

LONG-TERM RESPONSE TO SELECTION WITH INBREEDING
IN ALTERNATE GENERATIONS

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SUMMARY

The rate of genetic progress in selecting for a character with female phenotypes only was studied using two single-locus deterministic models and one simulation model with 32 loci (two alleles with initial frequencies of 0.5 at each locus). There was random mating in all generations or random mating and full-sib mating in alternate generations among the selected individuals.

For deterministic models the saving of time due to inbreeding in reaching a given proportion of the maximum response (50, 75 and 90 %) was about 20-40 %, increasing with the degree of dominance and with the proportion of the maximum response. For simulation the corresponding saving of time was about 10-20 %. It was concluded that the models generally exaggerate the advantage from the inbreeding method in real populations, the success depending decisively on the genetic composition of the base population.

INTRODUCTION

In animal breeding it is a common procedure to use random mating or to avoid matings between close relatives among the individuals selected to produce the next generation. However, if only genetic variation and the response to selection are considered, it has been known for a long time that some form of inbreeding might be of use (e.g. Wright 1942, Lush 1945). For instance, full-sib mating and random mating (or outbreeding) in alternate generations has been proposed (Dickerson 1973, Dickerson and Lindh  1977). Recently, this kind of method has been studied in Japanese quail by MacNeil et al. (1984a,b), and in flour beetles by Dion and Minvielle (1985). They found no advantage of the inbreeding method to the total response to selection. The present study compares some results on the subject got by deterministic models with those of simulation for a character manifesting itself in one sex only.

METHODS

Deterministic course of selection at one locus.

Model 1. The frequencies and the relative fitnesses of the genotypes in an arbitrary inbred generation t-1 are (fitness values of males are approximate in the full-sib selection based on sisters):

Geno- type	Fre- quency	Fitness		Frequency in the selected group	
		Females	Males	Females	Males
A_1A_1	P_1	1	1	$P_{f1} = P_1 / \bar{W}_f$	$P_{m1} = P_1 / \bar{W}_m$
A_1A_2	P_2	1-hs	1-hsr	$P_{f2} = P_2(1-hs) / \bar{W}_f$	$P_{m2} = P_2(1-hsr) / \bar{W}_m$
A_2A_2	P_3	1-s	1-sr	$P_{f3} = P_3(1-s) / \bar{W}_f$	$P_{m3} = P_3(1-sr) / \bar{W}_m$

where $h=(1-d)/2$ (d is the degree of dominance in terms of Falconer (1981)), s is the coefficient of selection and r is the coefficient of relationship by Wright. \bar{W}_f and \bar{W}_m are the mean fitnesses of females and males, respectively. The coefficient r between full-sibs was assumed to be a constant of 0.6 because each inbred generation was produced by full-sib mating (in fact there will be a slight increase in r in the course of generations).

In random mating among the selected individuals of generation t-1 the frequencies of different mating combinations (MC) and the genotype distribution in the progeny population t are:

MC in generation t-1	Frequency	Genotype distribution in generation t
$A_1A_1 \times A_1A_2$	$Q_1 = P_{f1}P_{m2} + P_{f2}P_{m1}$	$1/2 A_1A_1 \quad 1/2 A_1A_2$
$A_1A_1 \times A_2A_2$	$Q_2 = P_{f1}P_{m3} + P_{f3}P_{m1}$	A_1A_2
$A_1A_2 \times A_2A_2$	$Q_3 = P_{f2}P_{m3} + P_{f3}P_{m2}$	$1/2 A_1A_2 \quad 1/2 A_2A_2$
$A_1A_1 \times A_1A_1$	$Q_4 = P_{f1}P_{m1}$	A_1A_1
$A_2A_2 \times A_2A_2$	$Q_5 = P_{f3}P_{m3}$	A_2A_2
$A_1A_2 \times A_1A_2$	$Q_6 = P_{f2}P_{m2}$	$1/4 A_1A_1 \quad 1/2 A_1A_2 \quad 1/4 A_2A_2$

In the selected female group of generation t the proportions of the progeny of different mating combinations and the gene frequencies are:

MC in generation t-1	Proportion of progeny in the selected females	Frequency of allele A_1 in the selected females
$A_1A_1 \times A_1A_2$	$Q_{f1} = Q_1(1-hs/2)/\bar{W}_f$	$p_{f1} = 1/2(1+(1-hs)/2)/(1-hs/2)$
$A_1A_1 \times A_2A_2$	$Q_{f2} = Q_2(1-hs)/\bar{W}_f$	$p_{f2} = 1/2$
$A_1A_2 \times A_2A_2$	$Q_{f3} = Q_3(1-s(h+1)/2)/\bar{W}_f$	$p_{f3} = 1/4(1-hs)/(1-s(h+1)/2)$
$A_1A_1 \times A_1A_1$	$Q_{f4} = Q_4/\bar{W}_f$	$p_{f4} = 1$
$A_2A_2 \times A_2A_2$	$Q_{f5} = Q_5(1-s)/\bar{W}_f$	$p_{f5} = 0$
$A_1A_2 \times A_1A_2$	$Q_{f6} = Q_6(1-s(h+1/2)/2)/\bar{W}_f$	$p_{f6} = 1/4(2-hs)/(1-s(h+1/2)/2)$

In the selected male group of generation t the corresponding frequencies of A_1 are: $p_{m1}=3/4$, $p_{m2}=1/2$, $p_{m3}=1/4$, $p_{m4}=1$, $p_{m5}=0$ and $p_{m6}=1/2$.

In the next generation t+1, after random mating within the six classes of the selected group of generation t (full-sib mating), the genotype frequencies are:

Genotype	Frequency
A_1A_1	$P_1 = Q_{f1}p_{f1}p_{m1} + Q_{f2}p_{f2}p_{m2} + Q_{f3}p_{f3}p_{m3} + Q_{f4} + Q_{f6}p_{f6}p_{m6}$
A_1A_2	$P_2 = Q_{f1}((1-p_{f1})p_{m1} + p_{f1}(1-p_{m1})) + Q_{f2}((1-p_{f2})p_{m2} + p_{f2}(1-p_{m2})) + Q_{f3}((1-p_{f3})p_{m3} + p_{f3}(1-p_{m3})) + Q_{f6}((1-p_{f6})p_{m6} + p_{f6}(1-p_{m6}))$
A_2A_2	$P_3 = Q_{f1}(1-p_{f1})(1-p_{m1}) + Q_{f2}(1-p_{f2})(1-p_{m2}) + Q_{f3}(1-p_{f3})(1-p_{m3}) + Q_{f5} + Q_{f6}(1-p_{f6})(1-p_{m6})$

After this the calculation was continued as in generation t-1. In each generation the frequency of allele A_1 was calculated from genotype frequencies. The departure from Hardy-Weinberg proportions (F) was also calculated from genotype frequencies.

Model 2. In any generation the genotype frequencies and the relative fitnesses are:

Genotype	Frequency	Fitness of females
A_1A_1	$P_1 = p_f p_m (1-F) + pF$	1
A_1A_2	$P_2 = (p_f(1-p_m) + (1-p_f)p_m)(1-F)$	1-hs
A_2A_2	$P_3 = (1-p_f)(1-p_m)(1-F) + (1-p)F$	1-s

where p_f and p_m are the frequencies of allele A_1 among the selected females and

males of the previous generation respectively, and $p=(p_f+p_m)/2$.

The difference in the frequency of allele A_1 between the selected female group and the unselected population (Δp_f) is $(P_1+P_2(1-hs)/2)/\bar{W}_f-p$. The corresponding difference with respect to males in full-sib selection (Δp_m) is assumed to be $r\Delta p_f$. In the progeny population the frequency of A_1 is $p+(\Delta p_f+\Delta p_m)/2$. In inbred generations F and r were assumed to be 0.25 and 0.60 respectively, in other generations values of 0.0 and 0.5 were used.

In calculating results for models 1 and 2 there was no selection among males in generation 0 because the initial relationships were assumed to be unknown. In generation 0 the population was in Hardy-Weinberg equilibrium for an initial gene frequency of 0.5. In even generations there was random mating, otherwise full-sib mating (except for the case with random mating in all generations).

Simulation.

The method of simulation was as outlined in previous studies (Sirkkomaa and Maijala 1980, Sirkkomaa 1984). The character selected for was determined by 32 equivalent, practically unlinked loci which were initially in Hardy-Weinberg and linkage equilibrium. In generation 0 the phenotypic variance was 49.0. The initial heritability in the narrow sense was 0.075 or 0.250.

Females were selected by using phenotypic values. The males chosen to breed were full-brothers of the selected females, taken from the relevant sibships as evenly as possible. For maximizing the ultimate response half the population was selected in each generation ($(100\sigma+100\phi)/400$). In generation 0 males were not selected. In alternate generations full-sib mating was avoided and favoured as completely as possible. A male could mate with several females due to the random drawing of males for mating pairs.

RESULTS AND DISCUSSION

For a weak selection ($s=0.02$) the rate of change in the departure from Hardy-Weinberg proportions (F) was very similar to the case of a neutral locus (Table 1). During the first 20 generations only a minor increase in the frequency of the favourable allele was obtained (about 0.045). For the higher coefficients of selection the rise in gene frequency was considerably larger than that for the weak selection, being about 0.338 for $s=0.20$. The rise in F was lower for the strong selection than that for the weak one (Table 1).

A general observation from Table 1 is that for a weak selection F is about 1/3 in inbred generations almost all the time during which p changes from its initial value towards 1. For a strong selection F in inbred generations is clearly below 1/3 most of the time of gene frequency change. Thus, the weaker

Table 1. The departure from Hardy-Weinberg proportions (F) and the frequency of the favourable allele (p). The coefficient of selection is s. The degree of dominance over the unfavourable allele is 0.5. In generation 0 p was 0.5. In odd generations there was full-sib mating, otherwise random mating

s		Inbred generation (model 1)					
		2	4	6	8	10	20
.00	F	.250	.313	.328	.332	.333	.333
.02	F	.249	.311	.326	.330	.331	.332
	p	.503	.508	.512	.517	.522	.545
.11	F	.244	.303	.318	.321	.322	.322
	p	.518	.543	.568	.593	.617	.720
.20	F	.238	.294	.307	.310	.311	.313
	p	.533	.579	.623	.664	.701	.838

Table 2. The number of generations (G) needed to attain a given frequency of the favourable allele and the decrease in time due to full-sib mating (D) for deterministic models with various degrees of dominance (d) and coefficients of selection (s). The relative deviations from the results of simulation (Table 3) are also given (RD). The initial frequency of the favourable allele was 0.5. A: random mating in all generations; B: random mating and full-sib mating in alternate generations (B_1 = model 1, B_2 = model 2)

		Frequency of the favourable allele									
		0.750			0.875			0.950			
s	d	G	D(%)	RD(%)	G	D(%)	RD(%)	G	D(%)	RD(%)	
.02	.2	B_1	121	21.4		218	23.0		337	23.8	
		B_2	131	14.9		238	15.9		368	16.7	
		A^2	154			283			442		
	.5	B_1	129	23.7		244	27.2		394	30.0	
		B_2	140	17.2		268	20.0		436	22.6	
		A^2	169			335			563		
	.8	B_1	138	27.0		279	33.9		482	41.6	
		B_2	151	20.1		311	26.3		547	33.8	
		A^2	189			422			826		
.11	.2	B_1	22	21.4	-21.4	40	21.6	-20.0	61	22.8	-20.8
		B_2	24	14.3	-14.3	43	15.7	-14.0	66	16.5	-14.3
		A^2	28		- 9.7	51		-12.1	79		-13.2
	.5	B_1	24	22.6	-17.2	45	25.0	-16.7	71	29.7	-16.5
		B_2	25	19.4	-13.8	48	20.0	-11.1	78	22.8	- 8.2
		A^2	31		- 6.1	60		- 7.7	101		- 1.9
	.8	B_1	26	23.5	-10.3	51	32.9	-15.0	88	40.9	-10.2
		B_2	27	20.6	- 6.9	56	26.3	- 6.7	98	34.2	0.0
		A^2	34		- 8.1	76		+ 1.3	149		+21.1
.20	.2	B_1	13	13.3	-18.8	22	18.5	-21.4	33	23.3	-21.4
		B_2	13	13.3	-18.8	23	14.8	-17.9	35	18.6	-16.7
		A^2	15		-16.7	27		-12.9	43		- 6.5
	.5	B_1	13	23.5	-23.5	25	24.2	-16.7	39	29.1	-15.2
		B_2	14	17.6	-17.6	26	21.2	-13.3	43	21.8	- 6.5
		A^2	17		-10.5	33		- 5.7	55		+ 1.9
	.8	B_1	15	21.1	-16.7	29	29.3	-14.7	49	39.5	- 9.3
		B_2	15	21.1	-16.7	31	24.4	- 8.8	53	34.6	- 1.9
		A^2	19		- 5.0	41		+ 5.1	81		+20.9

the selection, the larger the advantage from inbreeding to the rate of response might be with respect to random mating in all generations. In general, this reasoning seems to be true in comparing the D values of different strengths of selection within the degrees of dominance (model 1, Table 2), but the differences are not large.

The approximate coefficients of selection at individual loci in simulation (Table 3) were calculated in the common way (e.g. Falconer 1981, p. 186). In general, the progress in gene frequency for the deterministic models was more rapid than that for simulation (RD, Table 2). The deviations from the results of simulation were lowest for random mating, except in the case of long-term response for a degree of dominance of 0.8. The results for model 2 were closer to simulation than those for model 1 (Table 2). The change of F given by model 1 would be realized only in a very large population.

Table 3. The number of generations (G) needed to attain a given mean frequency of the favourable allele at 32 loci and the decrease in time due to full-sib mating (D), results averaged from 50 replicate runs of simulation. The initial frequency of the favourable allele at each locus was 0.5. The proportion selected was $(100\sigma + 100\phi)/400$ in each generation.

d: degree of dominance; h^2 : initial heritability; s: coefficient of selection at each locus (approximately)

A: avoiding full-sib mating in all generations

B: avoiding and favouring full-sib mating in alternate generations

h^2	d	Frequency of the favourable allele						
		0.750		0.875		0.950		
		G	D(%)	G	D(%)	G	D(%)	
.075 ($s \approx 0.11$)	.2	B	28	9.7	50	13.8	77	15.4
		A	31		58		91	
	.5	B	29	12.1	54	16.9	85	17.5
		A	33		65		103	
	.8	B	29	21.6	60	20.0	98	20.3
		A	37		75		123	
.250 ($s \approx 0.20$)	.2	B	16	11.1	28	9.7	42	8.7
		A	18		31		46	
	.5	B	17	10.5	30	14.3	46	14.8
		A	19		35		54	
	.8	B	18	10.0	34	12.8	54	19.4
		A	20		39		67	

An explanation for the discrepancies in G between the calculated and simulated results is, of course, the finite population size existing in simulation. It was calculated in an earlier study (Sirkkoma 1984) that in the present simulation model the effective population size in random mating and with no selection would be about 134 for a parental group of $100\sigma + 100\phi$, since the number of gametes contributed per male to the breeding group of the next generation is not binomially distributed. In selection the effective size becomes still smaller (Robertson 1961). In addition, the decrease of effective size in the present simulation is pronounced because the breeding male group is chosen on the basis of relationship with the selected females. The random sampling effect is also increased because of the use of full-sib mating in the inbreeding method. In a simulation experiment using the present model for a population structure of $(10\sigma + 10\phi)/60$ without selection, the mean time until the fixation of either one of the two alleles at all of the 32 loci (initial gene frequencies 0.5) was in mating B about 12 % lower than that in mating A (the average result from 200 replicate runs).

In simulation the coefficient of selection (s) is not a constant over generations because of the random fluctuation in the number of measured individuals (on an average 200 females in each generation) and in the phenotypic variance. In the long term s will change due to the decrease in the phenotypic variance. The average response at several loci cannot be equal to the response at one locus, even in the absence of linkage and epistasis.

The saving of time due to inbreeding in reaching a given gene frequency is about 20-40 % for the single-locus deterministic models (D, Table 2) and about 10-20 % for simulation (D, Table 3). On the basis of the calculated models, in attaining a given response the saving of time due to inbreeding should increase with an increasing degree of dominance and with an increasing magnitude in the response (Table 2). Thus, the advantage from inbreeding should be largest for

a degree of dominance of 0.8 in the long-term selection. In general, these predictions are seen in the results of simulation (Table 3). However, there are exceptions from these rules (mainly in the stronger selection). The advantage from inbreeding should be somewhat larger for a weak selection than for a strong one (Table 2). This rule is striking in the results of simulation, with one exception (Table 3).

In the real populations with inbreeding there is usually a decline in the characters concerning fertility and viability, due to increasing homozygosity at all loci. The magnitude of this decline is not predictable in detail, but it depends decisively on dominance relations at loci and on the genetic composition of the base population. All kind of deterioration must have its effects on the efficacy of selection for any trait and on the effective population size. In the experiments of MacNeil et al. (1984a,b) and of Dion and Minvielle (1985) there was no advantage from alternate full-sib mating to the total response. However, these were short-term experiments of 15-17 generations. In the present simulation the responses at generation 20 of the inbreeding method for initial heritabilities of 0.075 and 0.250 were 8-20 % and 9-10 % larger than those of random mating, respectively (depending on the degree of dominance).

It is clear that the results given by most models exaggerate the advantage of inbreeding to the selection response because all the genetic complexity cannot be concerned in affecting them.

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