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The Role of Finite Population Size and Linkage in Response to Continued Truncation Selection

I. Additive Gene Action[1]

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Summary. In an attempt to analyse long-term response in finite dioecious populations, selection processes are simulated on a computer with situations of parental population size, linkages between loci, selection intensity, and heritability, specified in a 3^4 factorial design. A diploid polygenic system of 40 loci on 4 chromosomes is considered for additive genes. Linkage levels are specified as free recombinations, adjacent loci 5 map units apart, and as clusters on chromosomes with a distance of only .5 units between adjacent loci. Parental populations of 8, 16, and 64, truncation selection of 1/2, 1/4, and 1/8 of the progeny each generation, and initial heritability of 1, 1/3, and 1/9 are simulated for various populations.

For these populations, which are initially samples from a theoretical HARDY-WEINBERG situation, it is shown that an initial linear phase of response, which may last for only 2 or 3 generations in some cases, depends on the intensity of selection alone. The effects and interactions of all the above factors on the curvilinearity of response in later generations are analysed. It appears that linkages between loci have a strong influence in reducing the rate of response and the total response. In the extreme cases of gene clusters in a parental population size of 8 with low heritability, truncation selection is relatively almost completely ineffective in causing change in the mean over generations. The effect of tight linkage is also exhibited in causing more reduction in genotypic variance than can be accounted for by corresponding response.

The depressing effect of finiteness of population size on the rate of response and the total response appears to increase in geometric proportion with linkages between loci. The number of generations to fixation appears to be reduced in a similar manner. A strong interaction between population size and linkage is thereby found in various analyses. With parental populations as large as 64, linkage effects on response are negligible when recombinations between adjacent loci are .05 or more. In such situations there is a slower rate of response in later generations with linkage but the total response attained and the rate of fixation of inferior genes is about the same as for free recombinations. Increase in the intensity of selection appears to augment the effects of linkage in reducing the rate of response in later generations. This type of interaction is attributed to the accumulation of gametic disequilibria due to selection which are retained in the population over generations with linkage.

I. Introduction

To give the background and motivation for the studies described in this paper, it is necessary to review briefly the overall status of the theory of genetic selection. The separate directions of past study appear to be the following:

(a) Classical selection theory, as exemplified by the work of HALDANE (1925–27): In this development, population size is taken to be infinite and selective values of genotypes are generally taken to be constant throughout the progress of the population. This is essentially a single-locus theory. Later infinite population work has dealt with equilibria of two-locus systems (e.g., BODMER and FELSENSTEIN, 1967; LEWONTIN and KOJIMA, 1960).

(b) Finite population analogues to the work indicated in (a): This approach is to use probability transition matrices and, because these are in general unworkable, to turn to a continuization of the stochastic process in the form of differential equations. This line of work dates back to FISHER and WRIGHT, and has been pursued extensively by KIMURA. Reviews on these are given by MORAN (1962) and KIMURA (1964). By and large, the development has been made for the case of one locus. The arguments are essentially haploid, as indicated clearly by MORAN (1962). In these models, selection is weak and the selective values of gametes or genotypes are independent of the structure of the population and remain constant, i.e., independent of gene frequencies.

(c) Quantitative genetic selection along the lines of theoretical quantitative genetics initiated by FISHER (1918). The description of this by GRIFFING (1960) incorporates truncation selection and mating in which the selective value of a genotype is considered explicitly. This theory is possible to the present time only for weak selection over a period of time for which the statistical properties of the genetic population do not change and is thus valuable only for a few generations unless selection is very weak. LATTER (1965) has pointed out that the approximations followed in the development of this theory may lead to noticeable errors in the prediction of response in the case of genes of large effects, especially with strong selection. Moreover, this development

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is confined to the case of infinite populations so that the expected types and proportions of types selected are achieved, and the progeny of matings follow Mendelian expectations exactly. In recent years, the ideas categorized in (b) have been used to develop a theory of limits for quantitative selection in finite populations (ROBERTSON, 1960). This obviously combines the corresponding strengths and weaknesses of both the approaches.

In view of the above, we considered that an attempt should be made to obtain some understanding of selection in a polygenic system (which should really be termed poly-locus, multi-locus or some such term). We were particularly interested in the case of truncation selection based on phenotype, in finite populations with many loci some of which exhibit linkage. The aim is to form ideas regarding response to selection under these complex situations. A mathematical treatment of the problem is essentially impossible. The selection process is a stochastic process, but the incorporation of matings and selection is very difficult. A natural alternative is to use simulation on an electronic computer using Monte Carlo methods as first used in selection theory by FRASER (1957).

Monte Carlo work on similar lines by MARTIN and COCKERHAM (1960), FRASER (1960), and GILL (1965a, b) has provided general ideas on long-term genetic advance in polygenic situations. In the present study of a 40-locus system, selection processes are simulated with various levels of parental population size, selection intensity, and linkage so that the effects and interactions of these factors are investigated through comparisons. Parts of the results of this paper are from reports presented earlier in duplicated form (QURESHI, 1963; KEMPTHORNE and HAZEL, 1967).

II. Simulation Procedure

The Monte Carlo approach followed in this study is that of directly simulating on a decimal computer (IBM-7074), the processes of random mating, gamete formation, genotypic evaluation and truncation selection. The probabilistic events of the Mendelian mechanism are simulated with the help of uniformly distributed random numbers, $0 < u_i < 1$, generated as power residues by a properly defined congruence according to the requirements of the computer. An event with a given probability, say π, occurs if u is less than or equal to π. The genotypes are generated in the computer by representing each locus by a digit and a chromosome by a ten-digit machine storage word. The identification of genotypic arrays thereby conforms to the arrays in programming language. The i-th parental genotype randomly selected to produce a random gamete for progeny genotypes is determined as $i = N_s\, u$, where N_s is the number of male or female parents selected. If i is not an integer, the next higher integer is taken as i.

The formation of a random gamete from the genotype of a parent becomes a simple operation of performing a random walk along the stretch of the homologous chromosomes, if the recombination values are specified between adjacent loci. One can thereby calculate the probable recombination value between any two loci in the genotype. If r is the recombination value between all adjacent pairs of loci on a chromosome and if the cross-overs occur independently of each other, $[r + (l - r)]^k$ generates the frequencies of cross-overs and no-cross-overs on k recombination sites between locus i and locus j on a chromosome. Then the expected recombination value between genes A_i and B_j is

$$r_k = \sum_{\lambda=0}^{k} \binom{k}{k-\lambda} r^{k-\lambda} (1-r)^{\lambda}\,; \qquad (1)$$
$$(k - \lambda) = 1 \bmod (2)$$

since cross-overs at odd numbers of recombination sites between A, B, results in the production of a recombinant type gamete $A_i' B_j'$.

When we consider n loci each on m chromosomes, the average recombination value between random pairs of loci on a chromosome is

$$\bar{r}_c = 2/n\,(n-1) \sum_{k=1}^{n-1} (n-k)\, r_k\,, \qquad (2)$$

since there are $n\,(n-1)/2$ possible pairs of loci on a chromosome and the number of pairs of loci which are k recombination sites apart on the same chromosome is $n - k$. Similarly there are $n\,m\,(n\,m-1)/2$ possible pairs of loci in the genotype, $n^2\,m\,(m-1)/2$ of which are pairs with loci on different chromosomes. Hence, the average recombination value between any random pair of loci in the genotype is

$$\bar{r} = [2\,(n-1)\,\bar{r}_c + n\,(m-1)]/2\,(n\,m-1)\,. \qquad (3)$$

Symmetric models of gene action are well suited to the case of evaluation of genotypes in simulation studies. When the frequency and contribution to the genotypic value of the desirable or 'plus' gene at each locus is assumed to be similar, the genotypic value (g) can be expressed as a function of $--$, $+-$, and $++$ phases in the genotype. For the additive model of this study

$$g = n_1 + 2\,n_2 \qquad (4)$$

where n_1 is the number of $+-$ phases and n_2 is the number of $++$ phases in the genotype. By designating the $+$ allele by 1 and $-$ allele by 0 in the computer, a simple arithmetic addition of the two homologous chromosomes identifies the above phases in the genotypes.

The environmental component of the phenotype simulated in this study is independent of the genotype and is constant over generations. It is assumed to be normally distributed with zero mean and variance σ_e^2. σ_e^2 is specified in terms of heritability in the initial generation which is defined as $h_0^2 = \sigma_{g_0}^2/(\sigma_{g_0}^2 + \sigma_e^2)$, where $\sigma_{g_0}^2$ is the expected genotypic variance in the initial generation. The phenotypic value of an individual is therefore computed as $P = g + \sigma_e\, d$, where d is a normally distributed variable with zero mean and unit variance. The d_i are generated on the computer by the following transformation of u_i, as given by BOX and MULLER (1958):

$$d_1 = (-2 \log_e u_1)^{1/2} \cos 2\pi\, u_2\,,$$
$$d_2 = (-2 \log_e u_1)^{1/2} \sin 2\pi\, u_2\,.$$

III. The Populations Simulated

An equal number of diploid individuals of each sex are simulated and mating is random in the sense that parents are sampled with equal probability with replacement. The genotypes consist of 40 loci

located on four chromosomes, each with 10 loci. Two alleles are identified at each locus. The initial population is generated by random mating $N/2$ parents of each sex that are heterozygous at all loci. The plus and minus genes are assigned to these parental genotypes with equal probabilities and at random on a chromosome. The expected frequencies of coupling and repulsion phases in the initial population are therefore equal. A mean gene frequency of .5 is simulated in the initial population and this is a special case from the point of view of variance and chance of fixation of genes. For the additive model, the genotypic variance is maximum at this point and decreases with increasing gene frequency. If selection pressure is not very low, the chance of fixation of a plus gene with initial frequency of .5 is high for a parental population size of 8 or more. The number of the progeny produced in each generation is $N/2\,b$ in each sex, while $N/2$ parents of each sex or an upper fraction b of the progeny is selected on the basis of their phenotypic values.

All possible combinations of the following 3 levels each of size of parental population (N), recombination value between adjacent loci (r), fraction of progeny selected to be parents (b), and heritability in the initial generation (h_0^2) were simulated in 81 types of populations so that interactions between these factors could be examined.

$$N = 8,\ 16,\ 64$$
$$r = .005,\ .05,\ .5$$
$$b = 1/2,\ 1/4,\ 1/8$$
$$h_0^2 = 1/9,\ 1/3,\ 1$$

Four replications each were obtained for the 27 treatment combinations in the case of perfect heritability and two replications for each of the remaining 54 treatment combinations. For each run the selection process was continued for 30 generations, or less if fixation at all loci occurred earlier. For reasons of computer time involved, every population could not be followed to complete fixation. In a test run it took 140 generations to cause fixation at 38 out of 40 loci when the levels of N, r, b, and h_0^2 were 64, .5, 1/2, and 1/9, respectively. In the case of perfect heritability, fixation was always reached in less than 30 generations. Hence, total response and generation required to attain total response were studied for this case.

The levels of the factors specified are arbitrary and cover a large range of situations. They are chosen to obtain effects and interactions within these ranges of factorial values. The levels of N range from fairly rapid to very slow rates of inbreeding. The intensity of selection pressure may be assessed in terms of $\bar{\imath}\,h_0^2$ where $\bar{\imath}$ is the selection differential in standard units calculated from b on the assumption of normal distribution of phenotypes. For the levels of b and h_0^2 specified, $\bar{\imath}\,h_0^2$ ranges from .09 to 1.65 standard deviations as shown:

	$h_0^2 = 1/9$	1/3	1
$b = 1/2$	.09	.26	.79
1/4	.14	.42	1.27
1/8	.18	.55	1.65

Since σ_e^2 is simulated in terms of h_0^2 and is constant in succeeding generations, the heritability in succeeding generations will decrease with decrease in the genotypic variance. The following HARDY-WEINBERG expectation of h^2 for different values of gene frequency (p) and constant σ_e^2, may give some idea of the expected decrease with increasing p, ignoring the effects of N, r, and b.

p	$h_0^2 = .333$	$h_0^2 = .111$
.5	.333	.111
.6	.324	.107
.7	.296	.095
.8	.242	.074
.9	.153	.043

The role of environmental variance simulated is to reduce α/σ and thereby make selection pressure milder.

Close linkages between adjacent loci are specified for comparison with free recombinations. In a previous study, GILL (1965b) has shown that for non-epistatic models, appreciable linkage effects on response are found only when r is specified as .05 or less. In the genetic system of 4 chromosomes each with 10 loci, a variety of recombination values between various pairs of loci exist. With the specification of r equal to .005 and .05, the following values of certain recombination values defined in equations (1), (2) and (3) are calculated which may provide some idea of the linkage relationships in the genome.

	r_k	$\bar{r}_c$	$\bar{r}$
$r = .005$	.005 to .043	.018	.389
$r = .05$	.05 to .306	.151	.420

These values will, of course, be realized in very large populations. With r equal to .005, a situation simulating a gene cluster on each chromosome, there is very little chance of recombinations within a chromosome, but there is, of course, free recombination between chromosomes.

IV. Results

We denote the genotypic mean and genotypic variance in generation t, respectively as m_t and V_t, $(t = 0, 1, \ldots, T)$, where T is the number of generations to fixation at all loci. m_0 and V_0 are the mean and variance of the base population before selection, which are similar for all the populations simulated. The maximum value that m_t can attain, denoted by $m_{\max}$, is realized only when plus alleles are fixed at all the loci. We define response relative to $m_{\max}$ such that

$$R_t = \frac{m_t - m_0}{m_{\max} - m_0} \times 100; \quad t = 0, 1, \ldots, T. \qquad (5)$$

In attempts to describe the rate of change in genotypic mean over generations, it appeared that m_t was adequately represented by the following relationship.

$$m_t = \beta_0 + \beta_1 t + \beta_2 t^2 + \text{error}. \qquad (6)$$

With this representation, β_0 is the population mean in generation 0, β_1 is the initial rate of response, and β_2 a measure of curvature of response. Fitting of exponential functions were also tried but estimates of parameters in these failed to describe the observed response curves adequately. In some cases com-

parisons of the estimates β_1 and β_2 were found to be easier than the graphic comparisons of the response curves in describing the various effects and interactions on the rates of response. In some other cases, especially in the case of tight linkage, irregular estimates with large errors are not very useful for the purpose. It is interesting to note that there is a close relation between the estimates $\hat{\beta}_1$ and $\hat{\beta}_2$. They need to be examined together for the sake of comparisons. That there should be some dependence of $\hat{\beta}_2$ on $\hat{\beta}_1$ is not surprising because the larger $\hat{\beta}_1$ is, the greater the initial progress and therefore the greater the curvature. The occurrence of this relationship suggests that some other functional form involving only one parameter is possible, but the data are not adequate to give strong suggestions

Table 1. *Mean squares obtained from the analysis of variance of genotypic means in two replications*

Source of variation	d.f.	generation 1	generation 5	generation 15	generation 25
N	2	4.6	172**	1188**	1948**
r	2	4.5	275**	2894**	4304**
b	2	61.1**	502**	945**	697**
h^2	2	189.9**	1409**	2739**	1737**
Nxr	4	12.3*	35.2*	84.9**	113.1**
Nxb	4	3.5	9.5	10.4	14.6
Nxh^2	4	8.9	8.9	15.1	33.2*
rxb	4	1.4	37.9**	46.3**	30.7*
rxh^2	4	13.8*	25.2	91.3**	48.8**
bxh^2	4	7.9	35.1*	9.6	31.8*
$Nxrxb$	8	2.1	2.7	4.9	10.5
$Nxrxh^2$	8	5.3	13.1	20.5*	20.7
$Nxbxh^2$	8	3.1	7.9	19.2	24.3*
$rxbxh^2$	8	4.0	5.0	37.0**	53.0**
$Nxrxbxh^2$	16	4.6	21.3*	30.9**	31.3**
Error	81	3.4	11.1	9.6	12.1

*, ** significant at 5% and 1% level respectively.

Table 2. $\hat{\beta}_1$, $\hat{\beta}_2$, T, *and* R_T *averaged over four replications, for the various conditions of* N, r, *and* b *in the case of perfect heritability*

		$r = .005$			$r = .05$			$r = .5$		
$b =$		1/2	1/4	1/8	1/2	1/4	1/8	1/2	1/4	1/8
$N = 8$										
	$\hat{\beta}_1$	4.3	8.0	4.8	2.3	3.9	4.7	2.9	5.2	6.3
	$\hat{\beta}_2$	-.38	-.87	-.28	-.06	-.12	-.17	-.06	-.17	-.24
	T	10	6	9	23	15	13	22	14	12
	R_T	28	31	40	63	70	68	85	91	89
$N = 16$										
	$\hat{\beta}_1$	2.5	5.4	5.8	2.7	3.8	5.2	3.3	5.5	7.1
	$\hat{\beta}_2$	-.13	-.43	-.44	-.06	-.10	-.19	-.06	-.17	-.28
	T	14	8	9	27	16	15	22	15	13
	R_T	28	41	39	79	79	84	93	96	95
$N = 64$										
	$\hat{\beta}_1$	1.8	3.5	3.9	2.8	4.9	5.9	3.3	5.4	7.4
	$\hat{\beta}_2$	-.04	-.12	-.14	-.05	-.20	-.04	-.06	-.16	-.29
	T	23	18	17	26	16	14	22	19	11
	R_T	53	70	75	98	96	98	99	95	99

Table 3. $\hat{\beta}_1$ *and* $\hat{\beta}_2$ *averaged over two replications for the various conditions of* N, r, *and* b *in the case of low heritabilities*

		$r = .005$			$r = .05$			$r = .5$		
		$N = 8$	$N = 16$	$N = 64$	$N = 8$	$N = 16$	$N = 64$	$N = 8$	$N = 16$	$N = 64$
1/3	1/2	.7	1.7	1.8	1.7	.9	2.1	.3	1.6	1.9
		-.10	-.07	-.04	-.07	-.01	-.04	-.0	-.02	-.02
	1/4	5.4	1.9	1.2	1.3	1.9	2.6	2.5	2.2	2.9
		-.57	-.08	-.02	-.03	-.04	-.05	-.04	-.04	-.05
	1/8	2.7	1.9	1.7	1.5	1.9	2.7	2.9	3.2	3.4
		-.25	-.06	-.03	-.04	-.04	-.05	-.06	-.07	-.07
1/9	1/2	.9	1.4	.9	.8	1.2	1.4	1.0	.9	1.2
		-.11	-.04	-.01	-.02	-.02	-.02	-.02	-.01	-.01
	1/4	1.9	.2	1.7	1.5	1.3	1.8	1.6	1.7	2.1
		-.11	-.0	-.03	-.03	-.02	-.03	-.03	-.02	-.03
	1/8	.6	2.1	1.5	4.9	1.8	2.3	1.9	2.1	2.3
		-.09	-.08	-.02	-.02	-.03	-.03	-.04	-.03	-.04

Negative values are of $\hat{\beta}_2$.

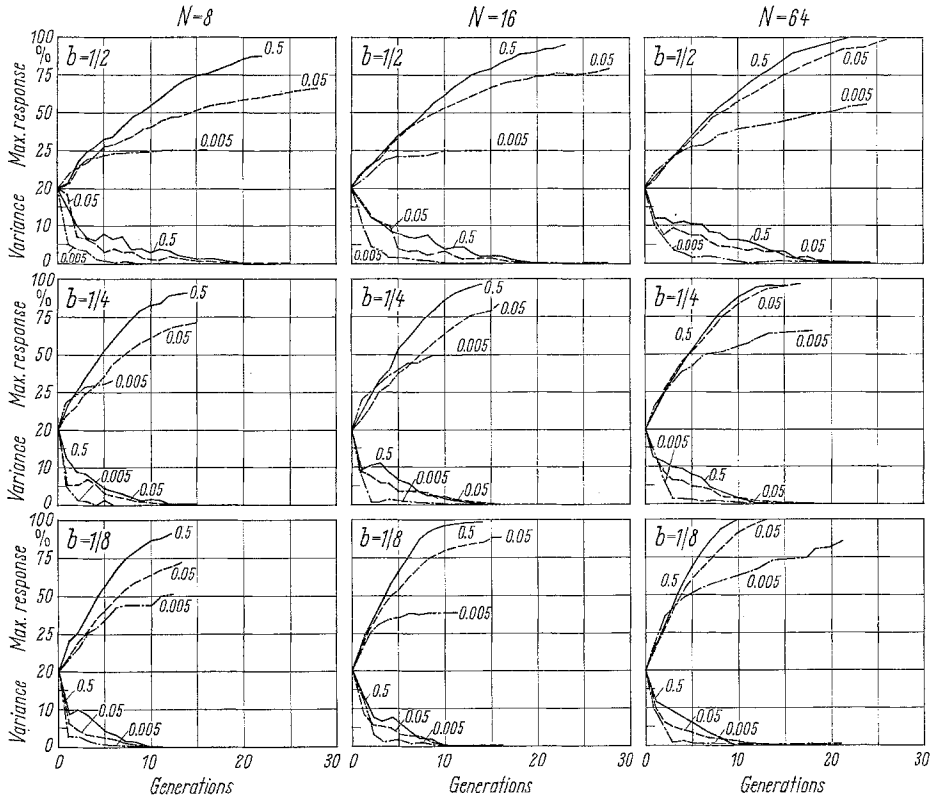

Fig. 1. R_t and V_t under various situations of N, b, and r in the case of perfect heritability; averaged over four replications

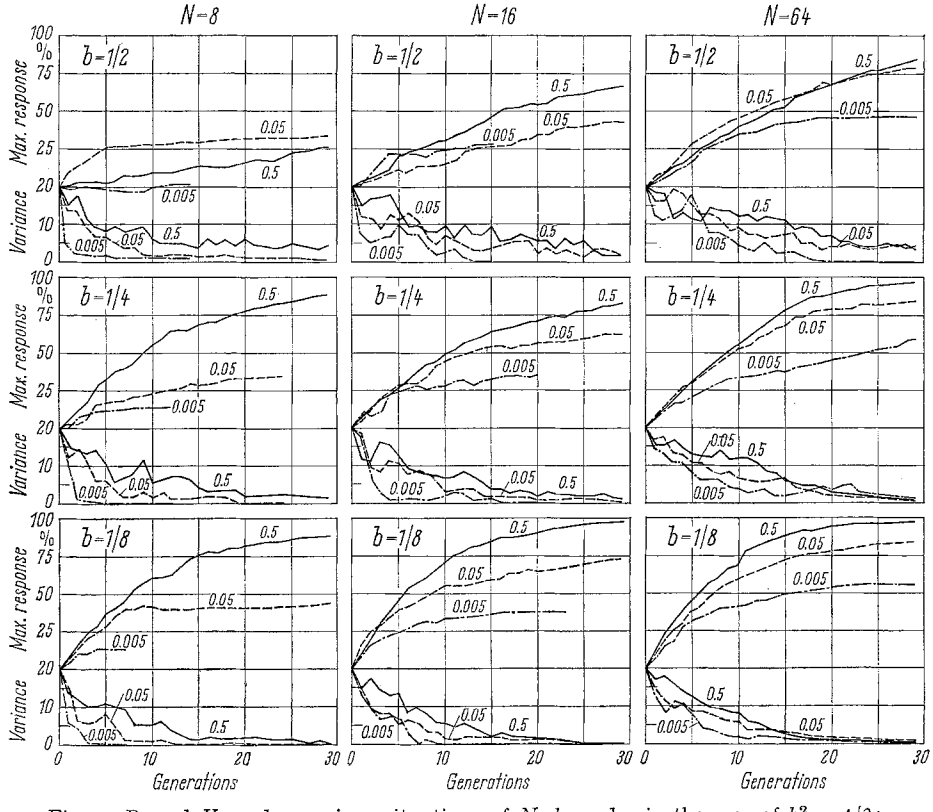

Fig. 2. R_t and V_t under various situations of N, b, and r in the case of $h_0^2 = 1/3$; averaged over two replications

Rates of Response

Except for sampling error, the initial structure of all the populations is the same. Response to the first cycle of selection therefore depends on b and h_0^2 alone. The effects of population size and linkage, and their interactions with selection build up in later generations. Table 1 gives a composite analysis of variance of genotypic means to illustrate this. It is interesting to note relatively small interactions involving N, b or h_0^2 in the Table. Besides main effects, interactions of linkage with selection pressure (b or h_0^2) or with population size appear to account for most of the differences.

Response curves given in Figures 1 to 3 illustrate the nature of these effects and interactions. Differences in response in the first three generations due to linkage appear only in small populations or when heritability is low. The differences due to linkage increase in successive generations and are very large in small populations. The effects of linkages between loci specified as r equal to .05 appear to be small compared to free recombinations in a population as large as 64. But this difference increases in smaller populations and with increased selection intensity. Tables 2 and 3 also show that the differences with respect to $\hat{\beta}_1$ and $\hat{\beta}_2$ between these linkage groups are smaller with weaker selection. In the case of r equal to .005, the effect on response in later generations is distinct. It is obvious that with smaller population size response in later generations is very much reduced. In this case, increased selection intensity appears to cause increased response only in its initial phase when the population size is 8 or 16. In parental populations of 64 alone, continued response is observed with tight linkage. It is also interesting to note that under conditions of low selection intensity and low h_0^2, the response curves for the various linkage groups are not as divergent as in the cases of stronger selection pressure.

Population size effects on the response curves in the case of free recombinations are slight. But with

linkages between loci population size appears to be an important factor in determining response in later generations. The estimates $\hat{\beta}_1$ and $\hat{\beta}_2$ given in Tables 2 and 3 also show that differences in rate of response due to population size are considerable with linkage. With milder selection and h_0^2 of 1/3 or less, population size differences are larger in all linkage groups, and with N equal to 8 the rate of response is very much decreased.

Increase in the rate of response with increased intensity of truncation is linear only in the first three generations. This phase of linear increase appears to last for about 8 to 10 generations in the case of parent populations of 16 or above and recombinations of .05 or more. The effect of increasing level of b in later generations is definitely reduced in populations of 16 or less and with r equal to .005. However, when h_0^2 is 1/3 or less and N is 64, increase in rate of response in later generations continues with increasing intensity of truncation for this case of close linkages. In smaller populations and close linkages the effect of increased truncation is irregular and insignificant. Response is more or less linear in parental populations of 64 and free recombinations, except a slight curvature after 8 to 10 generations under conditions of high truncation and h_0^2 of 1/3 or more.

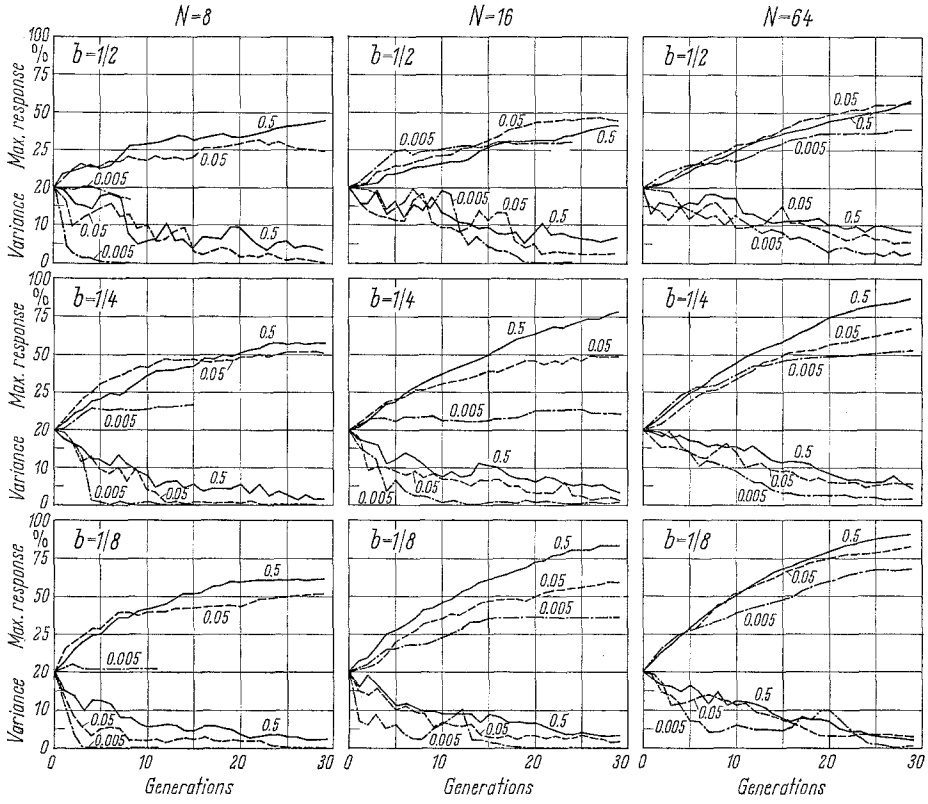

Fig. 3. R_t and V_t under various situations of N, b, and r in the case of $h_0^2 = 1/9$; averaged over two replications

Table 4. *Mean squares obtained from analysis of variance of genotypic mean at fixation (m_T) and number of generations to fixation (T) in the case of $h^2 = 1$ (4 replications)*

Source of variation	d.f.	$N = 8$	$N = 16$	$N = 64$
m_T:				
r	2	9359**	11280**	3959**
b	2	172	147	169*
$r \times b$	4	45	57	205**
Error	27	88	69	33
T:				
r	2	288.7**	256.4**	13.6**
b	2	178.5**	278.5**	296.3**
$r \times b$	4	24.6*	15.1	21.9
Error	29	7.8	14.6	9.4

*, ** significant at 5% and 1% level respectively.

The effect of environmental variance as it was simulated in this study is seen in Figures 2 and 3 and in Table 3. Primarily, its effect is to reduce effectiveness of the truncation level and to increase variability of response. The variability of response is higher in later generations since the genotypic component of phenotypic variance gets smaller while the environmental variance remains constant. With

Table 5. *Mean squares obtained from A.O.V. of m_T and T in the case of $h^2 = 1$ (4 replications)*

Source of variation	d.f.	$r = .005$	$r = .05$	$r = .5$
m_T:				
N	2	3984**	2784**	363.2**
b	2	776**	34	17.4
$N \times b$	4	81	30	27.8
Error	27	121	51	17.4
T:				
N	2	434.3**	16.7	4.7
b	2	83.1**	449.3**	300.1**
$N \times b$	4	7.7	3.7	10.7*
Error	27	15.9	11.7	4.2

*, ** significant at 5% and 1% level respectively.

Table 6. *Mean squares obtained from A.O.V. of m_T and T in the case of $h^2 = 1$ (4 replications)*

Source of variation	d.f.	$b = 1/2$	$b = 1/4$	$b = 1/8$
m_T:				
N	2	1890**	1626**	1992**
r	2	10469**	7003**	5942**
$N \times r$	4	180**	367**	353**
Error	27	31	86	73
T:				
N	2	96.4**	119.1**	23.0**
r	2	294.7**	105.2**	20.5**
$N \times r$	4	54.3*	39.8**	36.6**
Error	27	17.6	8.3	6.0

*, ** significant at 5% and 1% level respectively.

linkage and parental populations of 16 or more, there is slower approach to fixation and a steady rate of response with low heritability. But with a population size of 8 and linkage there is a faster approach to fixation and the increase in mean is seen only in the first few generations. With tight linkage and trunca-

Table 7. *Proportion of fixed loci for inferior allele in 30 generations, averaged over two replications*

		$r = .005$			$r = .05$			$r = .5$		
h_0^2	b	$N = 8$	$N = 16$	$N = 64$	$N = 8$	$N = 16$	$N = 64$	$N = 8$	$N = 16$	$N = 64$
1	1/8	.26*	.28*	.11*	.15*	.06*	.01*	.05*	.03*	.01*
	1/4	.39*	.26*	.13*	.11*	99*	.03*	.04*	0*	.03*
	1/2	.38*	.36*	.26*	.20*	11*	.01*	.05*	.03*	0*
1/3	1/8	.44*	.31*	.22	.29*	.13	.06	.06	.02*	.01
	1/4	.42*	.33*	.21	.32*	.18	.06	.05	.08	0
	1/2	.49*	.38*	.26*	.33*	.26	.02	.36	.12*	.04
1/9	1/8	.52*	.33*	.11	.25*	.19	.05	.14	.03*	.05
	1/4	.41*	.43*	.20	.24*	.26	.05	.18	.05	0
	1/2	.53*	.35*	.27	.37	.22	.16	.23	.24*	.08

* All 40 loci fixed.

tion of 1/2, there is a response of zero until all loci are fixed.

Total Response and Fixation of Genes

After examining the rates of response in the first few generations and in later generations, it is of interest to evaluate the effects of various factors on total response at fixation of all loci. Complete fixation was attained in less than 30 generations in the case of perfect heritability and in most populations with N equal to 8 or r equal to .005 as indicated in Table 7. For populations with perfect heritability, average percentage of maximum response attained (R_T) and the average number of generations to attain this response at fixation (T), are given in Table 2. It is obvious from the table that with free recombinations, response close to maximum is attained in parental populations of more than 64 with truncation of 1/2 or higher. In smaller populations, there is no difference in R_T when intensity of truncation is increased from 1/4 to 1/8 but with 1/2 truncation, there is a slight reduction in R_T.

In the case of r equal to .05, only in the case of population size of 64 is response close to the maximum attained. Increased level of truncation does result in slightly greater response but this level of linkage appears to impose a definite ceiling on response in smaller populations such that with 1/2 truncation and N equal to 8, only 63 percent of maximum response is attained. In the case of tight linkages this ceiling is very much lowered such that even in parental populations as large as 64 and with 1/8 truncation, only 75 percent of maximum response is attained. The relative increase in R_T with increase in N is not uniform for all linkage groups. Hence, a large and significant interaction mean square is observed in the analysis of variance as shown in Table 6. The other interactions with respect to R_T are small as shown in Tables 4 and 5. The tests of significance of these interactions are not accurate because of the heterogeneity of variance as seen by examining error mean squares.

In general, fixation is faster with lower N and r and with higher truncation selection. Only the interaction between population size and linkage appears to be meaningful and significant as shown in Tables 4 to 6. With free recombinations and r equal to .05, increasing N does not seem to increase T as much as in the case of r equal to .005. With tight linkage and small parental population, there is a very rapid approach to fixation, because blocks of genes rather than individual genes as a unit attain homozygosity.

Another way to analyse the effects of various factors is to examine the number of loci fixed for minus allele due to finiteness of population and linkage in spite of selection. Table 7 gives the proportion of such genes fixed among non-segregating loci in 30 generations of selection. The general conclusions are similar to those for total response except to show a higher variability in the pattern of fixation due to selection in situations of low heritability and small population size. With heritability of 1/3 or less, parental population of 8 and tight linkage, selection is almost completely ineffective in causing fixation of plus genes.

Changes in the Genotypic Variance

As discussed earlier, the genotypic variance is similar in generation 0 for all populations. The observed variance of the genotypic value in each generation for the various populations is shown in Figures 1 to 3. The reduction in variance over generations is attributable to the change in gene frequency due to selection, increased homozygosity due to finiteness of populations and due to gametic disequilibria arising with selection and chance. The present data do not allow the analysis of all these factors and it is taken up in detail in a separate Monte Carlo study (QURESHI and KEMPTHORNE, 1968).

Graphic comparison of the changes in variance under various conditions shows that linkages between loci definitely reduce variance beyond what can be accounted for by the corresponding change in response. With tight linkages there is an abrupt decrease in variance in the first few generations except in the case of large N and low heritability. When the parental population is 8, there is a distinct loss of variability due to linkage. The effects of population size and selection are regular in the case of free recombinations. Table 8 gives the linear parameter estimated from fitting the genotypic variance as a quadratic function of generation number, similar to that given in Equation (6) for the genotypic mean. Comparison of these figures gives a more concise picture of the various effects although the estimates are irregular.

Zusammenfassung

In der Absicht, das Verhalten einer begrenzten diözischen Population über einen langen Zeitraum zu analysieren, wurden Selektionsvorgänge auf einem Computer simuliert. Hierbei wurden die Größe der Elterpopulation, die Koppelung zwischen den Loci,

Table 8. *Initial rates of decrease of variance averaged over two replications*

		$r = .005$			$r = .05$			$r = .5$		
h_0^2	b	$N = 8$	$N = 16$	$N = 64$	$N = 8$	$N = 16$	$N = 64$	$N = 8$	$N = 16$	$N = 64$
1	1/2	5.3	9.5	2.0	1.1	3.0	1.1	1.4	1.6	1.1
	1/4	5.5	6.0	4.7	3.0	3.1	3.4	3.0	2.7	2.4
	1/8	13.0	10.8	4.2	2.9	4.0	3.6	2.2	5.1	3.8
1/3	1/2	2.1	3.6	1.4	2.0	.9	1.9	1.4	1.0	.6
	1/4	5.9	4.9	1.3	1.7	1.4	1.3	1.1	1.0	1.0
	1/8	5.4	2.1	1.0	1.4	1.5	1.2	1.2	1.3	1.6
1/9	1/2	3.3	3.3	1.4	.8	.5	.2	1.4	.8	.4
	1/4	6.9	1.7	2.1	2.4	.8	.8	2.0	1.0	.7
	1/8	5.8	2.9	1.3	1.4	1.2	1.0	1.0	1.0	.8

die Selektionsintensität und die Heritabilität in einem 3^4-faktoriellen Versuch variiert. Es wird ein diploides polygenes System mit vierzig Loci auf vier Chromosomen mit additiver Genwirkung zugrunde gelegt. Für die Koppelungsbeziehungen werden freie Rekombination, ein Abstand von fünf Rekombinationseinheiten zwischen benachbarten Loci und die Bildung von Genclustern auf den Chromosomen mit jeweils nur 0,5 MORGAN-Einheiten Abstand zwischen benachbarten Loci angenommen. Es werden elterliche Populationen des Umfanges 8, 16 und 64, trunkierende (stutzende) Selektion mit einer Fraktion von 1/2, 1/4 und 1/8 der Nachkommen je Generation und eine ursprüngliche Heritabilität von 1, 1/3 und 1/9 für verschiedene Populationen simuliert.

Für alle jene Populationen, die ursprünglich als Stichproben aus einer theoretischen HARDY-WEINBERG-Situation stammen, kann gezeigt werden, daß eine anfänglich lineare Phase der Reaktion, die in einigen Fällen nur über zwei bis drei Generationen anhält, allein von der Selektionsintensität abhängt. Die Wirkungen und Wechselwirkungen aller oben genannten Faktoren auf die Nichtlinearität der Reaktion in späteren Generationen wird untersucht. Es zeigt sich, daß Koppelung zwischen den Loci einen starken Einfluß auf die Reduktion der Reaktionsgeschwindigkeit und auf die Endreaktion ausübt. In dem extremen Fall der Gencluster in einer Ausgangspopulation des Umfanges 8 mit geringer Heritabilität ist die trunkierende Selektion hinsichtlich der Änderung des Mittels über Generationen hinweg praktisch völlig unwirksam. Die Wirkung enger Koppelung manifestiert sich außerdem in einer stärkeren Reduktion der genotypischen Varianz, als sie auf Grund der entsprechenden Reaktion erklärt werden kann. Der reduzierende Effekt der Begrenzung des Populationsumfanges auf die Reaktionsgeschwindigkeit und die Endreaktion erweist sich als geometrisch proportional zur Koppelung zwischen den Loci. Die Zahl der Generationen bis zur Fixierung wird in ähnlicher Weise reduziert. Hierbei wird eine starke Wechselwirkung zwischen der Populationsgröße und der Koppelung in den verschiedenen Untersuchungen beobachtet. Der Einfluß der Koppelung auf die Reaktion der Populationen kann vernachlässigt werden, wenn die elterliche Population den Umfang 64 hat und die Rekombination zwischen benachbarten Loci 0,05 übersteigt. In derartigen Situationen gibt es zwar eine langsamere Antwortrate in späteren Generationen mit Koppelung, jedoch ist die Endreaktion, die erreicht wird, und die Fixierungsrate überlegener Gene etwa die gleiche wie bei freier Spaltung. Eine Zunahme der Selektionsintensität scheint die Wirkung der Koppelung hinsichtlfch der Reduktion der Reaktionsgeschwindigkeit in späteren Generationen zu vergrößern. Dieser Typ der Wechselwirkung wird der Häufung gametischer Ungleichgewichte, die infolge der Selektion über Generationen in der Population erhalten werden, zugeschrieben.

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