SIMULATION OF SHEEP CROSSBREEDING SYSTEMS ¾ A RISK ANALYSIS

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SUMMARY

A static simulation study was performed to develop algorithms and a model for predicting crossbred performance. The model was built using @Risk software using quantitative risk analysis. Estimates of crossbreeding parameters were fitted with normal distribution functions as the model inputs. Sets of available population means were used as model target values. The standard deviations of the predicted means from the target values for all structured crossbreeding systems using up to 4 breeds were compared to predefined risk threshold criteria. This appeared to be a good approach to estimating robust, balanced trait parameters.

Keywords: crossbreeding parameters, simulation, risk analysis, probability distribution

INTRODUCTION

Prediction of crossbred performance is subject to the uncertainties of non-additive genetic variation, which results in performance prediction risk. This variation can only be estimated by carefully designed crossbreeding experiments (Garrick 2001).

A quantitative risk analysis approach (Vose 2000) was used, where uncertainties were quantified by probability distribution functions (Palisade 2002), based on the analyses of collated sheep crossbreeding parameter estimates (Wei *et al.* 2001). This paper briefly describes a simulation prediction of untested crossbred performance based on current crossbreeding theories.

MATERIALS AND METHODS

All published NZ data for weaning weight (WWT), litter size (LitSize) and loose wool bulk (Bulk), for Romney (Rom), Merino (Mer), Finn and Texel (Tex) breeds and their crosses were chosen to demonstrate the simulation algorithms.

Genetic model and design matrix. Direct and maternal additive breed effects as well as direct and maternal heterosis were assumed. A simple non-additive model was used, with dominance the only source of heterosis. 'Averaged' direct and maternal heterosis parameters for each trait were used (Kinghorn 1987;1997).

The model notation was:

$$\overline{G} = m + \sum_i \boldsymbol{a}_i ad_i + \sum_i \boldsymbol{a}_i am_i + \sum_{i<j} \boldsymbol{d}_{ij} dd + \sum_{i<j} \boldsymbol{d}_{ij} dm \qquad \text{(Equation 1)}$$

where $\sum_i \boldsymbol{a}_i = 1 \qquad \sum_{i \le j} \boldsymbol{d}_{ij} = 1 \qquad \sum_i ad_i = 0 \qquad \sum_i am_i = 0$

$\overline{G}$ =vector of mean values of each genotype in the given genetic group

m =general mean whose interpretation depends on the model used

$\boldsymbol{a}_i$ =proportion of genes from the ith source population in the genetic group

$\boldsymbol{d}_{ij}$ =probability that at a randomly chosen locus of a randomly chosen individual of the given genetic group, one allele is from the ith and the other allele from the jth source population

ad_i =additive direct effect of the ith source population

am_i =additive maternal effect of the ith source population

dd =averaged dominance direct effect

dm =averaged dominance maternal effect

The design matrix for a four-breed rotational or synthetic crosses assumed breeds were balanced at equilibrium.

Probability distributions. A normal distribution was assumed for all crossbreeding parameters. The available estimates of direct and maternal heterosis for each trait (Wei *et al.* 2001), were fitted as values drawn from normal distribution, using @Risk (Palisade 2002), where a risk quantifies the probability that a prediction can go beyond a target in this context. The **ad** value for each breed was added to **m** to provide breed **ad$_i$** normal distribution functions. Since there were generally less than five **am$_i$** estimates for each breed, the **am** distribution function was arbitrarily defined with reference to the available estimates with the sum of **am$_i$** effects set to zero. In each iteration, **m** was calculated as the average of the randomly sampled values from each **ad$_i$** function, and then subtracted from each **ad$_i$** sampled value, to give the input value for the ith source population to the model.

Simulation algorithm. For each trait simulation, distribution functions and relevant trait population means (Wei *et al.* 2001) were input into the genetic model for all structured crosses using up to 4 breeds. The population means were regarded as target values for corresponding genotypes. The maximum deviation (**MSD**) between the simulated means and target values were calculated and simulations stopped when **MSD** fell to a predefined arbitrary threshold level for WWT, LitSize and Bulk of 15%, 30% and 15% respectively. Other thresholds than **MSD** could have been used. Two thousand iterations were done in each run of the model using random samples from the distribution functions. The run outputs were evaluated by sensitivity analysis using @Risk®. The input functions were adjusted by changing the associated means and/or standard deviations until the **MSD** threshold or tolerance level was reached.
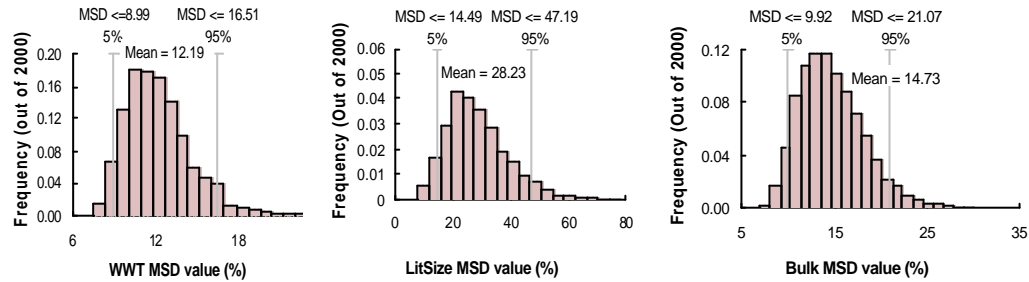
RESULTS AND DISCUSSION

The input distribution function for maternal heterosis for Bulk was not available (Table 1). All functions in Table 1 were assigned a minimum and maximum value to reflect the limits of biological performance.

Table 1. RiskNormal distribution functions (mean and standard deviation) used in the simulation models

	WWT (kg)	LitSize (lamb)	Bulk (cm³/g)
Direct heterosis	(1.84, 3.87)[1]	(-0.02, 0.17)[1]	(0.53, 3.03)
Maternal heterosis	(-0.27, 2.13)[1]	(0.08, 0.15)[1]	
additive direct			
Romney	(19.58, 1.89)	(1.53, 0.00)	(22.28, 1.09)
Texel	(28.28, 2.34)	(1.30, 0.00)	(30.16, 1.41)
Finn	(28.53, 0.00)	(2.10, 0.00)	(22.35, 0.00)
Merino	(20.54, 0.00)	(1.10, 0.00)	(27.16, 0.00)

[1]: Heterosis estimates from non-New Zealand sources were incorporated into the function definitions

Some functions (Table 1) had very small standard deviations (zero when only two decimal places were kept). This was because no additive maternal effect could have been estimated simultaneously with the additive direct effects due to insufficient input data of crossbred genotypes. The **MSD** histograms from the runs of 2000 iterations (Figure 1) show the distribution of different MSD values for each trait. The probabilities that MSD values can go beyond the thresholds, produced from the @Risk results for each trait, are: 12.2%, 37% and 42% for WWT, LitSize and Bulk respectively. These values could assist breeders to decide if crossbreeding decisions have a high element of risk in predicting performance from published information, eg. CrossSheep software (Cottle *et al.* 2001).

Figure 1. MSD histograms for traits (a) WWT (b) LitSize and (c) Bulk

Following the simulations, the means of each distribution function within each model were used to provide validated parameter point values (Table 2). These should be more robust and balanced for predicting crossbred performance across a wide range of crosses than those in Table 1, but were not necessarily the optimum solutions to the models, given that arbitrary adjustments of the input functions and only limited target data were used in the simulations.

Table 2. Validated crossbreeding parameters for WWT, LitSize and Bulk models

Model	m	ad$_1$	ad$_2$	ad$_3$	ad$_4$	am$_1$	am$_2$	am$_3$	am$_4$	dd	dm	MSD
WWT (kg)	24.50	-5.12	4.21	4.85	-3.95	0.73	-0.73	0.90	-0.91	2.12	0.84	9.58
LitSize (lamb)	1.50	0.06	-0.28	0.59	-0.36	-0.08	0.04	0.10	-0.05	-0.15	0.20[b]	6.28
Bulk (cm^3/g)	25.62	-2.62	4.15	-3.12	1.59	-1.99	1.70	-0.95	1.24	2.39	-0.58	9.42

[a]: subscript 1 =Romney, 2= Texel, 3= Finn, 4= Merino
[b]: Litsize **dm** value was unable to be tested as no relevant target value was available

The **MSD** point values for each model (Table 2) were calculated by the deterministic model when the parameter point values were used. These are lower than the corresponding MSD mean values in Figure 1 simply because those mean values were produced from simulation where randomly sampling were performed 2000 times. On completion of the simulation for different traits, it is easy to rank different crossbred genotypes on their aggregate economic returns using appropriate economic weights for each trait (Amer 2000), and the predicted merits for the genotypes. The ranking results should be useful to breeders for decision-making. This will be discussed in another paper.

The simulation algorithms and model appeared to be a practical, robust approach to the problem where crossbreeding trait parameter information is sparse (Wei *et al.* 2001). This approach showed promise by making full use of available NZ sheep crossbreeding data and incorporated genetic modelling and risk analysis technologies. It offers the flexibility of applying different target parameter values for specific environments. This study is not definitive and predictions will become more accurate when more data become available and as more sophisticated models are developed are developed.

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