

DYNAMIC SELECTION MODEL USING THE GENE FLOW METHOD

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SUMMARY

A dynamic selection model was developed extending the scope of the gene flow method in deterministic prediction of genetic response over time. The method depends on truncation selection across a series of groups, such as age groups, to determine the proportion to select from each group so as to maximize genetic change. A simple example is given to illustrate the method. Extensions to the method are being studied.

INTRODUCTION

Traditionally, Rendel and Robertson's (1950) equation has been used in comparison of breeding schemes to predict selection response. This equation estimates the asymptotic genetic response, assuming a constant breeding system such as constant selection intensity over generations. In practice, a population is composed of several groups, such as different age groups, with different genetic levels and variances due to genetic trend and selection. Selection is across these groups. Then, selection intensity within the group varies from generation to generation. As a consequence, the proportions of genes transmitted from each group also varies in subsequent generations. This dynamic selection process can be taken into account by the gene flow model. The objective of this study is to demonstrate how to use the gene flow method for dynamic selection across several groups.

METHODS

The algorithm of the dynamic selection model used here is similar to that of Ducrocq and Quaas (1988) but uses the gene flow matrix framework (Hill, 1974). A general situation is considered and a numerical example is presented. Definition of parameters, and of the variables used in the example are in Table 1. The equilibrium annual genetic gain is commonly expressed as: $G_a = (G_s + G_d) / (L_s + L_d)$, where G is a genetic superiority; L is the generation interval, and a , s , and d refer to individual, sire, and dam. Males and females can be divided into age groups (or other groups). Then, the proportion of genes transmitted from each group (p_i) can be calculated from the normal curve by numerical approximation (IMSL, 1984). Each p_i is computed for each time interval (year) and used in the transition probability matrix in the gene flow model. Let the gene flow model be (Jeon, et al, 1990): $M_t = T[M(t-1) + DG]$ ----- [1], where M_t is a vector of genetic means of animals at time t and for $M(t-1)$ at time $(t-1)$; T is a matrix of specifying the proportion of genes coming from each group and DG is a vector of genetic selection differentials for the groups. Expanding Equation [1] for the multiple ovulation and embryo transfer (MOET) example described below:

$$\begin{bmatrix} m0(t) \\ m1(t) \\ m2(t) \\ \text{-----} \\ f0(t) \\ f1(t) \\ f2(t) \\ f3(t) \end{bmatrix} = \begin{bmatrix} 0 & 0 & .5 & | & 0 & pd1 & pd2 & pd3 \\ 1 & 0 & 0 & | & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & | & 0 & 0 & 0 & 0 \\ \text{-----} \\ 0 & 0 & .5 & | & 0 & pd1 & pd2 & pd3 \\ 0 & 0 & 0 & | & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & | & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & | & 0 & 0 & 1 & 0 \end{bmatrix} \begin{bmatrix} m0(t-1) \\ m1(t-1) \\ m2(t-1) \\ \text{-----} \\ f0(t-1) \\ f1(t-1) \\ f2(t-1) \\ f3(t-1) \end{bmatrix} + \begin{bmatrix} DGm0 \\ DGm1 \\ DGm2 \\ \text{-----} \\ DGf0 \\ DGf1 \\ DGf2 \\ DGf3 \end{bmatrix} \quad [2]$$

where m, f refer to male and female, respectively; in row 1, .5 is the proportion of genes transmitted from sire to progeny; pd1, pd2, and pd3 are proportions of genes transmitted from selected females aged 1, 2, and 3 yr old, respectively; and the DG refers to the respective genetic selection differentials. The values of pd1, pd2, and pd3 depend on the genetic means and variances of the groups. The mean of the selected group of *i*th female age group is $f_i(t-1)$ plus its genetic selection differential of DGfi. For example, the genetic selection differential of 1 yr old breeding females, $DGf1 = i1.r1.\sigma_g$, where *i1*-selection intensity for 1; *r1*-accuracy of selection; σ_g -additive genetic SD. Then, *ij* is dependent on the common truncation point across all *j* groups. The truncation point varies depending on the variance of estimated breeding values in selection groups, which is due to the different amount of information available at selection, $r3 > r2 > r1$. Then,

$$P[\text{proportion selected}/x=z] = F1 \int_z^{\infty} f(x1) dx1 + F2 \int_z^{\infty} f(x2) dx2 + F3 \int_z^{\infty} f(x3) dx3 \quad [3]$$

where F_i is the proportion in each group. Here with 244 breeding females and survival of .8 across age groups, $F1=100/244$; $F2=80/244$; and $F3=64/244$. The common truncation point *z* in Equation [3] is found by an iterative method using the numerical integration of normal density function (IMSL, 1984). Then, *pdi* is evaluated, eg. $pd1 = .5(np1/nt)$, where *np1*-number selected from age group 1 (1 yr old); *nt*-total number selected from all age groups; and the sum of *pd1*, *pd2*, and *pd3* is .5. The selection intensity should be adjusted for the finite population size.

RESULTS

A simulation of the numerical example (Table 1.) is presented in Table 2. The average number of iterations to find the truncation point each year was about 17. Fluctuation in response occurred for about 15 years and then, the selection response reached an equilibrium state. The proportions of genes from each group reached an equilibrium state at the same time as the selection response. This study demonstrated the dynamic gene flow in transition probability matrix over the years can be taken into account. The model algorithm studied can be extended to other general situations.

DISCUSSION

Some authors, eg. Meuwissen (1989) suggest that the gene flow model is not suitable for predicting a dynamic selection system with variation in the

proportions selected from different age groups, and so varying generation intervals. By use of a common truncation level across groups, a dynamic gene flow model can be applied to deterministically optimize any breeding scheme. Effect of selection (linkage disequilibrium) and inbreeding also can be incorporated to improve the model predictions. Extensions to the method are being studied.

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Table 1. Definition of variables and parameters used in the numerical example.

Trait : milk yield
 Phenotypic SD : 1,500 kg
 Heritability (h^2) : .25
 Repeatability (r) : .50
 Conception rate (CR) : .70
 Survival rate (SR) : .80 (per yr)
 Breeding scheme : MOET breeding
 Mating ratio : 6 donors/sire
 Number of transferable embryos/donor : 5
 Population : a closed nucleus herd with MOET breeding scheme
 - no of females in i th age class (N_i) = $.8(N_{i-1})$, for $i=1$ to 4
 i.e., 125 (0 yr), 100 (1 yr), 80 (2 yr), and 64 (3 yr).
 - Selection candidates for donors = 1, 2, and 3 yr old females
 i.e., 72 females selected from 244 ($=100+80+64$) breeding females
 - Selection candidates for sire = 2 yr old males
 i.e., 12 males selected from 72 fullsib groups ($12 \times 6 = 72$)
 Selection method : truncation selection on selection index values
 Accuracy of selection :

	Age		
	1	2	3
Male :	-	.311	-
Female:	.282	.311	.609

Table 2. Proportions of genes transmitted from each age group and cumulative and annual genetic responses (kg/yr)

Time (year)	pd1	pd2	pd3	Cumulative response	Annual response
1	.178	.153	.169	338	338
2	.178	.153	.169	338	0
3	.354	.043	.103	430	91
4	.230	.193	.077	636	207
5	.229	.119	.152	696	59
6	.308	.086	.105	806	111
7	.246	.154	.100	960	154
8	.250	.118	.131	1049	89
9	.284	.107	.109	1165	116
10	.255	.136	.109	1297	132
11	.259	.119	.122	1400	103
12	.272	.116	.112	1517	117
13	.259	.128	.113	1640	122
14	.262	.120	.118	1750	110
15	.267	.119	.113	1867	117
16	.261	.125	.114	1985	119
17	.263	.121	.116	2099	113
18	.265	.121	.114	2215	117
19	.263	.123	.114	2332	117
20	.263	.121	.115	2447	115

pd1, pd2, and pd3 are proportions of genes transmitted from donors of 1, 2, and 3 age groups, respectively.