$$

where i_{2st} is the selection intensity obtained from two stage selection theory, r_{TI} is the accuracy of selection of bulls at stage 2, and σ_G is the genetic standard deviation for true EBI taken as €62.5.

For the progeny test scheme, it was necessary to establish the number of selection candidates available prior to stage 1 selection. In principle, this is a very large number and could potentially be interpreted as the total number of bull calves born. However, in practice, a large number of bull calves are unavailable for selection. For practical purposes, a value of 5000 was assumed, and projections of benefits from genetic progress were found to be relatively insensitive to this value. For example, doubling the number from 5000 to 10,000 resulted in the projected final superiority of bulls increasing by only 5%.

For schemes including genomic pre-selection to make selection of young bulls for progeny testing more accurate, the correlation r_{12} between stage 1 and stage 2 selection and the accuracy of bulls selected at stage 2 r_{TI} are updated to account for different information sources. The numbers of candidates and numbers selected after stages 1 & 2 respectively can also be manipulated depending on how many bull calves are tested.

Herd screening strategies for genomic selection of young bulls

Several genomic breeding strategies were considered whereby bulls were selected randomly for genomic testing from among all bull calves born in a year. In this instance, there is a single selection stage, and selection differentials for bulls can be predicted using standard selection intensity i and the accuracy of selection is computed from selection index theory capturing parent average and genomic test information. i.e.

$$SD_{Bulls.GS} = i \cdot r_{TI} \cdot \sigma_G$$

There is also potential for genomic selection strategies to be made more efficient by sourcing young candidate bulls for testing which are

a. Of higher average genetic merit than the industry average, and
b. Have more intensive and accurate recording practices than industry average

These enhanced genomic selection strategies allow for a higher selection differential at a given level of genomic testing through increasing the mean genetic merit of selection candidates relative to the average of all animals born in the same year and also by increasing the spread of estimated genetic merit of selection candidates through more accurate prediction.

A model was developed to simulate the amount of extra gain that might be realised with these strategies. Herds are divided into three categories,

a. mainstream herds from which no young bull candidates are sourced,
b. elite herds which are assumed to be 0.3 σ_G (~20 EBI units) superior to industry average, and
c. nucleus herds which are assumed to be 0.6 σ_G (~40 EBI units) or 1.2 σ_G (~80 EBI units) superior to industry average, and to have 10% (or 25%) higher accuracy leading to a 10% (or 25%) greater standard deviation of predicted EBIs of young bulls compared with elite herds.

It was assumed that 1000, 2000, or 5000 young bulls could be tested from elite herds, and 0 or 200 calves could be tested from nucleus herds. It is assumed that when only 2000 or 1000 young bulls from elite herds are tested, that they are taken from the herds with the best average EBI of calves, and that the standard deviation of elite herd means for EBI is 20 EBI units, such that the best 10% of elite herds are expected to average 35 EBI units above the average of all elite herds.

For the majority of simulations, it was assumed that bull calves for genomic testing would be taken at random from the elite herds. However, to test the likely benefits of a nationally co-ordinated breeding scheme, a further assumption was made that bull calves could be sourced from the best 15% available within the herd. To achieve this, cows would need to be genotyped to increase the accuracy of predictions of their genetic merit, and the best of the cows targeted to be bred to elite bulls chosen to become sires of sires. Within the model, this resulted in a lift by 1 genetic standard deviation of true genetic merit for the young bulls both being genomic tested, and the final 30 bulls that ultimately get selected for widespread use. These schemes with contract matings fit more closely the situations modelled in the McHugh study.

Accuracy of genomic predictions

The accuracy with which genomic predictions identify truly genetically superior animals is a key determinant of the efficiency of genomic selection schemes. Projecting what this accuracy will be is possible using theoretical formulae, although this is somewhat complicated by an apparent tendency for both accuracy obtained directly from genetic evaluation systems incorporating genomics and also genomic predictions to be inflated. For this study, formulae proposed by Daetwyler et al. 2010 with a slight modification proposed by John Woolliams to account for incomplete spread of markers across the Genome were used to predict the accuracy of direct genomic predictions, r_{GS} (i.e DGVs that do not include additional accuracy provided by parent average information) as follows:

$$r_{GS} = \sqrt{\frac{N_p \cdot h^2_{effective}}{N_p h^2 + M_e}} \cdot p_{spread}$$

where N_p is the number of individuals with phenotypes in the training population, p_{spread} is the proportion of the Genome covered by markers (as defined by Woolliams EAAP Crete and this parameter was used to tune genomic prediction accuracies to align with those observed from validation analyses in Ireland to date), $h^2_{effective}$ is the effective heritability of the phenotype used as the dependent variable in training, and M_e is the number of independent chromosome segments which is in turn computed using

$$M_e = \frac{2 \cdot N_e \cdot L}{\log(4 \cdot N_e \cdot L)}$$

where N_e is the effective population size and L is the length of the genome in morgans.

For the calculations used in this study, L was assumed to be 30 morgans and N_e was assumed to be 120 individuals. The N_e of 120 is higher than the value assumed in many studies dealing with pure Holstein cattle, but a higher value has been used here because of the contribution of both traditional (dual purpose type) Friesian and New Zealand type Friesian cattle to the training and prediction populations.

Calculations of r_{GS} were undertaken separately for $h^2_{effective}$ based on both high and low real heritability (h^2) traits. For example, in the report of Berry et al (The Economic Breeding

Index – A Generation On), milk yield traits with h^2 of 0.35 account for about 40% of variation in true economic merit, while calving interval (h^2=.04) and survival (h^2=.02) account for about 26% and 8% of the variation in true economic merit respectively. Thus, we calculated accuracy of genomic selection separately for traits with h^2=.35 and h^2=.03 and then took the overall accuracy of genomic predictions used in the genetic reponse models to be the average of these two values. The number of individuals with phenotypes, N_p, used in training was also varied. For example, in the base calculations, it was assumed that N_p =1100 for the how heritability traits, as calving interval and survival is unlikely to have been recorded accurately in daughters of both older bulls used in training, and also for training bulls sourced from Interbull MACE results. Realised accuracies (i.e. predictions verified by daughters) for low heritability traits have been very low in a number of practical situations around the world. It was assumed that N_p =3000 for the high heritability traits.

Actual heritabilities (h^2) need to be translated to the effective heritability scale ($h^2_{effective}$). For proven bulls used to train genomic selection, progeny information was used to predict the effective reliability of de-regressed daughter average proofs using

$h^2_{effective.Bulls} = \frac{p \cdot h^2}{(p-1) \cdot h^2 + 4}$ where p is the number of daughters per bull used in training and which was assumed to be 80 for the milk yield traits and to be 130 for the low heritability traits.

When modelling the additional information that could be provided by genotyping cows, the effective heritability ($h^2_{effective.Cows}$) was translated from the actual trait heritability as the square of the accuracy of selection calculated using selection index formulae assuming the cow had two repeated records (repeatability assumed to be 0.6 for the high heritability trait and 0.4 for the low heritability trait), 2 maternal half sibs with a single record and 2 repeated records on the dam. Paternal half sib information was ignored as many training individuals are likely to have the same paternal half sibs. The effective heritability used to compute r_{GS} was $h^2_{effective.Bulls}$, but the number of individuals with phenotypes in the training population was adjusted upwards to account for the extra training information provided by cows using

$$N_p = N_{Bulls} + N_{Bull.equivs}$$

where N_{Bulls} and $N_{Bull.equivs}$ are the number of bulls and bull equivalents (provided by the cow information) respectively with phenotype and genotypes used in training. The numbers of bull equivalents ($N_{Bull.equivs}$) provided by N_{Cows} training cows was obtained by solving to find the number of bulls at a training effective heritability for bulls that would give the same predicted accuracy as N_{Cows} (the number of cows used for training) at the training effective heritability for cows.

Results

Table 1 shows effective selection intensities for a range of different pure genomic selection schemes where the most elite herds are targeted for genotyping, and also considering opportunities created by the establishment of elite nucleus herds. The intensities give the expected superiority of selected sires over all bull calves born in the same year in units of standard deviations of estimated genetic merit. These values need to be multiplied by accuracy of selection and the standard deviation of true values of EBI in order to calculate the superiority of selected bulls over their contemporaries.

The extra selection intensity from genotyping more than 1000 bull calves as selection candidates is quite modest, for example, 8.6% increase in intensity when 5000 instead of 1000 young bull candidates are genotyped. This reflects the fact that the extra bull calves genotyped come from progressively lower average genetic merit herds.

The establishment of nucleus herds where 200 young male bull calves are also available as candidates with a higher mean and higher variance of predicted merit also results in modest improvements in intensity unless the nucleus herds have a much higher mean EBI than the majority of herds from which candidates are sourced. With nucleus herds that are 80 EBI units on average higher than the average of elite herds, and a 10 to 25% increase in spread of predicted breeding values due to more accurate recording, selection intensities are increased by approximately 10% if 1000 calves are genotyped from top herds, but only approximately 5% if 5000 calves are genotyped from top herds. Effectively, the lower numbers of bull calf candidates available from the nucleus herds moderates their contribution to higher selection intensities.

Table 2 shows how additional cows genotyped to train genomic predictions might contribute to higher accuracies of pure genomic predictions (DGVs). With low numbers of bulls and low effective heritability's for the non milk production traits, the predicted accuracy of genomic predictions for overall merit are quite modest at 0.66. Genotyping 2000 cows would add considerably to accuracy of prediction of the lower heritability traits in the EBI, with relatively modest incremental benefits beyond this with 5000 and 20,000 cows genotyped for training.

In theory, it has been argued that genomic selection should favour lower heritability traits over higher heritability traits. The Daetwyler prediction equations shown support this, but only when the numbers of animals with phenotypes contributing to training is the same for each trait category. Because lower heritability traits are typically associated with more recent recording practices and because bulls tend to be older before they can be accurately evaluated, there is typically many less training animals available for them. If we take the progeny test situation as a point of reference, the effective heritability for bulls for high heritability traits is 2.3 times greater than for low heritability traits. The ratio of genomic selection accuracies is lower than this value and further reductions with genotyping of cows are modest. This suggests that genomic breeding schemes should shift the relative progress more in favour of functional traits and less in favour of milk production traits. This is a natural bias that is independent of the economic weightings, rather it reflects relative shifts in accuracy ratios for the different types of traits.

Table 3 describes the expected sire superiority over contemporaries of the same birth year, full present value of returns, and annualised present value of returns. While sire superiority is of comparable magnitude between progeny testing and genomic selection schemes (in the absence of targeted matings), the much shorter generation interval of genomic testing schemes leads to considerably higher returns. Identifying elite herds for genomic testing of bulls resulted in a substantial leap in the value of genetic progress. Using targeted matings and identifying the most elite bull calves within targeted herds to lift the genetic merit of the bulls calves identified for genomic selection results in further substantial leap in the value of genetic progress.

Table 4 provides a summary of annual operating costs for each scheme. The progeny testing schemes are most expensive to operate, particularly if they incorporate genomic pre-selection. Schemes 7 and 9 provide the greatest present value of benefits relative to costs. However, all of the schemes provide a very high rate of return on investment relative to a situation of zero genetic progress in Ireland. Table 4 also shows the breakeven level of DGV accuracy for the EBI index for genomic selection schemes 7 to 10 to result in the same annualised benefit from genetic progress as a progeny scheme whereby each year 50 bulls have entered progeny test historically, and from now one, each year 100 bulls enter progeny test. In general, moderate reductions in accuracy are required before the annualised benefits of the genomic schemes fall below the 100 bull progeny testing scheme.

Figure 1 shows the sensitivity of projected returns to increases in the accuracy of genomic predictions for schemes 3, 7 and 10. Genomic pre-selection prior to progeny testing of 100 bulls (scheme 3) gave a lower proportional response to higher genomic prediction accuracy than pure genomic selection schemes 7 and 10. Scheme 3 relies on a significant proportion of its genetic progress coming from selection among progeny tested bulls at a point where daughter information has diluted down the influence of the genomic prediction in the selection decision. For schemes 7 and 10, benefits of genetic progress increase almost in proportion to the increase in genomic prediction accuracy. However, it should be noted from Table 2 that increases in genomic selection accuracy are not linearly proportional to the amount of investment in genotyping of training animals.

Table 1. Standardised selection intensities with alternative targeted genotyping strategies for pure genomic selection schemes.

Elite calves genotyped	Nucleus calves genotyped	Intensity A[1]	Intensity B[2]	Intensity C[3]	Intensity D[4]	Intensity E[5]
5000	200	3.31	3.42	3.53 (Scheme 10)	3.24	3.06 (Scheme 12)
2000	200	3.22	3.36	3.48	3.17	2.95
1000	200	3.11 (Scheme 9)	3.28	3.42	3.08	2.82
5000	0	3.26 (Scheme 8)	-	-		3.02
2000	0	3.15	-	-		2.89
1000	0	3.01 (Scheme 7)	-	-		2.73 (Scheme 11)

[1] Intensity A assumes that nucleus herds relative to industry average are 0.6 σ_G (~40 EBI units) superior with a 10% higher spread in EBI's of bull calves due to more accurate recording. Thirty of the best bull calves are selected for widespread industry use.

[2] Intensity B assumes that nucleus herds relative to industry average are 1.2 σ_G (~80 EBI units) superior with a 10% higher spread in EBI's of bull calves due to more accurate recording. Thirty of the best bull calves are selected for widespread industry use.

[3] Intensity C assumes that nucleus herds relative to industry average are 1.2 σ_G (~80 EBI units) superior with a 25% higher spread in EBI's of bull calves due to more accurate recording. Thirty of the best bull calves are selected for widespread industry use.

[4] Intensity D assumes that nucleus herds relative to industry average are 1.2 σ_G (~80 EBI units) superior with a 25% higher spread in EBI's of bull calves due to more accurate recording. Sixty of the best bull calves are selected for widespread industry use.

[5] Intensity E assumes that nucleus herds relative to industry average are 0.6 σ_G (~40 EBI units) superior with a 10% higher spread in EBI's of bull calves due to more accurate recording. Sixty of the best bull calves are selected for widespread industry use.

Table 2. Derived genomic prediction accuracies with various training information sources

	High h2 (=.35)						Low h2 (=.03)						Combined	Ratio
Situation	N_{Bulls}	$h^2_{effective.Bulls}$	N_{Cows}	$h^2_{effective.Cows}$	r_{GS}		N_{Bulls}	$h^2_{effective.Bulls}$	N_{Cows}	$h^2_{effective.Cows}$	r_{GS}		r_{GS}	r_{GS} low/high
Base	3000	.89	0	0	.73		1100	.50	0	0	.58		.66	1.26
2000 cows genotyped	3000	.89	2000	.53	.82		1100	.50	2000	.06	.62		.72	1.32
5000 cows genotyped	3000	.89	5000	.53	.84		1100	.50	5000	.06	.65		.75	1.29
20000 cows genotyped	3000	.89	20000	.53	.88		1100	.50	20000	.06	.75		.81	1.09

Table 3. Sire superiority, net present value over 20 years, and annualised benefits for 10 different breeding schemes. Genomic selection accuracy (DGV) for EBI assumed to 0.5 for schemes using genomic tested bulls.

Scheme	Description	Sire superiority (EBI €)	NPV over 20 years (€M)	Annualised benefits (€M)
1	30 bulls selected from 100 progeny tested	120	854.3	85.4
2	30 bulls selected from 50 progeny tested	90.6	432.3	43.2
3	Scheme 1 with genomic pre-selection	146.3	1231.5	123.2
4	Scheme 2 with genomic pre-selection	126.9	953.1	95.3
5	15 bulls selected from 1000 genomic tested	106.3	656.8	65.7
6	30 bulls selected from 1000 genomic tested	96.5	516.4	51.6
7	30 bulls selected from 1000 genomic tested from elite herds	127.9	968.2	96.8
7a	60 bulls selected from 1000 genomic tested from elite herds	116.0	797.2	79.7
7b	30 bulls selected from 1000 genomic tested with contract mating	190.4	1866.1	186.6
8	30 bulls selected from 5000 genomic tested in elite herds	138.6	1120.8	112.1
9	30 bulls sel. from 1000 tested in elite herds and 200 tested in nucleus herds	132.2	1029.3	102.9
10	30 bulls selected from 5000 tested in elite herds and 200 tested in extreme nucleus herds	150.0	1285.7	128.6
10a	60 bulls selected from 5000 genomic in elite herds and 200 tested in extreme nucleus herds	130.1	998.7	99.9
10b	30 bulls from 5000 tested in elite herds & 200 tested in nucleus herds with contract mating	212.5	2183.7	218.4

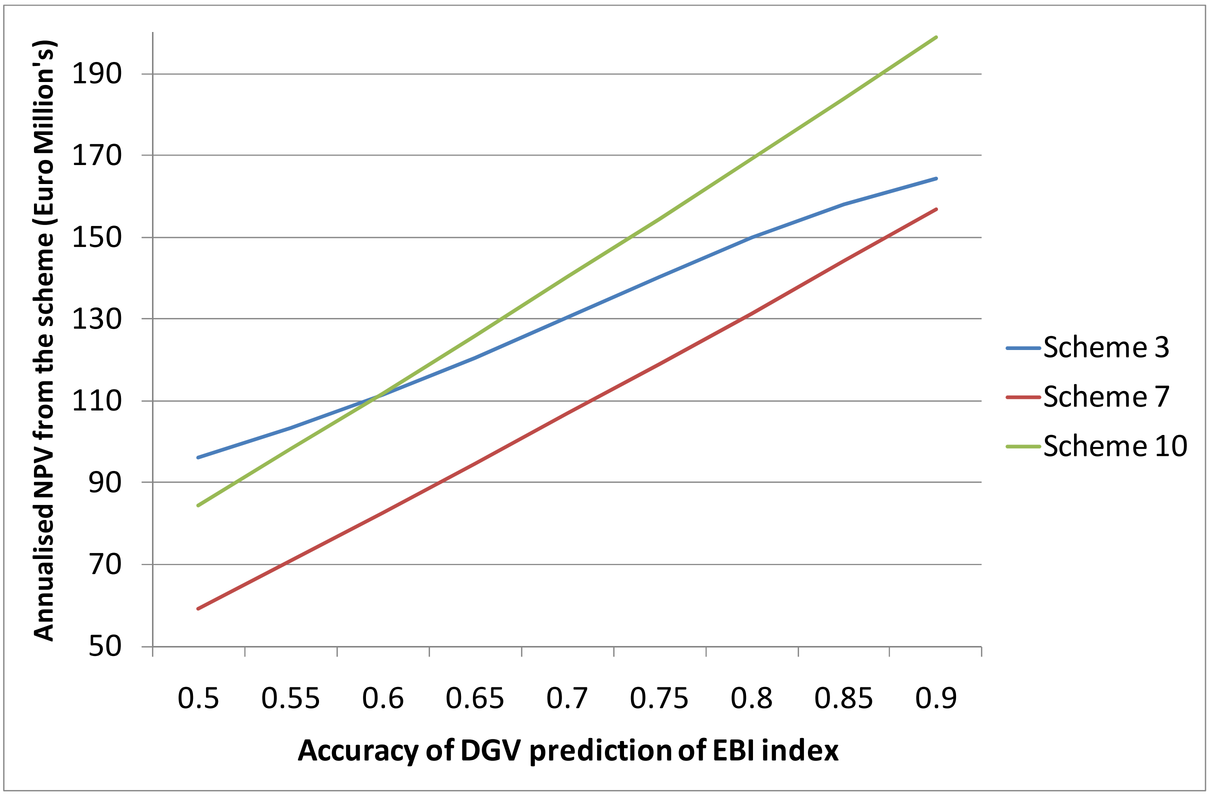
Table 4. Summary of annual operating costs by scheme relative to annualised benefits

Scheme	Description	Annualised benefits (€M)	Total costs €000	Bull costs €000	Low density. test costs €000	High density. test costs €000	Break-even accuracy of GEBV[2]
1	30 bulls selected from 100 progeny tested	85.4	1568	1568	0	0	
2	30 bulls selected from 50 progeny tested	43.2	784	784	0	0	
3	Scheme 1 with genomic pre-selection	123.2	1818	1568	250		
4	Scheme 2 with genomic pre-selection	95.3	1034	784	250	0	
5	15 bulls selected from 1000 genomic tested	65.7	326	216	0	110	
6	30 bulls selected from 1000 genomic tested	51.6	541	431	0	110	
7	30 bulls selected from 1000 genomic tested from elite herds	96.8	541	431	0	110	.55
7a	60 bulls selected from 1000 genomic tested from elite herds	79.7	973	863	0	110	.61
7b	Scheme 7 with contract mating	186.6	541	431	0	110	
8	30 bulls selected from 5000 genomic tested in elite herds	112.1	681	431	250	0	.51
9	30 bulls selected from 1000/200 tested in elite/nucleus herds	102.9	563	431	0	132	.53
10	30 bulls selected from 5000/200 tested in elite/nucleus herds	128.6	691	431	260	0	.47
10a	30 bulls selected from 5000/200 tested in elite/nucleus herds	99.9	1123	863	260	0	.55
10b	Scheme 10 with contract mating	218.4	691	431	260	0	

[1] A description of the schemes and a breakdown of the costings are presented in detail in Appendix 3.

[2] This gives the accuracy of the GEBV required for genomic selection schemes to give the same returns as a progeny test scheme with 50 bulls tested historically and 100 bulls entering progeny test from now on (i.e. Annualised benefits of € 618 M). The accuracy is currently assumed to be 0.68

Figure 1. Sensitivity of benefits from Schemes 3, 7 and 10 as the accuracy of genomic selection increases



Discussion

The return on investment in genetics

The estimated benefits of dairy cattle genetic improvement are expected to be very high relative to the level of investment required for all of the schemes considered. The annualised rates of progress predicted are high relative to benefits that might be counted from a single year of genetic improvement. However, the permanent and cumulative nature of genetic improvement is the key to the high level of benefits, and this is explained using a simple example in Appendix 2.

One factor that has not been accounted for in these calculations is the adoption rate by farmers of the superior bulls generated by the breeding programs. In general terms, the size of the benefits computed here assume a 100% adoption rate, such that all dairy farmers in Ireland rely on home generated bulls for their matings. Results can easily be adjusted for a long term market share for home generated bulls, for example, if the long term market share for homebred bulls is 70%, then 70% of the benefits shown can be attributed to the breeding strategy.

Importation is potentially an alternative option for genetic improvement of dairy cattle in Ireland. However, historically, reliance on importation delivered a very low rate of return, mainly because the economic importance of maintaining a tight calving interval is much higher in Ireland than in non seasonal production systems. It is likely though that importation of Semen from countries with more similar breeding objectives and production environments will contribute to genetic progress in Ireland, but the size of the benefits relative to the investment required for a domestic breeding scheme suggest that future reliance solely on importation is unjustified.

Genomic schemes versus progeny testing

The progeny testing scheme described here (Scheme 1 with 100 bulls tested per annum) generated a return of comparable magnitude to many of the genomic selection schemes, particularly if the accuracy of genomic selection is lower than the base levels assumed here. However, the level of investment required to maintain a scheme testing 100 bulls per annum is substantially higher than the genomic selection schemes. With the genomic selection schemes, less bulls need to be sourced and maintained, and also the period of time for which they need to be held is potentially much less. A key factor is the opportunity for much higher rates of progress with genomic selection if the accuracy of genomic predictions can be improved.

Building and maintaining the accuracy of genomic selection

The McHugh 2010 report identified the genotyping of females as a viable means of improving the accuracy of genomic selection. This study suggests that a project involving genotyping of 5000 cows (an investment of €250,000 at a low density test price of €50 per test) such that the accuracy of genomic predictions increased from .66 to .75 would result in the annualised benefits from genomic selection schemes increasing by at least €20 M per annum. The efficacy of cow genotyping to improve the accuracy of genomic predictions is currently unproven, although many research groups are attempting this, and so more information should be available shortly. It is important that all replacement heifers entering a herd have genotypes taken, and that recording in these herds be as accurate and comprehensive as possible. A further necessity is that stratification biases are eliminated. Thus, participating herds should have used a balance of at least 5 proven and young sires leading to good genetic links with other herds and across calving seasons, while maintaining close relationships with the young bull calves that are likely to become selection candidates.

In the future, routine genotyping of cows by commercial farmers wishing to enhance the accuracy of selection of their replacements could negate the need for additional investment at an industry co-ordinated level. However, much improvement in the analytical methods underpinning genomic predictions will be required to deal with the situation where only animals with desirable genotypes have phenotypes, and the efficiency of the data for training in this instance might be substantially compromised. Until the analytical issues are resolved, there is a case for co-ordinated genotyping of all first lactation cows in targeted herds where replacements have not been selected using genomic predictions.

Results of this study suggest that moderate falls in the accuracy of genomic selection would be required for benefits of genomic selection schemes to fall below those of a progeny testing scheme testing 100 bulls per annum from now on. Regular monitoring of realised accuracy (i.e. training predictions using a subset of bulls with daughters and then testing predictions on the balance) is required to ensure that genomic selection schemes are operating effectively.

Managing biosecurity issues

Bio-security risks need to be managed carefully irrespective of the final design chosen. Partitioning and isolation of groups of young bulls, along with application of extensive health testing protocols have been factored into the bull costing for the various schemes. Under a genomic selections strategy, there are two options for keeping a reserve pool of bulls.

The first option is to option is to select a larger pool of bulls using genomic selection. These bulls act as a reserve group, and would also then be available for widespread use once they are fully progeny tested. Cost benefit results for schemes 7a and 10a show the reductions in benefits of genetic progress that would occur if 60 instead of 30 bulls were selected and all of the retained bulls were used in genomic selection. The annualised benefits decrease by 18 to 22% which equates to €17 M to €28 M. Bull costs are also doubled (i.e. from €430,000 per annum to €860,000 per annum). The reduction in genetic progress would not necessarily be realised in years when the leading 30 bulls survived intact, as only the best 30 bulls could be used for widespread matings. However, the bull costs could only be avoided by identifying reserve bulls from an alternative source.

The second option is to retain genomically selected bulls that have had a single year of widespread mating for potential use in future years in the event of a bio security problem. Appendix 3 calculates the costs of retaining all bulls having undergone widespread mating until they have daughter records. The cost is an extra €4451 per bull which for 30 bulls equates to €134,000 per year. An additional advantage is that these bulls become a likely source of high merit daughter proven bulls, some of which are likely to be comparable in genetic merit to the genomic proven bulls. They would also be available to meet a likely ongoing demand by a proportion of farmers that prefer to use bulls whose merit is proven by daughter performance.

Retaining genomic selected bulls appears to be a much cheaper option for managing biosecurity risks than bringing extra bulls through the bull rearing and initial testing process to act as reserves. However, in the event of these bulls having to be used, they are likely to make a greater contribution to inbreeding and result in a dip in genetic merit of bulls used for industry matings. The dip in genetic merit should be substantially less than the level of genetic progress in one year, for the following reasons:

- not all of the young bulls should be taken out in one biosecurity event if bulls are reared in separate isolated groups and
- there should be able to replace some of the lost bulls with only the highest merit reserves from several year cohorts, and possible also from some bulls with daughter records.

Managing inbreeding

There are two potential mechanisms for managing inbreeding. The first mechanism is via breeding scheme structure, and the second mechanism is via active and enforced management and restriction of active bulls. Increasing the number of bulls selected for widespread mating as part of the genomic selection strategy has been shown to be a costly mechanism for managing inbreeding, both in terms of lost genetic progress and in terms of bull costs (i.e. comparisons of schemes 7 and 10 with 7a and 10a).

Limiting the number of matings by popular individual bulls through enforced withdrawal of them from the active bull list, and taking account of genetic diversity when selecting the pool of 30 bulls to be retained for the genomic selection strategies are likely to be much less costly mechanisms for managing inbreeding. Optimum contributions algorithms could easily be adapted to select teams of 30 bulls with constraints on co-ancestry among them and also taking into account their relatedness with the national cow herd and previous teams of genomically selected bulls.

Herd co-ordination

There is much to be gained in breeding scheme strategies that exploit variation in genetic merit both within and across herds. A structured approach to participating herds also provides the opportunity to apply effort to improve trait recording and or recording of novel phenotypes in an efficient way.

While operational and logistical challenges would not be trivial, there would be further substantial benefits available through targeted matings of elite cows to very high merit bulls that are not too closely related to the current cow population.

This opportunity could be enhanced via nucleus herds, whereby high merit cows are screened into the nucleus herds. Results from the simulations here suggest that these herds can make a modest positive contribution to the rate of genetic progress. However, other benefits of these herds would arise through specialised recording, industry demonstration of high merit herds in action, and contributions to research initiatives.

References

Jopson, N.B., P.R. Amer, J.C. McEwan 2004. Comparison of two-stage selection breeding programmes for terminal sire sheep. Proc. NZ Soc. Anim. Prod. 64:213-216.

Daetwyler, H.D. R Pong-Wong, B Villanueva, J.A. Woolliams (2010). The Impact of Genetic Architecture on Genome-wide Evaluation Methods. Genetics, Vol. 185, 1021-1031, July 2010

Appendix 1. Relevant literature studies

McHugh, Meuwissen, Berry, Cromie and Sonneson (2010). Genomic Selection in Irish Dairy Cattle. May 2010. ICBF Report

- Use genotyping as a pre-selection tool for potential AI sires on as many bull calves as possible considering the costs involved.
- Bulls that are selected to enter the progeny test should become selection candidates at two instead of three years of age, thus increasing genetic level and reducing the generation interval.
- The number of animals selected to enter the progeny test (100 to 20) has little effect on overall genetic level but an increase in the numbers chosen will result in lower rates of inbreeding and increase the reliability.
- The number of proven bulls may have little impact on the overall genetic level, but the greater the number of bulls that enter AI, the lower the rate of inbreeding within the population and the greater the reliability that is associated with the breeding scheme.
- Genotyping of females also holds the potential to increase both genetic level and the reliabilities associated with both the male and female populations.

Sonneson, Meuwissen and Cromie 2008. Genomic selection in Irish Dairy Cattle Breeding Scheme. December 2008. ICBF Report.

- Base system of 100 progeny tested bulls with 100 daughters with a single record for a trait with heritability of 0.15 (i.e. heritability of the index) gives .18 genetic standard deviations of progress per year
- Best genomic selection schemes using both genomic preselection of young bulls while maintaining a large progeny testing scheme. This gave .31 genetic standard deviations of progress per year, a 70% increase but would be very costly.
- The overall preferred scheme involved using genomic selection to screen 500 young bulls down to 100 progeny tested, then early widespread release of young bulls following the first crop of calves. This gave .28 genetic standard deviations of progress per year, a 55% increase over 100 progeny tested bulls.

Lillehammer, Meuwissen and Sonneson 2010. A comparison of dairy cattle breeding designs that use genomic selection (Journal of Dairy Science – In Press).

- Simulation better than deterministic models because changes to the breeding scheme design influence the ability to train genomic predictions into the future.
- Simulation based on Norwegian Red design but with some approximations to make the simulation tractable.
- Dropping progeny testing and selecting young bulls increases genetic progress for a medium heritability trait but need to select a reasonable number of genomically proven bulls to avoid inbreeding problems.
- Genomic pre-selection prior to progeny testing also increases the rate of genetic progress or else results in the same amount of genetic progress and inbreeding with smaller numbers of progeny tested bulls.

Pryce Goddard Raadsma and Hayes 2010. Deterministic models of breeding scheme designs that incorporate genomic selection. (Journal of Dairy Science – In Press)

- Deterministic model which can push boundaries with a wide range of options but it does not consider that choice of design could influence the ability to train bulls in the future
- Genomic pre-selection prior to progeny testing increases the rate of genetic progress by about 17% or else results in the same amount of genetic progress and inbreeding with smaller numbers of progeny tested bulls (50 instead of 100 selected for progeny testing).
- They conclude that little benefit from genotyping dams of cows and cite Schaeffer and Konig with similar conclusions. However, this likely based on 50k chip prices. However genotyping of females for training is posed as the solution to the problem of designs that limit opportunities for training in the future via progeny tested bulls.
- Young bull genomic selection program increased progress by about 60%.
- Additional benefits from genomic selection with widespread use of young bulls when additional training data used from other countries (an extra 17% over young bull genomic selection structure).

- Nucleus schemes using genomic selection and juvenile embryo transfer yielded highest rates of progress (25% to 50% higher rates than young bull genomic selection program)

Appendix 2. Understanding the value of response

Consider a lift by 10 EBI units in the genetic merit of all heifer calves born in a year. For 1 million cows, 210,000 heifers turn in to replacements. These heifers have 4 lactations on average and their daughters express one half of their genes again having 4 lactations, grand-daughters express one quarter of the genes, and so eventually, the cows genes effectively get expressed by twice the amount that she expresses them herself. That results in about 8 lactations worth of expressions. However, because a lot of the benefits occur a long time in the future, they get penalised. The net effect of the discounting penalty (at a 7% discount rate) leads to about 5 expressions of the cow's genes.

The EBI was designed for bulls, and so the true response in cows in euro's per lactation is actually twice the value of the EBI. Thus, each heifer and her descendants will be superior by 20 euros of profit for each of the 5 effective lactations. This equates to 100 Euros per heifer, which when multiplied by 210,000 heifers is worth 21 Million Euros. The following year, the heifers born will benefit from two years of genetic progress, but there needs to be a penalty of 7% because the total benefits all occur one year later. Thus, from the second year, we get 21 Million x 2 x .93 = 39 Million Euros. If we keep this up for ten years with compounding genetic gains, we get 21 + 39 + 55 + 69 +80 +90 +98 +105 + 110 +114 = 781 Million Euros. If we divide this by ten years of genetic improvement, we get 78 Million per year average return from the ten years of investment in genetic progress, even though the annual benefit was only 21 Million Euros. This is because of the cumulative, permanent and compounding nature of genetic improvement.

Appendix 3

Scheme Structures

PT (Figure 1), GS short (Figure 2), and GS long (Figure 3) timeframes are presented below. These represent timelines from bull calf birth (in February 2011) until the bull has finished testing. PT bulls are assumed to be retained until widespread use (5.25 years). Widespread use in GS bulls occurs after 2.25 years; two scenarios are modelled including GS short in which bulls are retained until widespread use only, and GS long in which bulls are assumed to be retained until their daughters are evaluated (4.5 years). The reason for inclusion of GS long is so that over time a progeny test (by commercial means) occurs and therefore allows the top GS bulls to replace those bulls that make up the “daughter proven” bulls likely to be sought after by a proportion of the industry.

Figure 1: Timeline of events for PT breeding scheme (6 years until industry calves are born, bull finishes test at 5.25 years)

February 2011	bull calf born
↓ 14 months	
May 2012	mated (in test)
↓ 9 month	
February 2013	progeny born
↓ 24 months	
February 2015	daughters calve
↓ 6 months	
August 2014	daughters evaluated
↓ 10 months	
May 2016	widespread use

Figure 2: Timeline of events for GS short breeding scheme (3 years until industry calves are born, bull finishes test at 2.25 years)

February 2011	bull calf born
↓ 14 months	
May 2012	mated (in test)
↓ 9 month	
February 2013	progeny born
↓ 4 months	
May 2013	widespread use

Figure 3: Timeline of events for GS long breeding scheme (3 years until industry calves are born, bull finishes test at 4.5 years)

February 2011	bull calf born
↓ 14 months	
May 2012	mated (in test)
↓ 9 month	
February 2013	progeny born
↓ 4 months	
May 2013	widespread use
↓ 9 months	
February 2015	Daughters calves
↓ 6 months	
August 2015	Daughters evaluated

Cost components

Cost components for each scheme (PT and GS) are outline in Table 1 below.

Table 1: Cost components of breeding schemes (PT versus GS)

Item	Cost (PT)	Cost (GS)
Purchase price [1]	€ 1,000	€ 1,000
Health Testing	€ 100	€ 138
AI Code [1]	€ 280	€ 280
ICBF Progeny Test Fee	€ 1,500	€ 1,500
Feed, vet, med, housing (per month) [2]	€ 83.3	€ 83.0
Fixed overheads (per month) [2]	€ 104.5	€ 104.5
Semen for progeny test (1000 straws * €2)	€ 2,000	€ 2,000

[1] Cost assumed to be incurred by the AI Company

[2] Cost assumed to be incurred by the AI Company after daughters evaluated (PT) and after widespread use (GS schemes)

Note that testing of bull candidates for genomic selection is excluded from here, as this is costed against the various schemes independently of the number of bulls actually retained.

Health testing is incorporated at €100 for PT and €138 euro for GS. PT costs were reported by ICBF, while GS health testing costs were based on costs associated with health testing bulls for Tully.

Total costs to keep a bull (feed, veterinary, and housing) in a disease free environment from 3 weeks-of-age to 14 month-of-age are assumed to be €1000 plus fixed overheads of €1463. This is assumed to be equivalent between PT and GS schemes. Ongoing yearly costs are assumed to be €1000 per bull. This calculation assumes 8 kg meal per day at €0.275 per kilogram, and ~€200 per year for labour, veterinary costs (including medicine), and housing. Fixed overheads are included at €105/ month (€1463/ 14), post 14 months-of-age.

Semen collection for testing was assumed to be at a cost of €2000 (1000 straws at €2 per straw) in both PT and GS schemes. Costs associated with collection for widespread use are assumed to be equivalent between PT and GS schemes, and are accounted for in per straw retail prices.

Cost divisions between AI Companies and industry (as per Table 1) results in €3740, €1280, and €5731 of the total costs per bull potentially being incurred by AI Companies in PT, GS short, and GS long, respectively.

Finally, survival is incorporated at each stage of the scheme to discount the likelihood of incurring the relevant costs.

Scheme costs

Tables 3, 4, and 5 outline the costs per bull for PT and GS short and long breeding schemes, respectively.

Table 3: Costs per bull for PT scheme (to 5.25 years)

		Progeny test			
Event description	Date	Time period	Cost	Probablilty of surviving to event	Effective costs
Bull calf born	February 2011				
		14 months	€ 7,509.20	1	€ 7,509.20
Mated (in test)	May 2012				
		9 month	€ 1,690.20	0.98	€ 1,656.40
Progeny born	February 2013				
		24 months	€ 4,507.20	0.9	€ 4,056.48
Daughters calve	February 2015				
		6 months	€ 1,126.80	0.85	€ 957.78
Daughters evaluated	August 2015				
		10 months	€ 1,878.00	0.8	€ 1,502.40
Widespread use	May 2016				
Total			€ 16,711.40		€ 15,682.26

Table 4: Costs per bull for GS short scheme (to 2.25 years)

Genomic selection - short					
Event description	Date	Time period	Cost	Probablilty of surviving to event	Effective costs
Bull calf born	February 2011				
		14 months	€ 7,543.00	1	€ 7,543.00
Mated (in test)	May 2012				
		9 month	€ 1,690.20	0.98	€ 1,656.40
Progeny born	February 2013				
		4 months	€ 751.20	0.97	€ 728.66
Widespread use	May 2013				
Total			€ 9,984.40		€ 9,928.06

Table 5: Costs per bull for GS long scheme (to 4.5 years)

Genomic selection - long					
Event description	Date	Time period	Cost	Probablilty of surviving to event	Effective costs
Bull calf born	February 2011				
		14 months	€ 7,543.00	1	€ 7,543.00
Mated (in test)	May 2012				
		9 month	€ 1,690.20	0.98	€ 1,656.40
Progeny born	February 2013				
		4 months	€ 751.20	0.97	€ 728.66
Widespread use	May 2013				
		21 months	€ 3,943.80	0.9	€ 3,549.42
Daughters calve	February 2015				
		6 months	€ 1,126.80	0.8	€ 901.44
Daughters evaluated	August 2015				
Total			€ 15,055.00		€ 14,378.92