

55th EAAP Meeting
September 3-8 2004
Bled Slovenia

Commission on Animal Genetics
Session III : Management of genetic variation
September 6th

MANAGEMENT OF SELECTED POPULATIONS: FROM THEORY TO PRACTICE

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Abstract

The methodologies available for improving the balance between genetic gain and inbreeding rate in selected populations were briefly reviewed. Emphasis was given to the long-term contribution approach. Such an approach was adapted to the main selection steps of dairy cattle and pig breeding. Details of the appropriate procedures were given. *A posteriori* tests were carried out in corresponding real populations in order to assess their potential for saving genetic variability while maintaining the genetic gains at their observed values. Generally speaking, these procedures were able to decrease kinship and inbreeding coefficients by about 20%.

1. Introduction

The improvement of evaluation methodology, the settlement of well-thought breeding programmes and, for some species such as cattle, the modification of reproduction methods have yielded dramatic genetic gains. First, at the expense of the general aptitude of animals to survive: awareness about this situation has been growing worldwide and has been inducing significant changes into selection methods and objectives. Second, at the expense of genetic variability. The corresponding damages are well-known: reduction of long-term genetic gains, reduced flexibility for new selection objectives, increased variability of response to selection, increased inbreeding depression and increased expression of genetic defects or diseases. In the long term, this might both discourage breeders and lead the public opinion to strongly disapprove 'modern' selection of domestic animals. The long-term trends extrapolated from the current situation are quite concerning (e.g., Boichard *et al.* 1997, Moureaux *et al.* 2000; for dairy cattle breeding, Maignel *et al.*, 1998, Maignel and Labroue, 2001 for pig breeding). Awareness is increasing worldwide as well, although the reaction on field does not seem to exhibit the same vigour as for functional traits.

Fortunately, research on Quantitative Genetics have been very active these last years and have succeeded in providing already valuable solutions, although further progress is certainly still possible. Then, the main current challenge is making this body of theoretical achievements to be definitely incorporated into every day's selection. We share the opinion of Kinghorn *et al.* (2002): for maximizing acceptance by practitioners, flexibility and legitimate constraints should be accounted for when trying to achieve this objective.

The objective of this communication will be to briefly review the weaponry of methods available for coping with the major problem faced and then to present a series of optimisation methods dedicated to each major step of any breeding scheme. (for dairy cattle and pig breeding). Their potential will be assessed based on real recent populations (three breeds for dairy cattle and one breed for pig).

2. Theoretical achievements

2.1 First approaches

All of these approaches, albeit very different, can be regarded as still related to the conventional approach for modelling breeding schemes: selected parents are used uniformly. Modifications proposed were biasing EBVs to temper family selection and inbreeding: either by using inflated heritability (Grundy and Hill, 1993) or by increasing the relative weight of Mendelian sampling deviation (Toro and Perez-Enciso, 1990; Verrier *et al.*, 1993.; Villanueva *et al.*, 1994). Another family of methods introduced penalties for individual's inbreeding coefficient (Villanueva *et al.*, 1994) or for the average coancestry between the candidate and the animals already selected (Wray and Goddard, 1994. Brisbane and Gibson, 1995).

Simulation showed that these methods were able to improve the balance between genetic gain and inbreeding rate. However, strong theoretical frame was lacking. Besides, in some cases; they would be hard to implement in reality because the first qualities repeatedly requested by practitioners about EBVs are unbiasedness and full accuracy. These were the reasons why Research progressively moved towards a more powerful and clear approach.

2.2 The long-term contribution theory

2.2.1 Optimising contributions

This concept was first introduced by James and Mc Bride (1958) for identifying the frequencies of different gene sources (represented by ancestors) in a population. Wray and Thomson (1990) established that in a randomly mating population, the inbreeding rate was related in a simple way with the squared long-term (stabilized) contributions of the basic ancestors and consequently with their variance. This work initiated a series of works on the methods of predicting inbreeding rates (beyond the scope of this communication: see Woolliams and Bijma, 2000) and the appropriate methods of containment while still selecting intensively.

Inbreeding rates also depend on the accumulation of squared contributions across generations of subsequent ancestors (Woolliams and Thomson, 1993; Woolliams, 1998; Woolliams and Bijma, 2000; Caballero and Toro, 2000). An equivalent expression of this accumulation is the average (weighted by the short term contributions of the current breeding animals) pairwise relationship coefficient in the population of current parents, including self-relationships. Equivalently, this coefficient is related to the number of founder alleles still present in the population (Crow and Kimura, 1970). or to the equivalent number of genomes (Caballero and Toro, 2000). Hence, the idea of setting this coefficient to a pre-determined value when implementing selection (Toro and Perez-Enciso, 1990; Meuwissen, 1997; Woolliams *et al.* 2002). Then, contributions of current parents are optimised. Extensions were proposed for overlapping generations (Meuwissen and Sonesson, 1998; Grundy *et al.*, 2000 .Sonesson *et al.* 2000.;Sonesson and Meuwissen, 2002; Sanchez *et al.*, 2003). They took into account the approximate expected contributions of existing cohorts in the future, 'approximate' because, at least on real populations, culling and intensity of use are fairly unpredictable. However, simulation showed the efficiency of this theory. Basically, the corresponding breeding schemes were found to generate more genetic gain (several tens of %) than a fixed contribution breeding scheme, for a given inbreeding rate, confirming the observation of Toro and Nieto (1984) .

2.2.2 The role of mating design

Several modifications to random mating were proposed: mainly minimum coancestry matings (MC) and compensatory matings (CM) either between parents of opposite contributions (Santiago and Caballero, 1995) or between parents of opposite coancestry with the population (Caballero *et al.* 1996) or even a mixture between MC and CM (Caballero *et al.* 1996). The impact of the mating design was quite clear in fixed contribution breeding schemes for reducing inbreeding rates but virtually vanished for breeding schemes with optimised contributions (Sonesson and Meuwissen, 2000) / However, genetic gains were enhanced: basically selection differential were improved through decreased average correlation between EBVs of candidates. Additionally, factorial matings were

shown to be more profitable than hierarchical matings (Woolliams, 1989; Sonesson and Meuwissen, 2000; Sorensen *et al.* 2002).

Due to these findings, Sonesson and Meuwissen (2000, 2002) recommended for the sake of simplicity and saving computation time, first to optimize contributions and second to optimize the mating design. CM is quite easy to implement and if MC is chosen, linear programming methods can be used (Toro and Perez-Enciso, 1990; Fernandez and Toro, 1993). Sonesson and Meuwissen resorted to the simulated annealing method, a MCMC method, for finding the best set of matings, given the calculated breeding allocations.

2.2.3 Combining both steps

This approach can be considered as a mixture between the contribution approach and the mate selection approach (Allaire, 1980) where the function optimized concerns progeny and not parents. Examples were given by Kinghorn (1987, 1998), Klieve *et al.* (1994), Fernandez and Toro (1993) with their 'weighted pair selection', Weigel and Lin (2000, 2002). Colleau *et al.* (2004) considered the average relationship in progeny modified by penalties for full-sibs. Calculations were carried out using the sparseness of the inverse of relationship matrix (Colleau, 2002). Despite these simplifications, calculations were more extensive than with the two-step approach.

The literature does not provide clear indication on whether this one-step procedure differs significantly in terms of efficiency from the two-step approach (Caballero and Toro, 2000; Sonesson and Meuwissen, 2000; Woolliams *et al.*, 2002). However, Fernandez and Caballero (2001) found out that the single step approach was definitely creating more inbreeding than a two-step approach.

3. Dynamic management of genetic variability in dairy cattle breeding

3.1 General outline

The objective is to develop management methods of genetic variability dedicated to each major step of any dairy cattle breeding scheme, *i.e.*, when:

- i) procreating young bulls to be progeny-tested (and possibly young females within selection nuclei)
- ii) selecting young bulls for progeny-testing
- iii) using service bulls on non-elite cows.
- iv) approving recently progeny-tested bulls for AI use

These different procedures share common characteristics. First, the objective is to minimize the average pairwise relationship coefficient (including self-relationships) in the population of individuals to be born and of existing individuals so as to maximize the number of founder genes still present. Second, as a major constraint, the average EBV of the future individuals for an overall combination of many traits of economical importance is set to a desired value. This operational choice is preferred to the symmetrical approach (*i.e.*, constraining the average pairwise relationship coefficient while maximizing the average EBV). It is considered that practitioners might be inefficient, because reluctant, if major emphasis were given to a parameter they are still unfamiliar with. These procedures are detailed in Colleau *et al.* (2004).

3.2 Procreation of young bulls

Relationship coefficient is minimized after considering additionally the population of young bulls waiting for completion of progeny-test. The average EBV of the individuals to be born from the programmed matings is set to a desired value. Besides, a second major constraint, reproduction cost, is added. Practitioners may wish to set this parameter to a desired value. Then, they are prompted to define the different reproduction profiles they consider to be feasible if recommended (*e.g.* a single AI, or one superovulation followed by AI or two superovulations followed by AI) and the corresponding costs. The optimisation method defines the dams undergoing the different reproduction regimes and the sires involved at each elementary reproduction step. For example, a dam chosen for being superovulated twice and finally inseminated can be mated to 1, 2 or 3 different sires. Finally, the output of the procedure is a ready-for-use recommendation.

3.3 Selection of young bulls for progeny-testing

Usually, much more young bulls are procreated than really needed for progeny-testing. An additional selection step occurs based on the most recent EBVs of parents and especially dams. Then, practitioners set the average EBV of selected young bulls to a desired value. The selection procedure minimizes the average relationship coefficient in the population of selected individuals and previous bulls still waiting to be progeny-tested. The analytical optimisation progressively builds the set of individuals to be retained and the set of individuals to be dismissed.

3.4 Use of service bull on non-elite cows

Individual cows in the existing population are not considered due to the very high calculation cost incurred. Instead, the general population of existing females is split into sire* maternal grand-sire groups where relationships between and within groups are calculated only based on the exact relationships between the males involved (either sires or MGS or both). As a result, the problem amounts to find out, for each group, the optimal proportions of females to be served by the different AI sires. Then, the overall optimal use of a given AI sire is obtained after considering group frequencies in the population and specific within-group optimal use of this sire. These indications allow extension services of AI organizations to orientate the effective use by breeders, according to the groups their cows belong.

The only constraint is here the desired value of the average EBV of selected bulls (after weighting for the recommended intensity of use). Analytical developments are much simpler than for young bull procreation.

3.5 Selection of young bulls for service

In some countries, official approval of bulls, mainly based on EBV, is needed. Ideally, genetic variability should be accounted for when taking this decision. The selection procedure directly stems from the procedure used for finding the optimal use of service bulls. Available service bulls and recently progeny-tested young bulls are made to compete for use on the female population. Finally, young bulls can be accepted for use provided their optimal contribution were not null.

4. Dynamic management of genetic variability in pig breeding

4.1 General outline

Management of genetic variability in pure breeding herds is needed at two major steps of the breeding scheme

- i) selecting available boars for service on sows already selected for reproduction
- ii) selecting male and female replacements (in order to define future availability)

Pig reproduction cycle is very fast so that decisions should be taken very often at the herd level (typically each three weeks). The relationship approach method used in dairy cattle breeding is relatively time-consuming. For this reason, it is preferred to switch towards the less demanding method of Meuwissen and Sonesson, where contributions are optimised based on the average pairwise relationship coefficients between selected parents, not between their progeny, and where matings are determined subsequently so as to minimize inbreeding coefficient of progeny. The average EBV of parents is still constrained to a desired value.

4.2 Use of boars and mating design

Breeders give the list of sows to be bred next month and the list of available boars either AI boars or NS (natural service) keeping in mind that 'NS' boars are very often collected for semen and subsequent home use. Furthermore, individual breeders can set to specific values the average EBV of the boars they want to use and the number of sows to be served by NS boars. If there is only a single NS boar (at the beginning or at a given optimisation step), then the contribution of this boar is known. The optimisation procedure minimizes the average relationship coefficient in the population of the sows and of the selected boars, after accounting for the different cohorts of existing animals in the whole population (other boars, other sows, young animal still under performance-test and current

gestations). Finally, the list of selected boars is obtained with the corresponding numbers of sows (proportional to the optimized contributions). Matings are programmed to obtain the minimum average inbreeding coefficient using a method very close to Meuwissen and Sonesson's method.

4.3 Replacement

The method envisioned (yet untested) is analogous to the one described in 3.3. Complications arise from the fact that female and male replacement should be considered simultaneously and that numerous constraints should be accounted for: desired number and average EBV of young sows and young NS boars in each herd. The same is true for AI boars. The size of linear systems to be solved is much higher than in 3.3, constraining one to use iterative resolution methods. Finally, it is anticipated that the method will be able to give an optimal ranking of young females within herds and of males between and within herds so as to determine the best boars for AI or NS. Selected young boars are finally added to the list of available boars to be further submitted to the selection procedure described in 4.2.

5. Validation principles and data sets

5.1 General outline

The general objective was:

- i) informing breeders about the optimality of their current selection practices concerning genetic variability
- ii) providing them with solutions integrating out their constraints and using extensively the most efficient concepts proposed by Research worldwide.

For this reason, testing of methods was based on real populations and aimed at answering this simple question: *would have the proposed methods been able to save genetic variability while maintaining the genetic levels recently observed in the population?* In other words, the testing procedure can be considered as an *a posteriori* optimisation.

5.2 The cattle data sets

The data originated from the three main dairy breeds exploited in France. The Holstein breed was represented by OGER-MIDATEST's population and the Montbéliarde breed by UMOTEST's population. The Norman population could be considered as a whole because selection operations are coordinated by a single organization: GNA (Génétique Normande Avenir).

As to testing the procreation step of young bulls, young bulls entering performance-test stations between March 1, 2001 and February 28, 2002 were considered *i.e.*, 499, 359 and 401 for the Holstein, Montbéliard, Norman breeds respectively. 4 previous annual groups of animals still under progeny-test were also considered for representing the background population of young bulls *i.e.*, 585, 708 and 626 according to the different breeds (in the same order.) Optimisation was carried out so that the expected average ISU (overall index, see Colleau and Regaldo, 2001) was equal to the observed one. Besides, for each breed, the overall actual reproduction costs and the current panel of breeding profile were introduced into the optimisation equations.

As to testing the selection step before progeny-testing, the number of really selected bulls was maintained *i.e.*, 204, 144 and 156 respectively. The average ISU for the selected individuals was constrained to be the observed one.

As to testing the method of optimizing use of AI bulls, inseminations between October 1, 2001 and September 30, 2002 were examined. Selected cows (219169, 124937, 135771 respectively) were born from known sires and MGS (1875, 1861 and 2075 sire-MGS groups) and were inseminated by 50, 52 and 42 approved bulls, respectively.

As to testing the approval step, the batches of young bulls born in 1996 were considered *i.e.*, 208, 130 and 152 respectively. The numbers of bulls really selected were 32, 15 and 19 respectively. The average constrained ISU of selected bulls was the same as the current average ISU of AI bulls augmented by the desired genetic gain *i.e.*, 4 ISU points per year.

5.3 The pig data set

The test data were provided by the French Landrace breed where inbreeding is increasing very fast. The average inbreeding coefficient was 3.4% in 1995 (Maignel *et al.*, 1998), 4.2% in 1999

(Maignel and Labroue, 2001) and 6.4% in 2003 (this study). The 2445 sows mated between September 15, 2002 and February 9, 2003 and belonging to 26 herds were chosen in order to represent the unit time of the pig cycle (21 weeks) *i.e.*, sows were mated successfully only once during this period. The section of time was split into 5 monthly periods in order to roughly mimic the usual pace of decisions in pig breeding. For each monthly period, boars currently available for natural service or for AI were identified. For each sub-period, the number of sows varied from 360 to 617, the number of available AI boars from 123 to 131 and the number of available NS boars from 53 to 63.

The optimisation procedure was run five times, successively for each monthly period, accounting for the background population and for the recommendations already calculated during the previous monthly periods. Finally, it yielded the number of sows allocated to each selected boar. For finding the optimal mating design, an additional constraint was considered given the main question raised in 4.1. : herd averages for the EBVs of the selected boars should be as close as possible to the corresponding observed values. Adding this constraint into the system of equations was not possible because the average relationship coefficient between parents depended only on the overall use of boars over herds and not on their specific use in each herd. Then, herd allocations for selected AI boars were obtained by a Monte-Carlo method. Sampling allocations were given to each herd and were equal to the numbers of sows to be sired by AI (equal to the observed values). The overall use of AI was 69%, varying between 0% and 100 % according to the herd*month combination. Sampling was carried out randomly across herds until completion. In the herd currently considered, an AI boar was sampled from the still unused AI allocations, using a fitness function adapted to the local herd average. Herd averages for the EBV's of boars selected in this way were very close to the observed ones. Finally, matings were determined by independent herd optimisations in order to obtain the lowest possible inbreeding coefficient for future progeny.

6. Results obtained in dairy cattle breeding

3.1 Procreation of young bulls

The results of Table 1 clearly showed that optimization would have save substantial genetic variability, despite the constraints met, by decreasing the average kinship coefficients (Malécot, 1948), *i.e.*, the probabilities of identity by descent, within the population of new young bulls and between populations of new or previous young bulls.

Table 1 Young bull procreation: average kinship coefficients

N=new young bulls P = previous young bulls

Vertically : Holstein, Montbéliard, Norman

Kinship (%)	Real	Optimized	Decrease (%)
P*P	6.47 5.88 6.07	Idem	0
P*N	6.28 5.44 5.87	4.71 3.82 4.13	25 30 28
N*N	7.76 7.25 7.03	6.05 5.54 5.10	22 24 27
(P+N)*(P+N)	6.65 5.84 6.07	5.65 4.92 5.00	15 16 18

The origin of such a difference was certainly complex: directional selection (as strongly suggested by the literature), threshold selection instead of selection on overall EBV, imperfect view of the relationships due to remote generations, subjective decisions about the use of breeding animals, especially males. The last point could be tested indirectly in one breed because practitioners would

have preferred that the optimization be run under additional operational constraints: a large proportion of males candidates for reproduction should have been given either minimal or maximal allocations. The algorithms were modified accordingly. The main result was that under these circumstances, the efficiency of the optimization was dramatically impaired (decreased by 50%). Finally, the results of Table 1 both challenged the current practices and showed that the solution envisioned was reasonably efficient.

The calculated recommendations corresponded to significant and even brutal changes as a result of an attempt to correct the unfavourable current situation. For instance, in one breed, the best bull for ISU was totally excluded from the sire list. Consequently, the point of the full acceptance of this kind of recommendations by practitioners in the future might not be trivial.

Although the procedure was not specifically designed for minimizing inbreeding coefficients of the young bulls, it succeeded in generating significant decreases : from 5.30, 4.20, 4.18% as observed in the three breeds to 4.11, 2.96, 3.15% respectively.

3.2 Young bull selection

The results of Table 2 showed that additional protection of the genetic variability might have been obtained at this step, especially when considering the average pairwise kinship coefficient between selected animals. It should be pointed out that this improvement had nothing to do with 3.1 because the procedure considered the set of animals as it stood, where contributions of parents were not themselves optimized. Then, implementing both 3.1 and 3.2 could have led to somewhat additive improvements.

Table 2 Young bull selection for progeny-test: average kinship coefficients

S=selected young bulls P = previous selected young bulls

Vertically: Holstein, Montbéliard, Norman

Kinship (%)	Real	Optimized	Decrease (%)
P*S	6.17	5.75	7
	5.40	4.84	10
	5.72	5.12	11
S*S	7.71	6.88	11
	7.22	6.24	14
	7.34	6.11	17

The ranks obtained for each candidate after the procedure were transformed into normal scores and could be reasonably predicted (R^2 equal to 0.68, 0.77, 0.78 for each breed respectively) by a linear function considering three variables: ISU, the average kinship coefficient between the individual and the other candidates, k_1 , its counterpart k_2 after considering the previous young bulls. Expressing kinships in % , the regression formulae were: (1.3 to 4.2) ISU - (0.42 to 0.49) k_1 - (0.36 to 0.62) k_2 . Because the standard deviations of ISU and of the k 's were about 5 and 1 respectively, penalties could be considered at first sight as relatively mild. However, ISU was related to the k 's (r about 0.30) and both k 's were strongly related (r about 0.60). Hence, directional selection for ISU was clearly discouraged.

3.3 Use of service bulls

The results of Table 3 were as clear as those of Table 1, showing that the optimisation could have led to less relationship between the future females or between them and the existing female population.

Table 3 Use of service bulls: average kinship coefficients
N=new females P = previous females
 Vertical ranking of breeds: Holstein, Montbéliard, Norman

Kinship (%)	Real	Optimized	Decrease (%)
P*P	6.86 6.76 6.20	Idem	0
P*N	4.11 4.06 3.82	3.61 3.27 3.30	12 19 14
N*N	5.52 5.47 5.20	4.45 3.86 4.08	19 29 21
(P+N)*(P+N)	6.27 6.18 5.60	6.14 6.00 5.46	2 3 3

In the three breeds, the correlation coefficient between the real use and the optimized use of service bulls was almost zero. This was not surprising at all, because for the present being, fame of bulls is primarily based on the EBV profile for the major traits. The challenge for the future will be making individual breeders to consider also genetic originality. The publication of an overall EBV penalized for kinship would certainly be useful for helping them to classify bulls more correctly than they currently do. The relevant coefficients to be used would not be given *a priori* but after extensive optimisation calculations, analogous to those mentioned in 3.2.

3.4 Approval of young bulls

The real decisions were somewhat questioned by the optimisation procedure in the three breeds. Considering the breeds in the same order than in the tables, only 16, 16 and 12 young bulls should have been approved instead of 32, 15 and 19, although they included 6, 7 and 2 bulls dismissed in reality. These last bulls always exhibited a relatively low ISU. Nevertheless, the procedure saved them due to their originality. Very clearly, practitioners should consider this parameter when choosing bulls at the verge of exclusion by directional selection and should keep rare origins.

7. Results obtained in pig breeding

The results of Table 4 show that the optimisation succeeded in reducing substantially the kinship coefficients concerning males (reductions from 14% to 24%). The largest reduction was obtained for kinships between males, despite the number of selected males was only around 40-50 according to the periods. The inbreeding coefficients of progeny were also reduced by 16% in comparison with the real data. The additional constraint concerning the herd averages for the EBVs of selected bulls prevented the optimisation from obtaining an extra reduction of kinship coefficient of about 0.2%. Then, maintaining this constraint in the future for real implementation would lead to a reasonable cost. The % of AI was considered as a basic management parameter and it would not have made sense to examine the effect of a constant use of AI across herds.

Table 4 Optimisation of pig matings: average kinship coefficients

P = previous population (males +females)

M=selected males

F= females

Kinship (%)	Real	Optimized	Decrease (%)
M*P	7.21	6.05	16
M*M	8.65	6.55	24
M*F	6.88	5.88	14
Inbreeding of progeny (%)	6.42	5.32	17

Finally, this procedure will be proposed to French pig breeders, after checking its efficiency on other pig populations. A pending question is the optimisation of replacement of males and females and the settlement of an overall EBV accounting for genetic originality (see 4.3 and 3.2). The corresponding work is under way.

Repeated implementation of both approaches (optimized matings and replacements) is expected to decrease inbreeding coefficient in the short term and inbreeding rate in the long term.

8. Conclusion

Based on some real examples from dairy cattle and pig breeding schemes, it can be concluded that genetic variability might be better protected by using optimising procedures without any short term loss of genetic gain. Basically, contributions of breeding animals and mating design are *calculated* in a rational way. This finding is in agreement with the assessment of Bijma *et al.* (2002): *'by using these (optimized) procedures, breeding organisations can make the same ? G as they do at present whilst reducing the rate of inbreeding generated.* Breeding schemes are fairly complex and involve several selection steps. It is of the utmost importance that genetic variability be considered fully and repeatedly at each step. The methods described in this communication can be considered as an attempt to meet this basic need.

Practitioners, especially those involved in dispersed breeding schemes, might be reluctant to fully implement these approaches. However, because they are already trained in mating science, as mentioned by Weigel (2001), they might be less interested in mating parents complementary for some traits and much more in mating relatively unrelated parents, given the troubles to be expected if they do not so. Another point is how to make them to perceive the correct hierarchy of their breeding animals. For this purpose, the settlement of a modified overall EBV integrating out the degree of genetic originality would be certainly useful for national and international classification, provided that the coefficients used be not set *a priori* but be the result of extensive appropriate calculations. In contrast, specialized and centralized breeding schemes as those met in poultry and rabbit breeding and partly in pig and goat breeding, can very rapidly implement these approaches, if not already done.

In some countries and in some species (such as dairy cattle), marker-assisted selection is starting to be implemented. For many reasons, tracing back QTLs from markers is easier within larger families and selected animals are more likely to originate from fewer families than after conventional selection. Efficient approaches, based on the theory of optimized contributions, have already been proposed (Villanueva *et al.* 2002, Woolliams *et al.* 2002). The scope of this communication was clearly conventional selection but it is obvious that in the long term, the corresponding optimizing procedures should be extended to MAS.

Although maintaining genetic gains at their current levels while better managing genetic variability is still possible, it will be no longer true in the future. Besides, the functions optimized might be forced to account for inbreeding depression. Then, the future can be regarded as somewhat

tougher than the past, but certainly much less than with the genetic troubles occurring from repeated under-management of genetic variation.

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