

Optimal system of contract matings for use in a commercial dairy population

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Managing the contribution of prominent animals to the pedigree of livestock populations is a topic of increasing importance worldwide. The aim of this study was to evaluate methods of controlling the accumulation of inbreeding in the Irish Holstein-Friesian population through the methodology used to arrange contract matings. Two non-random mating systems were investigated, linear programming (LP) and sequential programming (SEQ); these were compared with random mating (RAN) and mating of the best sires to the best dams (TOP). All mating systems were compared across a range of objectives: to maximise genetic merit for the economic breeding index (EBI) used in Ireland, to minimise population coancestry with breeding females (R-value), and a dual objective of simultaneously maximising EBI and minimising coancestry with breeding females. Algorithms were developed to identify elite dams and sires from the national herd for use in the contract mating programme. One thousand contract matings were generated using each selection method, with the aim of producing 83 test sires (the number of bulls which it is feasible to test annually in Ireland) for use in a progeny testing scheme. The top 1,000 matings, as selected by the LP and SEQ methods, performed similarly when maximising the dual objective (average progeny EBI of €145 and an average coancestry of the progeny to the population of breeding females of 0.93%). The TOP and RAN methods both selected phantom progeny with higher coancestry with the breeding female population (1.21% and 1.34%, respectively) than the LP and SEQ methods. However the matings from the TOP method generated progeny of higher genetic merit (EBI = €199), whilst the progeny generated from the RAN method had lower genetic merit (EBI = €127) than those selected by the LP or SEQ methods.

Keywords: coancestry; contract matings; Holstein-Friesians; inbreeding

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Introduction

The potential for the rate of inbreeding to get out of control in domestic populations due to improved technology (AI) and computational advances (BLUP) (Wray and Goddard, 1994), together with the inbreeding depression exhibited in some species (Pariacote, Van Vleck and MacNeil, 1998; Smith, Cassell and Pearson, 1998; Norberg and Sørensen, 2007) has led to interest in developing methods to control inbreeding within breeding programmes (Meuwissen, 1997; Lopez-Villalobos, Harris and Price, 2004; Haile-Mariam, Bowman and Goddard, 2007). Strategies have been designed to control inbreeding either in the short term (Weigel and Lin, 2000) or the long term (Lopez-Villalobos *et al.*, 2004). In the short term, on-farm computerised mating schemes are useful to help breeders avoid lines already in the pedigree of the herd. Alternatively, the cost of inbreeding depression can be offset against potential genetic gain from sires highly related to the breeding population in genetic evaluations. However farmers can only use the germplasm which is available to them, which, if using AI, is dictated by the AI companies. Therefore farmers have little influence over the change in inbreeding in the population as a whole. Long term control will rely on minimising the genetic relationships both among the population of young test bulls (Weigel and Lin, 2002) and between the population of young test bulls and the future breeding female population.

In Ireland, genetic merit of dairy animals is measured using an economic breeding index (EBI), which is the sum of five sub-indices; milk production, fertility, calving performance, health and beef production (Berry *et al.*, 2007). To date, no systematic approach has been taken in selecting young test bulls for progeny testing and subsequent widespread

use in the national population. Although this approach has been sufficient to date, selection on genetic merit alone may limit the potential for genetic gain in future generations. Selection decisions made now will influence future relatedness within the Irish Holstein-Friesian population and an accumulation of inbreeding in the population may reduce the genetic variation in the Irish Holstein-Friesian population resulting in reduced long-term response to selection (Wray and Goddard, 1994). The level of inbreeding in the Irish Holstein-Friesian population has been increasing at a rate of 0.10% per year over the past decade (Mc Parland *et al.*, 2007a). Thus modifying the current dairy breeding programme to reduce the accumulation of relatedness within the population is of increasing importance.

The selection of mating pairs, or contract mating, is defined as the simultaneous selection and mating of males and females according to predicted progeny merit (Jansen and Wilton, 1985) and is a commonly discussed method to slow down the accumulation of relatedness within populations. Alternative solutions include ignoring relatives' records when estimating BLUP values (Brisbane and Gibson, 1995), imposing restrictions on the number of siblings selected from any particular family (Brisbane and Gibson, 1995) and altering family information in evaluations (Villanueva, Woolliams and Simm, 1994).

Contract mating has been demonstrated to be effective in dairy cattle breeding populations (Sørensen *et al.*, 2006). In addition, the introduction of multiple goals into the breeding programme to simultaneously reduce relatedness and increase genetic merit in a population has also proved successful (Tozer and Stokes, 2002; Lopez-Villalobos *et al.*, 2004).

The objective of this study was to evaluate various contract mating options for

implementation in the Irish national breeding programme. Two alternative contract mating methods were compared for their effectiveness at simultaneously increasing genetic gain and reducing the accumulation of relatedness within the Irish population of Holstein-Friesians. Although the principles of such contract mating methods are applicable to any livestock species (excluding populations under genetic conservation), the data edits used in the present study to identify the candidate parents are specific to the Irish, seasonally-calving Holstein-Friesian population.

Materials and Methods

Pedigree information on 3,581,380 Holstein-Friesian animals was extracted from the Irish Cattle Breeding Federation database together with all available production and performance records. Holstein-Friesians were defined as any animal which had Holstein and Friesian as its main breed fractions and where the sum of the Holstein and Friesian proportion was at least 50%

Selection of candidate parents

Using current Irish cattle population statistics, the maximum feasible number of young test bulls that could be progeny tested was determined and the number of candidate parents required to generate these young test bulls was calculated. Consideration was given to potential bulls lost from the system because of sex ratio (52%; Berry and Cromie, 2007), perinatal mortality (4%; Mee, Berry and Cromie, 2008), pre-weaning mortality (2%; Berry *et al.*, 2006), bull infertility (7%) and loss of daughters to unrecorded herds (3%). The remainder of this study involved selection of the most appropriate parents of these animals and the evaluation of various algorithms for generating the contract matings. The candidate parents

were selected from the national database following stringent assessment of pedigree and performance.

Sires The top 500 AI bulls, ranked on EBI, with semen available in Ireland were considered as potential candidate sires. A consultation group was formed that comprised representatives from the Irish Cattle Breeding Federation (who operate the national breeding programme), breeding company representatives, sire analysts and geneticists. This group decided that the candidate sires should be predominantly Holstein-Friesian with at least three full generations of pedigree known. To be considered as eligible, candidate sires were required to have a standardised predicted transmitting ability (PTA) of at least -2 for both the mammary composite and feet and legs composite. The mammary and feet and legs composite traits are subjective scores encompassing all mammary and feet and legs traits respectively. In addition, candidate sires were required to have a PTA for calving interval of less than 2 days and a PTA for survival of greater than -1% . A total of 61 candidate sires were selected for the contract matings. Furthermore, it was decided by the consultation group that the contract matings generated should be involve a maximum of 30 different bulls.

Dams Candidate dams were defined as being both genetically and phenotypically superior to the population average. Although phenotypic performance is largely affected by several environmental factors (including management), cognisance must be taken of phenotypic performance to ensure acceptance by farmers and breeding companies. To ensure phenotypically sound cows were selected, only milk recorded animals were considered and minimum and maximum threshold values were set for the economically

important traits, following discussion with the consultation group. Cow performance had to be within the thresholds set for all traits.

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 $\geq 4,000$ kg with a protein concentration ≥ 33 g/kg. This threshold was imposed to identify cows with proven performance for production above the population mean. Cows were required to have an average calving interval of ≤ 400 days and no calving interval between parity 1 and parity 5 could exceed 500 days. This threshold was imposed to ensure only cows with consistently good fertility were selected for entry to the contract mating programme. In addition cows must have calved for the first time between 22 and 38 months of age, be no greater than ninth lactation and have calved in the 12 months prior to data extraction. 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. This restriction removed any cows with known poor conformation from the data set.

Restrictions were placed on cow pedigree information and only cows of $\geq 78\%$ Holstein-Friesian ancestry with at least two complete generations of pedigree known were considered. In the pedigree of Irish Holstein-Friesian cows as well as the young test bulls currently in layoff, three sires, Galtee Merci, Newhouse Sjoerd and Collins Royal Hugo are particularly prominent. The daughters and grand-daughters of these sires were removed and, as no candidate sire had these bulls in its pedigree either, it ensured that any young test bulls produced from the programme would be unrelated to these three prominent bulls. Restrictions were also

placed on cow genetic merit. 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 ≥ -2.5 kg. Finally, all cows were required to have positive milk and fertility sub-index values (Berry *et al.*, 2007) and have an EBI of $\geq \text{€}90$. Following these edits, of the 408,375 living milk-recorded Holstein-Friesian cows in Ireland, 8,748 remained. Restrictions on pedigree information and on the most recent calving date were the main reasons why potential candidates were removed from the list.

A customised economic index, hereafter known as the customised index (CUI) was derived for each cow, using the economic weights for the 2008 EBI for milk production (but at a lower milk price of 28 c/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 in the multi-trait analysis was set to zero. This was done because estimated breeding value for calving interval is influenced by milk yield due to the higher heritability of milk yield and its antagonistic genetic correlation with calving interval. Yet, the objective of this study was to identify fertile, high-producing 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.

Contract mating

Every possible mating combination between the candidate sires ($n = 61$) and dams ($n = 3,000$) was undertaken to generate 183,000 “phantom” progeny. For each phantom calf, its inbreeding coefficient (F), and average coancestry with the breeding female population (R -value) were computed (Meuwissen and Luo, 1992). Breeding females were defined as all Holstein-Friesian females with at least two complete generations of pedigree, and 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 as the average of its parents’ EBI in 2008; 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 to eliminate any phantom progeny which were unbalanced in terms of milk and fertility.

The minimum and maximum number of matings per candidate sire was decided upon by the consultation group. The thresholds were based on the representation of germplines in the population, presence in the pedigree of young test bulls 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 was applied only to the random method.

Methods tested

Linear programming (LP) optimises a linear objective function subject to linear equality and inequality constraints and has been proposed as a tool to select breeding stock for production (Jansen and Wilton, 1984). The LP approach was implemented in the present study using Proc LP (SAS Institute Inc., Cary, NC).

The sequential programming method (SEQ), as defined in the present study, selects the best matings in terms of a pre-defined objective, subject to linear equality and inequality constraints. Matings were ordered sequentially in terms of the objective to be achieved. From this list, the top mating was selected and all further potential matings of the selected dam were removed. Sires were removed from the selection list when they had reached their maximum number of matings allowed. This procedure was terminated when 1,000 phantom progeny were selected.

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 the resulting 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 dams and sires used. Therefore the RAN method of selection was used only as a control for the purpose of the study.

The TOP method selects the top matings according to a pre-defined objective with no constraints. As the concept of operating a breeding programme without constraints is impracticable, this method was used as a control for the purpose of the study.

The EBI and R -values of the phantom progeny were standardised to 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 case, 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.

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.

Results and Discussion

This study involved comparing two systems of contract mating (LP and SEQ) with two controls (RAN and TOP). 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 population of breeding Holstein-Friesian females. Due to the editing criteria used, the results are specific to the Irish seasonally calving Holstein-Friesian population only.

Number of contract matings

Assuming a progeny daughter group size of 100, it is feasible to test only 83 young bulls annually in Ireland. This is partly

due to the low level of milk recording in Irish herds. Of the 1,087,900 dairy cows in Ireland, only 41% are milk recorded annually (ICBF, 2008). Other factors include the low level of AI usage, particularly for young test bulls (5%), sex ratio, perinatal mortality, pre-weaning mortality, infertility within 2 years and loss to unrecorded herds.

To reduce any unnecessary computational load, the minimum number of contract matings which would be required to obtain 100 bull calves was determined. Seven hundred contract matings were required to get 100 young test bulls taking into account the sex ratio, perinatal mortality and pre-weaning mortality, along with the failure of herds to meet the required health status (20%), pregnancy rate to first and second service (65%), and unwillingness of a breeder to sell (20%) or to become involved in the scheme (30%).

Other factors which may influence the number contract matings required include the number of animals available for selection and resources to purchase and manage the subsequent young test bulls (Wray and Goddard, 1994). Because of other potential losses as well as potential growth in the market for young test bulls, it was decided that 1,000 contract matings should be generated.

Genetic merit of candidate sires

A summary of the performance of the 61 candidate sires chosen is provided in Table 1. The EBI and sub-index performance of the candidate sires was superior to the national average (ICBF, 2008) and age ranged from 6 to 16 years. There was no relationship between age and R-value ($r = -0.06$) nor was there a relationship between age and EBI ($r = -0.03$). This was contrary to expectation since younger animals are expected to be genetically superior due to on-going genetic gain. It

Table 1. Summary of the performance of the 61 bulls selected as potential bull sires

Trait	Mean	s.d.	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 ¹ for milk yield (kg)	211.3	165.3	-177.0	599.2
PTA for fat yield (kg)	9.7	6.1	-5.0	22.5
PTA for protein yield (kg)	9.3	4.0	-1.5	20.3
PTA for fat concentration (g/kg)	0.3	1.5	-2.7	4.2
PTA for protein concentration (g/kg)	0.4	0.6	-1.1	2.0
PTA for calving interval (days)	-3.1	1.5	-6.3	0.3
PTA for survival	2.4	1.2	0.0	6.3
PTA for calving difficulty (score)	2.8	1.3	0.8	7.4
PTA for gestation length (days)	-1.4	0.9	-3.7	0.7
PTA for carcass weight (kg)	-1.8	5.3	-17.2	10.4
PTA for somatic cell count	0.0	0.1	-0.2	0.2
Overall type score ²	-0.4	1.5	-2.9	4.0
Overall feet and legs ²	0.3	1.0	-1.6	3.1
Overall mammary ²	-0.1	1.5	-2.9	3.5

¹ PTA = predicted transmitting ability.

² Normalised value.

was also expected that the younger sires would have a greater relationship with the breeding females due to the increase in inbreeding in the Irish Holstein-Friesian population recorded over the past decade (Mc Parland *et al.*, 2007a).

Performance of candidate dams

Table 2 describes the genetic merit of the top 3,000 candidate dams as ranked by CUI 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 and their phenotypic performance is summarised in Table 3. It is evident that the process used to identify genetically excellent cows with satisfactory proven performance for milk, fertility and conformation was successful. However a considerable

number 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.

Relative weighting on genetic merit and coancestry

The optimal rate of inbreeding is not clearly defined for any population. This creates difficulties when weighting the cost of coancestry in breeding programmes. It has been suggested that any restriction on the rate of inbreeding should be relative to the cost of reduced performance associated with inbreeding depression, or if inbreeding depression is not a major concern, to base the rate on maintenance of genetic variation (Wray and Goddard, 1994). Inbreeding depression is currently of limited economic concern in Ireland

Table 2. Genetic merit of the 3,000 cows selected as potential bull dams

Trait	Mean	s.d.	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 ¹ for milk yield (kg)	130.2	147.2	-337.0	661.0
PTA for fat yield (kg)	8.9	5.3	-2.5	29.0
PTA for protein yield (kg)	8.5	4.5	-2.5	22.5
PTA for fat concentration (g/kg)	0.8	1.1	-2.7	4.9
PTA for protein concentration (g/kg)	0.8	0.5	-0.6	3.0
PTA for calving interval (days)	-2.9	1.5	-8.3	2.3
PTA for survival	1.3	0.6	-0.5	3.8
Weighting on parents data (%)	46.7	12.7	16.0	65.0

¹ PTA = predicted transmitting ability.

Table 3. Summary of phenotypic values for fertility, milk production traits and conformation for the 3,000 cows selected as potential bull dams

Trait	N	Mean	s.d.	Minimum	Maximum
Age at first calving	3000	25.7	3.4	22	38
Calving interval (days)					
Parity 1	3000	363	26	300	499
Parity 2	2189	366	27	300	490
Parity 3	1342	367	27	301	488
Parity 4	732	372	32	306	498
Parity 5	365	371	31	308	490
Milk yield (kg)					
Parity 1	2830	5909	933	4009	10637
Parity 2	2999	6840	1047	4006	11595
Parity 3	2142	7299	1097	4070	11811
Parity 4	1309	7523	1109	4060	12215
Parity 5	701	7637	1066	4573	11292
Milk fat concentration (g/kg)					
Parity 1	2830	40.9	4.3	21.8	60.6
Parity 2	2999	40.2	4.6	22.1	58.6
Parity 3	2142	40.3	4.6	23.9	60.5
Parity 4	1309	40.3	4.7	25.3	55.4
Parity 5	701	40.3	4.5	26.2	53.7
Milk protein concentration (g/kg)					
Parity 1	2830	35.6	1.6	33.0	42.8
Parity 2	2999	36.2	1.7	33.0	47.4
Parity 3	2142	36.2	1.7	33.0	49.9
Parity 4	1309	36.2	1.6	33.0	43.3
Parity 5	701	36.1	1.6	33.0	41.8
Overall type score ¹	218	78	3	65	85
Overall feet and legs ¹	218	78	4	70	88
Overall mammary ¹	218	78	4	70	87

¹ Scale 1 to 100.

(McParland *et al.*, 2007b). Therefore our main interest was to preserve genetic variation by keeping a low average relationship within the population.

The effects on the average EBI and R-value of the progeny selected by the SEQ method when the weighting on EBI was changed relative to a constant R-value are illustrated in Figure 1. Similar results were obtained for the matings selected by the LP method. As the weighting on EBI increased, average EBI of the selected phantom progeny increased although a concomitant increase in the average R-value between the selected progeny group and the population of breeding females was also observed (Figure 1). The weighting used in this study in the dual objective of maximising genetic merit under the constraint of future inbreeding was to place twice as much weighting on maximising EBI as on minimising R-value. This weighting was selected

subjectively through comparisons of the loss in genetic gain against increases in R-value. As the ratio of weighting on EBI: R-value increased above +2: -1, little gain in EBI was expected; the mean EBI achievable with a weighting of +10: -1 (EBI: R-value) was €148.63 compared to €145.21 with a weighting of +2: -1. However above a weighting of +2: -1, the average R-value continued to rise steadily, increasing from 0.93% at a weighting of +2: -1 to 1.29% at the weighting of +10: -1. There was a 2.4% increase in EBI relative to a 38.7% increase in R-value when the weighting on EBI increased from +2: -1 to +10: -1.

Comparison of methods

Computing time was low for both of the non-random mating options. Time taken to undertake all procedures, once the data had been appropriately set up was 0.49 and 7.66 minutes for the LP and SEQ

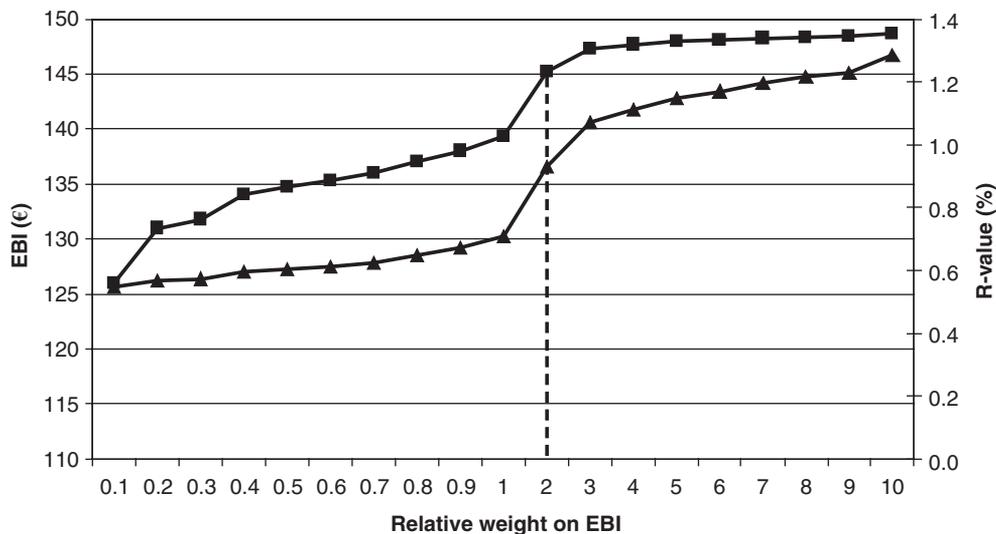


Figure 1. Effect of increased EBI (average economic breeding index) weighting, relative to a weighting on the R-value of -1, on the EBI (-■-) and R-values (-▲-) of 1,000 progeny selected by the sequential programming method (dashed line represents the weighting on EBI used in the dual objective).

procedures on a 64-bit quad core, 1.86 GHz processor with 8 Gb of RAM.

For each of the four selection methods examined, the three 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 4. Average EBI, R-value and inbreeding coefficient of the groups selected by both LP and SEQ were similar across all objectives. LP, SEQ and TOP matings all performed better than RAN in achieving the set objectives. In a study comparing the effect of non-random mating strategies to a random mating design, DeStefano and Hoeschele (1992) found only small differences in progeny merit when non-random mating designs were employed.

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. Lopez-Villalobos *et al.* (2004) investigated the use of goal programming to achieve objectives similar to the objectives in this study: to maximise breeding worth (BW; the breeding objective in New Zealand), to minimise population

inbreeding, and random mating. Results from the present study corroborate those of Lopez-Villalobos *et al.* (2004) in that the random mating method resulted in intermediate BW and inbreeding when compared to the greater BW and greater inbreeding arising from selecting on an objective that maximised BW, and the lower BW and lower inbreeding arising from selection on an objective that minimised inbreeding. This demonstrates the conflict between the alternative objectives and highlights the need to combine these individual objectives into a multiple or dual selection objective.

When maximising EBI, the TOP method selected a phantom progeny group with a higher average EBI than either the LP or SEQ methods. Yet the average R-values for the groups selected by the three methods were similar (Table 4). Thus TOP appears to be the best method to maximise EBI. However, TOP did not constrain the maximum number of progeny per sire. The high EBI of the phantom progeny achieved when maximising EBI arose from using only two high EBI sires, which were moderately related to the population. This extreme selection inten-

Table 4. Average EBI, R-value (coancestry with population of breeding females) and inbreeding coefficient (F) of phantom progeny from the 1,000 contract matings selected by linear programming (LP), sequential programming (SEQ), the top ranked (TOP) method and by random selection (RAN)

Objective	Variable	Contract mating system			
		LP	SEQ	TOP	RAN
Maximise EBI	EBI (€)	149	149	200	127
	R-value (%)	1.39	1.36	1.39	1.34
	F (%)	1.19	1.14	1.44	1.48
Minimise R-value	EBI (€)	125	125	116	127
	R-value (%)	0.55	0.55	0.22	1.34
	F (%)	0.40	0.47	0.68	1.48
Maximise dual objective	EBI (€)	145	145	199	127
	R-value (%)	0.93	0.93	1.21	1.34
	F (%)	0.69	0.71	0.98	1.48

sity is unrealistic as such heavy use of two sire lines would be detrimental to future genetic diversity, although the impact on the next generation would be small as suggested by the low R-values. In contrast, all 61 sires were represented as sires of sires with the RAN method, while between 20 and 22 sires were represented with the LP and SEQ methods.

The coancestry among the phantom progeny selected using the LP, SEQ and TOP methods was 1.93% (s.d. 0.45%), 1.93% (s.d. 0.47%) and 13.24% (s.d. 1.06%), respectively. The high coancestry among the phantom progeny selected by TOP indicates that the phantom progeny as selected by TOP are genetically similar and highlights the unsuitability of this selection method.

Although mean EBI and R-values of the phantom progeny were similar for the LP and SEQ methods when maximising the dual objective, their distributions differed (Table 5). SEQ selected more phantom progeny from the highest class of EBI values (>€210) than the LP method, however the SEQ method also selected more

phantom progeny than the LP method from the lowest EBI class (<€120). Thus although the average EBI of the selected phantom progeny from the LP and SEQ methods were similar, the LP method sacrificed mating the highest EBI sires to the highest EBI dams and instead selected an increased number of the moderate EBI phantom progeny (between €120 and €210) resulting in a tighter distribution (or a more homogenous group of animals). In contrast, to achieve the same average EBI, the SEQ method selected the highest EBI progeny by mating the highest EBI sires to the highest EBI cows but due to restrictions imposed, the SEQ method had then to mate lower EBI sires to lower EBI cows. The distributions for the R-values were similar for the two groups (Table 5).

The LP method is favoured for use as a method of contract mating in the Irish Holstein-Friesian population due to the lower potential risk associated with this method. Of the 1,000 contract matings generated, only 83 phantom progeny are required for progeny testing. The risk associated with the more intensely selected SEQ phantom progeny, is that those phantom progeny in the highest EBI class may not be in the final 83 phantom progeny which become available as young test bulls. This will result in a lowering of the average EBI of the group. In contrast, the LP method selected a more homogenous group of phantom progeny.

When the objective was to maximise EBI using the LP method, the average R-value for the group selected was 1.39% (Table 4), which is lower than the level of inbreeding (1.5%) in Irish Holstein-Friesian females in 2004 (Mc Parland *et al.*, 2007a). 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,

Table 5. Percent of matings in EBI and R-value classes for the 1000 contract matings selected by the LP, SEQ and TOP methods

	Contract mating system ¹		
	LP	SEQ	TOP
EBI (€)			
<120	0.5	2.8	0.0
120–150	69.4	68.3	0.0
150–180	24.6	22.4	0.1
180–210	5.3	2.3	91.2
>210	0.2	4.2	8.7
R-value (%)			
<0.5	11.5	11.1	0.1
0.5–1.0	43.5	42.5	29.1
1.0–1.5	36.4	38.7	49.9
1.5–2.0	8.5	7.5	20.9
>2.0	0.1	0.2	0.0

¹ See Table 4.

through the incorporation of minimising R-values in the population into the breeding programme. This agrees with Weigel and Lin (2002) who concluded that the average genetic merit of a selected group will always be higher if inbreeding is ignored.

Performance of phantom progeny

The predicted progeny performance as well as the performance of the dams and sires of the progeny selected by LP when the aim of the method was to achieve the dual objective is summarised in Table 6. Comparisons between Table 1 and Table 6, and Table 2 and Table 6 demonstrate that the 21 sires and 1,000 dams selected by LP are above the average of the initial full list of candidate sires and candidate dams for EBI, as well as for milk and fertility genetic merit. The average EBI of the dams selected was €135, which is higher than the average EBI of the group of 3,000 dams (€119) and is also higher than the EBI of the dams of young bulls tested in 2008 (€119).

Mean EBI for the phantom progeny (€145) is higher than the average EBI of bulls on the active bull list (€131) in the Irish breeding programme (www.icbf.com). The average R-value between the phantom progeny and the breeding female population was 0.93%, which is lower than the current level of inbreeding in the population (Mc Parland *et al.*, 2007a). This indicates that using these bulls on the population should aid in reducing mean population inbreeding level. In addition, mean inbreeding for selected sires of sires, dams of sires and progeny were also below the population average (Mc Parland *et al.*, 2007a).

Conclusions

The option of contract mating to simultaneously maximise genetic merit and reduce coancestry within the population of Irish Holstein-Friesians, through the use of linear programming, is a practical method of selecting potential young test bulls. The theory of contract matings will

Table 6. Predicted performance statistics for phantom progeny and their parents as selected by the linear programming method¹

Trait		Mean	s.d.	Min	Max
EBI (€)	Progeny	145	17	115	217
	Sire	156	31	123	262
	Dam	135	15	106	195
Milk sub-index (€)	Progeny	60	16	28	111
	Sire	64	21	39	114
	Dam	57	27	1	142
Fertility sub-index (€)	Progeny	70	14	31	120
	Sire	77	21	35	131
	Dam	63	20	0	125
Inbreeding (%)	Progeny	0.69	0.70	0.00	3.11
	Sire	0.86	1.11	0.00	4.15
	Dam	0.95	1.90	0.00	26.66
R-value (%)	Progeny	0.93	0.37	0.23	2.07
	Sire	0.92	0.49	0.29	1.87
	Dam	0.94	0.57	0.07	2.37
Average matings per sire ²	-	48	24	20	100

¹ Relative weightings used in objective +2 for EBI to -1 for R-value.

² Average number of matings assigned to bulls using the LP method.

work for a small commercial population as exists in Ireland, but only with the support of all AI companies and breeding organisations involved in the national breeding structure. The programme will however be put under threat by competing AI companies that consider only short-term genetic gain thereby appearing to offer better bulls to their customers. This approach is also very much applicable with recent technological advances in animal breeding such as genomic selection.

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