Technical aspects of the Animalplan system

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ABSTRACT

Animalplan is an integrated set of data processing packages that meets the pedigree and performance recording requirements of many animal species in a unified way. The package offers much flexibility in terms of specification of breeding objectives, the traits to be recorded and presentation of reports.

Technical aspects discussed include breeding objectives, trait adjustment for non-genetic effects using standard or flock/herd specific adjustments, prediction of breeding values using selection index techniques, restricting a trait to zero genetic change and the estimation of direct and maternal effects.

Keywords Performance recording; breeding objectives; breeding values; selection index; genetic gain

INTRODUCTION

The National Flock Recording Scheme (NFRS) for sheep was developed in 1968 and updated (to Sheeplan) in 1976. The National Beef Recording Scheme was developed in 1963 and updated (to Beefplan) in 1973. Goatplan was developed in 1984 from certain options in Sheeplan and similarly Deerplan in 1985 from options in Beefplan. In 1988, MAFTech released Animalplan, an integrated set of data processing packages that meets the pedigree and performance recording requirements of sheep, beef, deer and goats in a unified way. The Animalplan package is available for IBM compatible personal computers or through a bureau service.

The technical background to NFRS was described by Clarke (1967, 1968) and to Sheeplan by Clarke and Rae (1977). Callow *et al.* (1986) outlined proposed enhancements to Sheeplan, these leading on to the development of the Animalplan system.

The basic philosophy behind Animalplan is one of maximum flexibility and consistency of use regardless of the species or trait concerned. The ultimate objective of all breeders is to increase net farm income. Performance recording provides a scientifically based method of assessing and ranking animals in flocks or herds such that consistent breeding decisions can be made. It involves identifying those animal characteristics that contribute significantly to economic profit and optimising the productivity of animals within the flock/herd for these characteristics.

Animalplan has great flexibility as to the traits a breeder can record; there is a broad range of *official* traits about which there is an established base of research information to enable the prediction of breeding values. The breeder is also able to define his own *ad hoc* traits to satisfy other specific recording requirements.

The technical background relating to the processing of these performance traits in order to identify genetically superior animals is the subject of this paper.

Breeding Objectives

The main aims of genetic improvement programmes can be expressed in terms of the component traits which contribute to overall economic profitability. The cost and returns associated with change in the level of expression of each trait can be summarised in terms of relative economic values (REVs) which provide appropriate economic weightings for derivation of an overall breeding objective.

A breeding objective then can be thought of as

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a set of traits of economic importance with a corresponding set of REV's. Animalplan allows the breeder to set up one or more breeding objectives of relevance to the breeding programme. As a guide, a set of standard objectives for each species is used by Animalplan, these being the outcome of discussions with industry.

The breeding value (BV) concept is used to describe an animal's genetic worth for a particular trait - it simply looks into the future and describes the likely merit of the animal's progeny. The traits in an objective determine the BV's to be estimated, the weighted sum of individual trait BV's by their corresponding REV's is an index (estimate) of aggregate breeding worth for each animal. For example

570c x BV(NLB) + 27c x BV(LW8) + 440c x BV(FW12)

is the index (or aggregate BV for net financial return) for the objective comprising number of lambs born (NLB), 8 month live weight (LW8) and 12 month fleece weight (FW12) with corresponding REVs of 570c per lamb, 27c/kg and 440c/kg respectively.

Sometimes a breeder may wish to control the genetic change in a particular trait, for example, the objective may be to improve fleece weight without any genetic change in the average flock level of fibre fineness or one may wish to avoid genetic change in the mature live weight of breeding females. Animalplan provides the option to specify whether a trait included in the breeding objective is to be restricted or not (Cunningham *et al.*, 1970)

Adjusting Records for Non-Genetic Variation

A breeding value is an estimate rather than an absolute value that can be measured directly on an individual animal. The performance of an individual may be considered as the sum of two components -

(i) a genetic component (G) which represents the total additive effect of the individual genes the animal carries and which influence the trait under consideration, and

(ii) an environmental component (E) which represents the combined effect of all non-genetic influences that affect the animal's performance.

When assessing the breeding merit of an animal it is the G component that is important since it is only a sample of the animal's genes which is passed on to the next generation. Thus, an estimate of G, the breeding value, is the desired goal. The accuracy of prediction of the G-component depends on the ratio of genetic variation (var G) to phenotypic variation (var G + var E), that is, the heritability. Thus, reducing the influence of environmental variation (var E) allows for greater accuracy of selection.

The environmental component (E) can be further split into two components -

(i) identifiable sources of non-genetic variation such as age of the animal, age of dam or birth and rearing status, and

(ii) all other sources of environmental variation (random noise).

Animalplan takes two approaches to the adjustment of data for the first type of non-genetic variation. The first approach is a two-stage process -

(i) the use of standard correction factors - these are specified for each species and breed group within species and have been derived from analyses of research and commercial data,

(ii) deviation from contemporary group average - the effect of different contemporary groups is accounted for by deviating an animal's adjusted performance record from the average adjusted performance of all animals in the same group. This is typically used for environmental effects which are due to management and which are likely to be more variable from flock/herd to flock/herd and year to year.

This standard correction procedure was the method used by Sheeplan except that different management groups (mobs) were not always accounted for.

If the flock/herd size is large enough (≥100 animals per sex group), Animalplan combines stages (i) and (ii) above to derive adjustment factors that are appropriate for the particular environmental conditions under which the animals are reared using a method known as least-squares. Eikje and Johnson (1979) discussed the merits of within flock/herd *v* standard correction procedures. This approach is always used for traits where standard adjustments are not appropriate, e.g. assessed carcass fat. In addition, deviations derived from either method are standardised so that variation in adjusted performance conforms to a standard appropriate for the trait to facilitate prediction of breeding values from more than one trait.

Prediction of Breeding Values

The basis of selection is the resemblance between relatives. The selection index approach (Hazel, 1943) is used in Animalplan to combine the relevant measured trait information on different types of relatives.

Animalplan allows for six different types of relative's information (referred to as kintype) for use in BV prediction of young replacements and these can be chosen by the breeder. The kintypes are -

I individual
PHS paternal half sibs
MHS maternal half sibs
FS full sibs
D dam of individual
P progeny of individual

For dam and sire summaries the kintypes are pre-set - a sire summary BV will generally be based on the progeny of that sire while for a dam, the lower number of progeny can be enhanced by inclusion of half sib information.

Relatives' records may be the only source of information when the individual concerned does not have a record or for a sex limited trait, e.g. assessing the fertility of flock/herd replacements using information on the dam. Similarly the BV for carcass weight could be predicted using the individual's own live weight and the carcass weight of half sibs. This last example shows that it is not necessary to be able to measure directly the various component traits in the objective.

As well as relatives' records, increased accuracy of prediction can be gained through correlated information on other traits, this is termed indirect selection. A genetic association arises between two traits when some of the individual genes that control expression of one trait also have some influence in the expression of the second trait.

The *predictor set* defines, for a particular objective, a list of traits that the breeder has measured that are used to predict the BV's of traits in the objective. The definition of predictor set also includes the type of relative each predictor trait refers to. For example, if we consider the breeding objective for sheep, referred to earlier, defined as

570 BV(NLB) + 27 BV(LW8) + 440 BV(FW12)

then a suitable predictor set for the selection of flock replacements, might be -

Predictor traits NLB LW8 LW8 FW12 FW12Relatives/kintype D I PHS I PHSCutoff 88 87 88 87 88

which includes NLB measured on the dam, LW8 and FW12 measured on the individual itself and the average LW8 and FW12 of paternal half sibs. In some circumstances it may be desirable to have relative's information included for more or fewer years than that comparable with the individual. The animal's dam will have had another opportunity to produce offspring by the time the animal is included on its final selection list. So the *cutoff* date for inclusion of the dam's fertility records is one year later than for inclusion of records on the animal itself. Similarly, for the paternal half sib average if the animal's sire was mated again in the year following the one in which the animal being evaluated was born. Once a cutoff date is specified Animalplan will include the appropriate records up to and including that birth/recording period.

Each row of Table 1 corresponds to a subset of the above predictor set, giving the accuracy of the prediction and the value of each component in the predictor in terms of its contribution to overall economic gain. If a predictor does not have an entry in the table in a given row then that predictor has not been included in that subset. It is assumed that the dam has 3 lambing records and that the paternal half sib averages contain 40 observations (not including the individual's own record).

TABLE 1 Selection index features for prediction of aggregate BV:
570 BV(NLB) + 27 BV(LW8) + 440 BV(FW12).

		Value of predictor			
Accuracy	NLB D_3	LW8 I	LW8 PHS_{40}	FW12 I	FW12 PHS_{40}
0.44	6	4		33	
0.51	5	2	2	15	7
0.47	5	2	7	28	
0.50	5	3		15	11
0.46	6		9	43	
0.42	7	17			30

I = individual's record
D_3 = three lambing records on dam
PHS_{40} = forty paternal half sibs
value = percent reduction in accuracy (overall economic gain) if the corresponding predictor information is not used.

Fleece weight contributes most to the prediction with the value of the paternal half sib average for fleece weight being around 7% to 11% depending on the inclusion of the corresponding information on live weight. The PHS information plays an even greater role if the corresponding trait information on the individual is missing.

Maternal Effects

Maternal effects refer to influence of the dam on the environment of her offspring. For example, the milking and mothering ability of the dam will have an effect on the growth and survival of her offspring. These maternal effects are environmental as far as the offspring is concerned but have a genetic component as far as the dam is concerned.

A path diagram (Fig. 1), with genetic relationships indicated by broken lines and genetic influence by solid lines, illustrates the situation where G_I denotes the direct genetic component for the expression of the individual's own genes on its performance (P_I) and G_M denotes the maternal genetic effect as expressed by the dam on the performance of its offspring. The path correlation coefficients are indicated where h_I and h_M are the square roots of the heritabilities for direct and maternal effects respectively, and r_{IM} is the correlation between them.

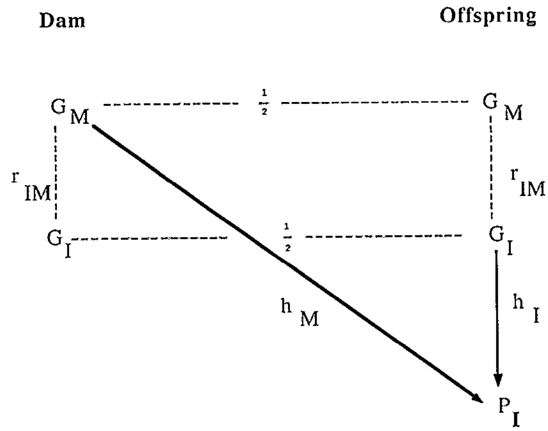

FIG. 1 Path diagram denoting direct genetic components and maternal genetic components of performance.

In Animalplan, BVs for direct and maternal effects can be estimated on most traits up to weaning. In dual-purpose breeds the flock/herd is maintained by rearing replacement females and selection for higher milk production and mothering ability will often be an objective. Hence, estimation of both G_M and G_I is necessary. The breeder will also need to specify REVs for the two components (usually an equal value for each component will be chosen). For terminal sire breeds, the daughters of the sire are not required for reproduction, hence the maternal breeding value is not relevant and it is the direct breeding value which is required.

For a breeding female the most important information for predicting maternal performance is provided by the performance of her progeny. For selecting flock/herd replacements the closest relative of relevance is the dam and so maternal half sib information (progeny of the dam) is important. Table 2 shows the importance of different relative's information for weaning weight (WWT) when predicting both the direct and maternal BV's for WWT, BV(WWT) and BV(WWTM).

The individual's own weaning weight together with the PHS average weaning weight play the dominant role for predicting BV(WWT) while for BV(WWTM) the ewe's progeny information is most important and to a lesser extent her MHS average weaning weight with the latter rising to

TABLE 2 Selection Index features for the prediction of direct (BV(WWT)) and maternal (BV(WWTM)) breeding values for weaning weight.

	Accuracy	Value of predictor			
		WWT I	WWT PHS_{20}	WWT $MHS_{5/4}$	WWT $P_{3/2}$
BV(WWT)	0.43	20	23	0	2
BV(WWTM)	0.61	0	1	6	44

I = individual's record
PHS_{20} = twenty paternal half sibs
$MHS_{5/4}$ = five maternal half sibs from 4 birth periods
$P_{3/2}$ = three progeny in 2 birth periods
value = percent reduction in accuracy (genetic gain) if the corresponding predictor information is not used.

prominence if no progeny information is available. The figures in Table 2 are only a guide as they will vary depending on the numbers of progeny and half sibs involved.

Genetic and Phenotypic Parameters

In Animalplan, breeding value calculations are based on parameter sets stored as part of the processing package for different species, breeds and traits. A typical sheep subset which contains the information used to derive the index features presented in the tables is shown in the appendix.

The parameter estimates in Animalplan will be updated regularly as new research information becomes available.

Data Export

Facilities are available in Animalplan for the breeder to export data for further statistical analysis, which may include -

(i) analyses to update the genetic parameters which form the basis of BV prediction
(ii) use of Best Linear Unbiased Prediction (BLUP), for example within flock/herd to estimate genetic trends or to allow comparisons among animals across flocks/herds such as in sire referencing
(iii) national 'on-farm' assessments of different breeds and crosses
(iv) evaluation of alternative breeding and management strategies or provision of industry statistics.

CONCLUSION

Animalplan is a flexible performance and pedigree recording system designed to meet the varied requirements of breeders of different animal species. The package is a powerful tool to

APPENDIX

Genetic and phenotypic parameters for dual-purpose sheep.

	NLB	WWT	WWTM	LW8	FW12	SD	t	c^2
NLB	**0.1**	0	0	0.1	0	0.57	0.15	0
WWT	0	**0.12**	-0.16	0.8	0.2	3kg	-	0.2
WWTM	-	-	**0.18**	0	0	-	-	-
LW8	0.05	0.8	-	**0.25**	0.25	3.5kg	-	0
FW12	0	0.3	-	0.35	**0.3**	0.45kg	-	0

Genetic correlations above diagonal, phenotypic below, heritabilities on diagonal
NLB = number of lambs born
WWT = weaning weight (individual)
WWTM = weaning weight (maternal)
LW8 = 8 month live weight
FW12 = 12 month fleece weight

SD = phenotypic standard deviation
t = repeatability
c^2 = proportion of environmental variation common to full sibs

assist breeders in identifying genetically superior animals, within their flocks or herds, accurately and efficiently.

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