

USE OF GENETIC MARKERS TO AID CONSERVATION DECISIONS FOR GROUPS OF RARE DOMESTIC BREEDS

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ABSTRACT

An approach to balancing genetic diversity and genetic merit in animal conservation programs is presented and illustrated by simulated example. Microsatellite markers are used to characterise the genetic variation among animals selected to join a conservation program. This is done by consideration of genetic variation within and between breeds at the marker loci. Perceived mean merit of the breeds is also considered. A weighting factor balancing diversity and merit is varied to give a range of possible outcomes. The resulting frontier of diversity and merit combinations is characteristic of the total animal resource, measurements made on it, and the size of the conservation program. It is suggested that practitioners choose an appropriate solution from this frontier. Extension of the method seems possible to help make decisions on factors such as rationalising breeds via crossbreeding and investment in conservation facilities.

KEYWORDS: Genetic markers, genetic conservation, endangered breed, differential evolution

1. INTRODUCTION

Quantitative genetic techniques are successfully used to increase animal productivity, which is the ultimate goal of most animal breeders and producers. More than 7,600 breeds in FAO's Global Databank for Farm Animal Genetic Resources, 190 have become extinct in the past 15 years and a further 1,500 are considered "at risk" of extinction [1]. Many of these breeds are threatened, and genetic diversity itself is also threatened, because of wide preferential use of just a few breeds in each of the key species. The obvious example is in the dairy cattle industry, where Holstein-Friesian is now the dominant breed and is spread throughout the world [2]. Recent studies in Canada and US report that inbreeding rates in this breed are now approaching 1% per generation. In addition, convergence of breeding objectives and high selection intensity with new reproductive technologies such as artificial insemination (AI), multiple ovulation embryo transfer (MOET) and *In vitro* fertilization (IVF) can substantially accelerate the loss of animal diversity.

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Plans for conservation of animal diversity should consider not only endangered and threatened domestic breeds, including those with little or no current use, but also those that are well used and involved in animal improvement programs [2]. The level of biodiversity can be specified through consideration of animal phenotype, but it is preferable to use a measure of genetic diversity [3]. The approach taken in this paper is to use both, in an attempt to balance maintenance of both animal merit and genetic diversity.

Among the genetic markers, microsatellite loci are common in all eukaryotic genomes, and highly polymorphic, making them very useful for the study of genetic variation [4]. In this paper, we simulate use of microsatellite markers to measure genetic variation within and between endangered breeds, combining these to give a measure of genetic diversity within a conservation program. We present a method for optimizing the balance between genetic diversity and perceived genetic merit within such a program. The method as presented here relies on a subjective decision on strategy in the light of a range of predicted outcomes, each determined by a different relative emphasis on diversity and merit. This is analogous to the strategy used to balance genetic merit and long-term inbreeding used by Meuwissen [5] and Kinghorn [6].

2. MATERIALS AND METHODS

The scenario used for this paper assumes that a number of breeds are threatened, but that animals are available for importation into a conservation program in which security of genetic resources is assured. The problem is to decide what proportion of the conservation facilities or resources to use for each breed. In the example used in this paper, numbers of animals to be included in the conservation program are dealt with. This assumes an equal contribution by each animal, and thus a simple extension is required to consider each sex separately, and to accommodate animal relationships, if known. Extensions can also be made to satisfy logistical constraints and costs, such as setting minimum numbers of animals per breed and cost effective patterns of migration into conservation areas or facilities.

Genetic diversity within the conserved group of animals could be measured from genetic marker data in a number of ways, including mean heterozygosity and functions of genetic distances. For this short paper, we have used variation in allele status at each genetic marker site, within and between breeds, as follows:

Variation within breeds:

$$\frac{\sum_j \frac{\sum_i n_i \left(\frac{\sum_k p_{ijk}(1-p_{ijk})}{\sum_k k} \right)}{\sum_i n_i}}{\sum_j j}$$

Variation between breeds:

$$\frac{\sum_j \frac{\sum_k \frac{\sum_i n_i \left(p_{ijk} - \frac{\sum_i n_i p_{ijk}}{\sum_i n_i} \right)^2}{\sum_i n_i - 1}}{\sum_k k}}{\sum_j j}$$

where

n_i is the number of animals conserved for the i^{th} breed.

p_{ijk} is the frequency of the k^{th} allele at the j^{th} locus for the i^{th} breed

3. RESULTS AND DISCUSSION

The scenario simulated has twelve breeds with 1000 animals each currently available, and space to conserve a total of 120 animals in a secure facility. Mean merit of each breed (*Merit*) was sampled randomly (range 95 - 114 units).

The breeds were characterised genetically by typing all available animals for five microsatellite loci, with a maximum of five alleles segregating at each locus. Underlying allele frequencies, used when generating animals, were generated at random in a scheme that results in occasional fixation. The measure of genetic diversity within the candidate conserved group of 120 animals (*Diversity*) was chosen arbitrarily as variation within breeds plus five times variation between breeds. This weighting was chosen in recognition of the fact that variation between breeds is much more accessible and useful than variation within breeds. More work is required to find diversity criteria of high utility, possibly including genetic markers for specific traits, and recognition of rare genetic attributes.

The overall criterion to be maximised was $Merit + \lambda.Diversity$. Weighting factor λ was varied to give a set of results with differing emphasis on *Merit* and *Diversity*. For each value of λ , the optimal solution of numbers of conserved animals from each population was obtained using a modified version of differential evolution [7]. The results are shown in Figure 1 and Table 1.

Table 1 shows that with no emphasis on *Diversity* ($\lambda = 0$), all conserved animals were drawn from the breed with the highest *Merit* (breed 6, 114 units). As more emphasis was placed on *Diversity*, more breeds were included (Table 1), *Diversity* increased and mean *Merit* decreased (Figure 1).

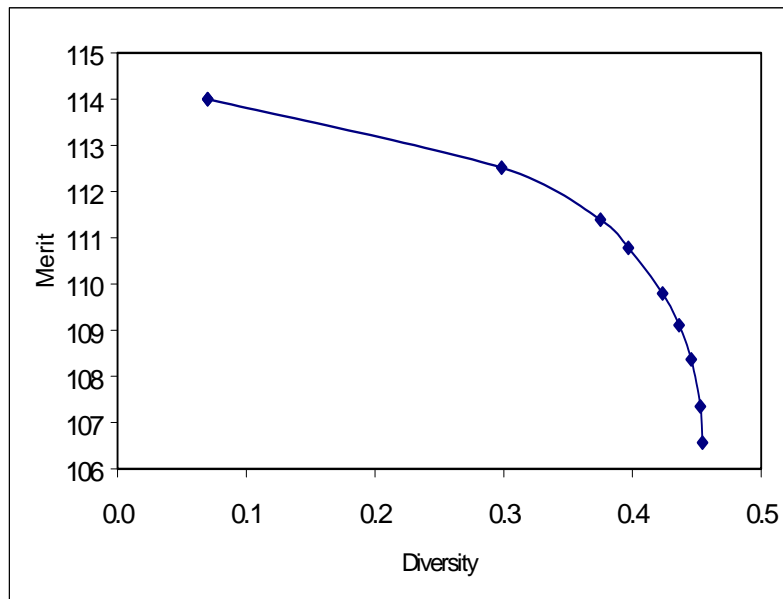


Figure 1 The range of conservation options possible. Each point is a possible solution, and is represented by a row in Table 1

The shape of the curve in Figure 1 depends on the breeds involved, their *Merits* and their microsatellite genotypes. The best solution to choose depends on the uniqueness of the breeds involved, their security outside the conservation program, their potential future use to mankind, and the attitude of the practitioners involved.

Table 1 Number of animals conserved from each population for various weights on diversity, λ

λ	Population number											
	1	2	3	4	5	6	7	8	9	10	11	12
Merit:	108	99	101	107	109	114	111	104	112	95	102	104
0	0	0	0	0	0	120	0	0	0	0	0	0
14.55	0	0	0	4	14	63	2	0	37	0	0	0
23.08	0	0	0	18	15	45	28	0	14	0	0	0
33.54	1	0	0	25	15	39	30	0	8	0	2	0
47.63	6	0	0	28	11	35	28	0	1	0	11	0
69.20	6	0	0	31	8	31	26	0	0	0	18	0
109.7	12	2	0	32	4	26	22	0	0	0	22	0
225.9	11	10	0	33	0	21	21	0	0	0	24	0
∞	8	16	0	33	0	16	21	0	0	0	25	1

An approach analogous to that put forward here has proved to be very flexible in handling a range of decision issues in animal breeding [8]. In the current context, it is suggested that extensions could be made to include decision making on issues such as size of conservation programs, rationalisation of breeds through crossbreeding and money to be spent on facilities development.

It is the method of finding solutions that makes such extensions possible. Differential evolution and related stochastic algorithms work by evolving better solutions. The method does not need to ‘understand’ the problem at hand, in that no analytical optimisation is required – it only needs to be able to evaluate the ‘fitness’ of each possible solution it confronts. This means that arbitrary logistical constraints can be easily handled (a broken constraint renders the solution worthless), and the cost implications of any possible solution can be simply incorporated in its fitness.

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