

# MATING PLANS FOR SELECTION ACROSS BREEDS

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## SUMMARY

This paper presents an approach to the design of breeding programs in which no design is purposefully aimed at. The design emerges as a consequence of a policy implemented at the level of the breeding pair or mating group. The method proposed accounts for both genetic and cost factors in a single index, and uses an algorithm which optimises the mating structure. The method is discussed with particular reference to crossbreeding systems. Stochastic simulation is used to demonstrate the emergence of various designs according to prevailing genetic and cost parameters.

## INTRODUCTION

The design of breeding programs is a highly complex subject. In addition to defining breeding objectives, many genetic, cost and logistical factors must be taken into account. The most common approach is to fit these factors into one of a number of theoretical frameworks, resulting in a set of rules to be followed. This set of rules gives rise to a pattern which is the design of the breeding program. In many cases, no single body of theory is sufficient, and some trial and error is involved in developing a preferred design.

This paper presents a different approach, where the the program design is not purposefully aimed at, but emerges as a consequence of a breeding policy implemented at the level of the breeding pair or mating group. The method proposed will be discussed with reference to programs involving crossbreeding, but the approach can be developed for use in other types of program. It is simply driven by the aim of maximising the genetic merit of the next generation, after accounting for the costs of running the program. It involves two central features:

- 1) The Multibreed Selection Index (Kinghorn, 1982). This index is similar in concept to the additive index described by James (1966), which provides a means of suitably weighting breed means and within-breed deviations. However, the multibreed selection index also exploits non-additive heterotic effects. Kinghorn (1984) incorporated cost factors, such as purchase price and transport costs, into this index.

- 2) An algorithm to set up mating pairs or groups in a manner which optimises the expected genetic merit of offspring while taking proper account of operating costs.

This paper describes the algorithm referred to in 2) above, and illustrates the emergence of various designs from simulated breeding programs.

#### A MATING ALGORITHM

Where only additive effects are of importance, the pattern of allocation of mates is not expected to affect the average merit of the next generation. However, where non-additive genetic effects (such as direct heterosis) and/or interactions in cost factors (mating neighbours is cheaper than mating geographically separated individuals) are important, the pattern of mating can be critical.

The algorithm proposed can be described conceptually, with reference to figure 1. Candidates of each sex are grouped according to breed, and any other factor involving non-additivity. This description considers direct heterosis to be the only non-additive factor involved. [Note that maternal heterosis is additive in this context as its expression does not depend on mate genotype]. Animals are ranked within genotype groups on an index of all additive factors. As is common practice with indices, this index describes twice the expected contribution to progeny. It includes three components:

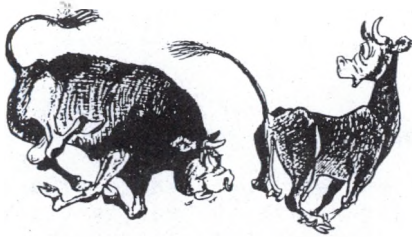
- 1) Breed Genetic Value (BGV) corrected for direct heterosis, or Average Breed Value (Kinghorn, 1983)
- 2) Twice the Breed Maternal Value, (BMV, Kinghorn 1984), for female candidates only. Doubling is necessary here as the full maternal effect is expressed in progeny.
- 3) The within-breed estimate of breeding value.

Highest ranking animals are set adjacent to the matrix of non-additive values, as in figure 1. This matrix contains the non-additive components of merit expected to be expressed in progeny of each combination of male and female groups. In this case the matrix contains direct heterosis values.

For each potential mating among highest ranking animals, the expected progeny value (after penalising for cost factors) is the average of the additive indices of the members of the pair, plus the non-additive component relating to the two groups involved. This criterion is used to select the first mating pair. In this case the value expected is  $(382.2 + 426.6)/2 + 25.0 = 429.4$  Kg.

If single pair mating is required, the two animals selected are removed from their groups, and the next-highest ranking animals are candidates for selection of the next pair, and so on.

However, where a number of females are to be mated by each male, only the selected female is removed. The next pair selection is based on the same criterion, but choice is restricted to the row to which the selected male belongs. In this way the selected male has a second mate allocated to him. This procedure continues until his mating group is complete, and then he is removed along with his last mate.



				FEMALE QUEUES		
				BREED 1	BREED 2	F1 (1X2)
				344.6	370.2	398.2
				348.5	376.4	401.1
				353.9	377.0	407.6
				361.0	384.0	412.5
				365.5	388.1	416.2
				369.1	388.6	419.4
				372.2	391.2	426.6
BREED 1				349.3	355.0	362.7
BREED 2				359.0	370.0	379.8
BREED 3				363.4	375.0	382.2
F1 (1X2)				355.3	362.5	378.2
F1 (1X3)				358.7	365.0	381.0
				0.0	25.0	12.5
				25.0	0.0	12.5
				25.0	25.0	25.0
				12.5	12.5	12.5
				12.5	25.0	18.75

**Figure 1.** A conceptual description of the method proposed for setting up mating groups. This description is based on the genetic parameters used in simulation 5, which relates to breeding for yearling weight in beef cattle (see Table 1). One queue is set up for each breed genotype within each sex, three male candidates or seven female candidates are shown in each queue. The additive value for each candidate is entered in the queues. For males this is the Breed Genetic Value corrected for heterosis expressed, plus the within-breed estimate of breeding value. For females this is the same plus twice the Breed Maternal Value. Cost factors can also be included, but these have been ignored here. The middle ranking candidate in each queue has its estimate of breeding value set to zero, for illustration alone. The bottom right corner of the figure contains the 3 x 5 matrix of direct heterosis values (Kg) expected to be expressed in the 15 breed genotypes possible in the next generation.

When this procedure has been completed, mating pairs will have been constructed in an assortitative manner with respect to additive effects. If this is not desired, mate allocation can be randomised in a manner which retains the numbers of matings in each group x group cell. This maintains the favourable expression of non-additive effects expected in the progeny.

A simulation study showed that where there is only one animal per group, this algorithm is about 90 percent efficient for up to eight groups. The loss in efficiency arises from losing later options to exploit non-additive superiority when groups are eliminated by early selections. Large simulations of this type are not possible due to the number of permutations of mate allocation involved. However, in animal breeding programs many candidates per group usually exist, or if males are rare, they are usually fecund. Under these circumstances it seems reasonable to predict that the algorithm proposed is close to optimal.

This algorithm exploits non-additive effects, such as heterosis. It should not be confused with reciprocal recurrent selection, where purebreds are selected on the expression of heterosis in their crossbred progeny.

## SIMULATION OF BREEDING PROGRAMS

Several stochastic simulations will be used to illustrate how use of a multibreed selection index with the mating algorithm proposed can set up a range of breeding program designs. To aid in conception, they will relate to beef cattle, with yearling weight as the trait of interest. However, these simulations are based on a very simple model, with perfect balance, discrete generations and no fixed environmental effects. It is emphasised that results are only of value in illustrating properties of the method, and results relating to specific scenarios should be interpreted with caution. All simulations will be based on the same population model, which will be described now.

### Population Structure

The "home" population is the population or farmed unit of interest. The objective is to maximise the profitability of this enterprise. Industry-wide objectives are not involved here, but will be discussed later.

The home population is initially of breed 1 alone. However, ten populations exist from which a given number of male and female candidates are available for selection, at a given purchase price. These "foreign" populations are of breed 1, 2, 3, 4 and the six first cross combinations 1x2, 1x3, 1x4, 2x3, 2x4 and 3x4.

### Population parameters

The following set of parameters acts as a 'mask' for the simulations to be presented:

Number of bulls used at home per generation . . . . .	40
Number of cows per bull at home . . . . .	25
Number of progeny per cow per generation . . . . .	4
Male candidates per foreign breed . . . . .	50
Female candidates per foreign breed . . . . .	1000
Import cost per bull . . . . .	0
Import cost per cow . . . . .	0
BGV's (Kg), Breeds 1 to 4 . . . . .	355, 370, 375, 357
BMV's (Kg), Breeds 1 to 4 . . . . .	+3, +7, -4, -6
Direct heterosis values (Kg), all F1 crosses . . . . .	25
Maternal heterosis values (Kg), all F1 dams . . . . .	20
Within-breed standard deviation (Kg) . . . . .	40
Within-breed heritability . . . . .	0
Genetic progress in foreign populations . . . . .	0
Genetic correlation between environments . . . . .	1

Setting within-breed heritability to zero helps to clearly demonstrate the emergence of various designs.

### Selection Criterion

Estimation of breeding value within breed group is based on individual phenotype, for simplicity of illustration. The full index used in these simulations is as given by Kinghorn (1984) - for the  $i$ th candidate for selection:

$$Index_i = (BBV_i + 2.BMV_i) + h^2.(Phenotype_i - BGV_i) - COST_i \quad (1)$$

- where BBV is Breed Breeding Value (Kinghorn, 1982), which is related to the expected BGV of progeny. This value depends on mate genotype, which is determined by the mating algorithm. COST is the net cost of selecting the individual (purchase, transport etc.) expressed in units of breeding value. Use of this index is equivalent to the procedure illustrated by figure 1, except that that latter ignores cost factors to simplify illustration.

### Simulation Parameters

Table 1 shows the parameter values used for each simulation, where they deviate from the parameter mask given above. These values were chosen to illustrate the setting up of a number of different program designs. It should be noted that no input to these simulations contains instructions on setting up specified designs. Designs emerge as a consequence of the method used for selecting and mating individuals

Table 1. Parameter values, best crossbred genotype and its value (Kg), for simulations 1-5. Only deviations from the parameter mask given in the text are shown.

Simulation	Parameter Deviations	Best Genotype	Value
1	none	Three breed cross, 3x(1x2)	418.75
2	Import cost \$200 per cow, \$400 per bull	Two breed rotation, breeds 2 and 3	404.0
3	No direct heterosis	Backcross, 3x(2x3)	395.25
4	No maternal heterosis	F1 cross, 3x2	404.5
5	Heritability = 0.3	----- See simulation 5 -----	-----

### Assumptions

In addition to the assumptions indicated above, the following are assumed for these simulations:

1) Heterosis expressed is proportional to heterozygosity with respect to breed of origin of genes.

2) The proportion of genes from each breed in an individual is the average of those in its parents.

3) Heterosis values are unaffected by selection response within breed groups. Breed Genetic Values are fixed at generation zero values for simple illustration, and within-breed response to selection is treated separately

## RESULTS

The first four simulations assume a heritability of zero. This is done in order to give a clear demonstration that optimal strategies emerge from use of the method - lack of genetic variation (and variation due to cost factors) between individuals within breed groups results in one of the classical crossing structures being optimal. For each of these simulations, Table 1 shows the optimal crossing structure and its value.

### Simulation 1 - Three Breed Cross

For each of the five generations covered by this simulation, Table 2 shows the population mean components of merit (Breed Genetic Value, Breed Maternal Value, phenotypic deviation and phenotype), the total numbers of imported bulls and cows, and the proportion of genes derived from each of the four pure breeds. In each generation, breed 3 bulls and F1 1x2 cows were imported as the sole breeding stock, giving crossbred progeny of expected value:  $BGV + BMV = 393.75 + 25.0 = 418.75$  Kg. The population mean phenotypic deviation from this expectation has no genetic component as heritability is zero.

The three breed cross which emerges here is the best possible. It can be seen that breed 3, with a good direct value but a poor maternal value, is well suited as a terminal sire breed, and that the F1 1x2 cow has a suitably high value as a dam.

### Simulation 2 - Two Breed Rotation

This simulation differs from the previous one only in the cost of importing breeding stock. An approach to incorporating cost factors into the index is described by Kinghorn (1984). This will be treated very simply here for illustration.

Assume that the net cost of importing heifers is \$200 per head, accounting for purchase, transport etc., but discounted for the effect of releasing a homebred heifer from the breeding role. Assuming an expected four progeny per lifetime, and a marginal value of \$1 per Kg yearling weight, a candidate needs to leave progeny which are genetically superior by  $\$200 / (4 \times 1\$/\text{kg}) = 50$  Kg in order to compensate for this cost. This progeny value corresponds to a parent index value of 100 Kg - and this is the 'COST' value which acts as a penalty in index 1) for this simulation.

As bulls are much more fecund than cows, their COST values are correspondingly lower. Assuming a net dollar cost of \$400 per bull, and 100 progeny per lifetime, the COST value for imported bulls is  $2 \times 400 / (100 \times 1) = 8$  Kg, which is the value used in this simulation.



**Table 2.** Results from simulations 1 - 5, represented by the five blocks in the table. Results shown are: generation number (GEN); population mean weight values (Kg, to nearest 100g) for Breed Genetic Value (BGV), Breed Maternal Value (BMV), phenotype within breed group (P-BGV) and phenotype (P); numbers of imported sires and dams; population mean breed proportions for genes derived from each of breeds 1 - 4.

GEN	POPULATION MEAN VALUES				IMPORTS		BREED PROPORTIONS			
	BGV	BMV	(P-BGV)	P	SIRES	DAMS	1	2	3	4
<b>Three breed cross:</b>										
0	355.0	3.0	-0.4	357.6	0	0	1.00	0.00	0.00	0.00
1	393.8	25.0	-0.8	417.9	40	1000	0.25	0.25	0.50	0.00
2	393.8	25.0	-0.5	418.3	40	1000	0.25	0.25	0.50	0.00
3	393.8	25.0	-1.0	417.7	40	1000	0.25	0.25	0.50	0.00
4	393.8	25.0	0.2	418.9	40	1000	0.25	0.25	0.50	0.00
5	393.8	25.0	0.1	418.9	40	1000	0.25	0.25	0.50	0.00
<b>Two breed rotation:</b>										
0	355.0	3.0	0.7	358.7	0	0	1.00	0.00	0.00	0.00
1	390.0	3.0	0.2	393.2	40	0	0.50	0.00	0.50	0.00
2	392.5	19.5	-0.6	411.4	40	0	0.25	0.50	0.25	0.00
3	390.0	23.3	0.7	414.0	40	0	0.13	0.25	0.63	0.00
4	389.3	14.6	-0.4	403.6	40	0	0.06	0.63	0.31	0.00
5	390.0	18.3	0.0	408.3	40	0	0.03	0.31	0.66	0.00
<b>Backcross:</b>										
0	355.0	3.0	0.7	358.7	0	0	1.00	0.00	0.00	0.00
1	373.8	21.5	-0.3	394.9	40	1000	0.00	0.25	0.75	0.00
2	373.8	21.5	-0.1	395.1	40	1000	0.00	0.25	0.75	0.00
3	373.8	21.5	-0.2	395.1	40	1000	0.00	0.25	0.75	0.00
4	373.8	21.5	0.1	395.4	40	1000	0.00	0.25	0.75	0.00
5	373.8	21.5	0.2	395.5	40	1000	0.00	0.25	0.75	0.00
<b>F1 cross:</b>										
0	355.0	3.0	-0.3	357.7	0	0	1.00	0.00	0.00	0.00
1	397.5	7.0	-0.5	404.0	40	1000	0.00	0.50	0.50	0.00
2	397.5	7.0	-0.4	404.1	40	1000	0.00	0.50	0.50	0.00
3	397.5	7.0	-0.6	403.9	40	1000	0.00	0.50	0.50	0.00
4	397.5	7.0	-0.4	404.1	40	1000	0.00	0.50	0.50	0.00
5	397.5	7.0	0.0	404.5	40	1000	0.00	0.50	0.50	0.00
<b>Multicross:</b>										
0	355.0	3.0	0.4	358.4	0	0	1.00	0.00	0.00	0.00
1	390.3	21.5	23.5	435.3	26	1000	0.32	0.28	0.30	0.11
2	387.6	21.5	33.6	442.6	10	631	0.24	0.33	0.32	0.11
3	387.3	20.7	42.5	450.5	9	672	0.21	0.34	0.33	0.12
4	386.9	20.3	44.7	451.9	7	618	0.21	0.37	0.33	0.10
5	385.9	19.8	56.6	462.3	4	587	0.20	0.38	0.31	0.11

Table 2 shows the results of this simulation up to generation 5. The high COST of importing cows has effectively closed the home population to such imports. In generation 1, breed 3 bulls are imported to give the best possible progeny - the cost of importing these bulls is more than covered by the value of using them. In the next generation, breed 2 bulls are imported to give three breed

cross 2 x (3x1) progeny. Again, the cost of importation is justified. In the following generations, bulls of breed 2 and 3 are imported rotationally, and a classical 2 breed rotation emerges.

#### Simulation 3 - Backcross

This simulation differs from the first only in the absence of direct heterosis. The results, shown in Table 2, are as expected. The expression of full direct heterosis, as in a three breed cross, is no longer of value. The 2x3 F1 dam is still preferred, but a breed 3 bull is now favoured for its high purebred value. The 3 x (2x3) backcross is set up and maintained each generation.

#### Simulation 4 - F1 Cross

This simulation differs from the first only in the absence of maternal heterosis. In this case, F1 cows cannot be better than the best purebreed, yet direct heterosis favours crossbred progeny. The best design is the 3x2 F1 cross, giving a high BGV and exploiting the high maternal value of the breed 2 cow. Breeding stock are imported each generation to maintain this design.

#### Simulation 5 - "Multicross"

This simulation differs from the first only in the setting of heritability to 30 percent. Table 3 shows the matings set up in the first generation of this simulation. In order to properly exploit within-breed genetic variation, animals were selected from a range of breed groups, with simultaneous consideration being given to group values and optimal mating patterns. All of the 1000 matings are either three breed crosses or four breed crosses, indicating efficient use of both direct and maternal heterosis.

However, the best crossbred genotype (3 x (1x2), from simulation 1) is only the second most represented cross here (155 matings). This is because the pool of breed 1 candidates (2000 homebred plus 50 foreign bulls) is much larger than that of breed 3 candidates (50 foreign bulls), giving a better selection intensity for within-breed merit. The best mates for breed 1 sires are 2x3 F1 cows, and 335 such matings were set up (Table 3).

Table 4 shows the matings set up in the third generation of this simulation. The 'best' crossbred genotype is now most represented (147 matings). Of the 34 male genotypes available for selection, 15 are represented, and 11 of these are homebred. Although a wide range of genotypes are in evidence, the population mean breed proportions are already approaching those of the optimum synthetic for the genetic parameters involved. For breeds 1-4 respectively these are (to the nearest percentage) 21, 34, 33, 12 at generation 3, and 18, 39, 32, 10 theoretically from equation 5 of Kinghorn (1982). The mean breed value (BGV + BMV) of this optimum synthetic is 400.3 Kg, and yet, despite compromising due to within-breed effects, the population mean BGV + BMV equals 408.0 Kg in generation 3 of the simulation (Table 2). This is because the method used sets up non-random matings to more fully exploit heterotic effects.



**Table 3.** Matings set up in the first generation of simulation 5. Genotype 1x2 is an F1 cross between breeds 1 and 2. The number of matings for each pair of genotypes is shown. Unselected genotypes are not shown. Each of the 40 selected sires has 25 selected dams individually allocated to him.

MALE GENOTYPE	NUMBER SELECTED	FEMALE GENOTYPE					
		2x3	1x2	1x3	2x4	1x4	3x4
BREED 1	14	335	.	.	15	.	.
BREED 3	8	.	155	.	45	.	.
BREED 2	5	.	.	79	.	5	41
3x4	4	.	100	.	.	.	.
2x3	3	.	.	.	.	75	.
2x4	3	.	.	75	.	.	.
1x3	2	.	.	.	50	.	.
1x4	1	25	.	.	.	.	.
<b>TOTALS</b>	<b>40</b>	<b>360</b>	<b>255</b>	<b>154</b>	<b>110</b>	<b>80</b>	<b>41</b>

**Table 4.** Matings set up in the third generation of simulation 5. Layout is as for Table 3, except that breed genotype is here described by three percentage figures - these are the percentages of genes derived from breeds 1, 2 and 3 respectively. The percentage of breed 4 genes is 100 minus the sum of these three figures. Only 743 out of 1000 matings are shown.

MALE GENOTYPE	NUMBER SELECTED	FEMALE GENOTYPE					
		0 50 50	50 50 0	0 50 0	25 37 25	50 0 50	25 50 25
0 0 100	6	.	147	2	.	.	.
25 37 25	6	67	1	.	10	7	8
12 37 37	5	.	30	.	30	11	7
37 25 25	4	80	.	.	4	.	4
25 25 50	4	.	8	86	2	.	.
25 25 37	3	20	.	12	13	.	18
25 37 37	2	.	.	15	6	.	.
37 37 25	2	13	.	5	11	1	2
25 50 25	2	.	.	.	.	7	.
12 25 37	1	.	10	.	4	.	10
37 25 37	1	.	.	23	.	.	.
12 37 25	1	.	.	.	.	18	.
0 100 0	1	.	.	.	.	25	.
0 0 0	1	23	.	.	.	.	.
0 50 50	1	.	.	.	.	3	.
<b>TOTALS</b>	<b>40</b>	<b>203</b>	<b>196</b>	<b>143</b>	<b>80</b>	<b>72</b>	<b>49</b>

Table 2 shows the components of response for the first five generations of this simulation. Within-breed additive response accumulates due to the presence of genetic variation within breeds. This component of response is expressed in homebred animals only (as the expected genetic progress in foreign populations is set to zero) making homebred animals more liable to be selected in later generations. This is demonstrated by the decreasing level of importation as the simulation progresses, and the approach to an optimal set of breed proportions, as described above.

It is of interest to compare the components of response in this simulation with those achieved by a policy of restricting selection in a manner which gives rise to the best crossbred genotype (3 x (1x2)) alone. Results of this comparison are shown in Table 5 for two values of the expected genetic progress in foreign populations - zero and 20 Kg per generation. The restricted policy does give rise to some selection response, as the best 40 breed 3 sires are selected out of 50 candidates each generation. However, it can be seen that the unrestricted method gives much better response within breed groups (P-BGV) at little expense in between-group merit. As might be expected, a higher level of importation is maintained when progress in foreign populations is high.

Table 5. Population mean values and numbers of imports in generation five. Parameters are as for simulation 5, except where foreign progress is varied and/or generation of the best three breed cross is forced (FIXED as opposed to FREE). Results are averaged from five replications in each case. Variation between replications within case was small for all results.

FOREIGN PROGRESS Kg/generation	MATING TYPE	BGV	MEAN VALUES			IMPORTS	
			BMV	(P-BGV)	P	SIRES	DAMS
0	FIXED	393.8	25.0	2.2	421.0	40	1000
0	FREE	386.3	19.9	58.2	464.4	4	575
20	FIXED	393.8	25.0	101.0	519.8	40	1000
20	FREE	388.9	21.5	123.2	533.7	19	856

#### DISCUSSION

Results from the simulations carried out show that the method proposed does set up designs which are appropriate to the prevailing genetic and cost parameters. Simulations not described here have, for example, set up two cow groups at home and maintained both phases of a 2 breed rotation simultaneously, or used a terminal sire over 2 breed rotation cows. The method encompasses the classical decision process for this type of problem (Cunningham, 1976), but makes balanced use of each option.

The population structures, selection criterion and assumptions made for these simulations have been rather simplistic, for the sake

of simple illustration. However, it is proposed that this type of approach can be used profitably in relation to more complex, real situations.

Without direct application, the method can be used in computer programs written to closely simulate existing breeding problems. All available information about population means, population sizes, age structures, dystocia problems, heritabilities, genotype-environment interaction, costs, etc. can be incorporated in such a simulation. Results may reveal unpredicted design options which influence decision making.

The method can also be used directly in a breeding program, although this may involve some development work:

1) Some knowledge of population means and heterosis, as well as within-breed genetic parameters, is required for the environment(s) concerned. After the first one or two generations of crossing, the effects of epistasis on the expression of heterosis may become important, such that the prediction of breed genetic and breeding values needs to be carried out on an ad hoc basis, probably from within the program itself.

2) Where between-breed effects are considered to be fixed, they can be simply weighted by economic weights for the traits in the breeding objective. However, where these effects are considered as random, a knowledge of the variance-covariance structure between breeds is required. This is not of great importance where there is a large amount of suitable data available to estimate breed group means - such that there is little error variance in the variance of these means.

3) The within-breed component of index 1) can be replaced by any method of predicting breeding value, using information from relatives and a number of traits. However, where relatives belong to one or more different breed groups, proper account must be taken of the between-breed parameters involved.

4) In some cases, the wide range of breed genotypes emerging may not be desired, even though quite a narrow range of broad groupings (where breed proportions are within about 10 percent) is usually observed. If this is a real problem, the method can be objectively restricted to generate no more than a certain number of genotypes, or broad groupings.

5) Application of this method would be facilitated by a comprehensive recording scheme which gathers information about animal performance and selling prices for breeding stock. Such a scheme could advise the farmer on the exact composition of his mating groups, and which breeding animals to buy, if any. The logistical problems in such a scheme would be most challenging.

The question of how appropriate the designs which emerge really are is not simple. One potential flaw in the method, as presented, is that it only aims one generation ahead at each stage, which defines goals to be relatively short-term. The between-breed component of index 1) can be regressed in a manner which improves

long-term response at the cost of short-term response (Kinghorn, 1983). However, this is not a full solution to the problem - under some population structures it may be appropriate to generate certain genotypes for specified rôles as parents in the next generation, and this is not achieved by the regression method.

A solution to this problem would at least help develop the approach to a level where the breeding objective covers a structured group of populations, rather than a single 'home' population. This would involve a range of component objectives, either setting up some populations to provide breeding material for others, or optimising the design of an existing industry structure.

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