THEORETICAL CONSEQUENCES OF TRUNCATION SELECTION BASED ON THE INDIVIDUAL PHENOTYPE

By B. GRIFFING*

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Summary

Theoretical consequences of truncation selection based on the individual phenotype are examined for the following cases of increasing genetic complexity: (i) an arbitrary number of alleles at a single locus, (ii) an arbitrary number of alleles at each of two linked loci, and (iii) a completely general genetic situation.

The analyses are facilitated by generalizing the concept of hereditary units to include not only the gene but also units of higher levels of organization.

Analyses fundamentally based on higher-order units but with a gene interpretation permit a detailed examination of the consequences of selection and relaxation following selection for the two-locus case. It is shown that the immediate response to selection may be different from that predicted on the basis of gene analysis if an additive $\times$ additive type of epistasis occurs. However, due to the "mutability" of these higher-order inheritance units, the population mean, on relaxation of selection, decays to that predicted by the gene-analysis approach.

I. INTRODUCTION

Apart from the abbreviated presentation in Section 7 of the remarkable paper by Kimura (1958), there seems to be no generalized treatment of the theoretical response of a population to continuous artificial selection. However, various intuitive suggestions have been made without an extensive rigorous mathematical treatment. For example, Lush (1948) makes the following comprehensive statement:

> "Epistatic variations are in small part transmitted; i.e. they are correlated as between parent and offspring although not as highly correlated as the genic differences are. Therefore we do expect to recover temporarily in the offspring some fraction of whatever epistatically caused phenotypic differences in the parents led to our selecting those parents in the first place. When mating is random, this fraction would be about half of the two-gene epistatic interactions, one-fourth of the three-gene interactions, one-eighth of the four-gene interactions, etc. Therefore only a little of the epistatic variance would be removed unless nearly all epistasis is from simple two-gene and three-gene interactions. The phenotypic gains from selecting for epistatic differences come from distorting the gametic array and soon disappear after selection is relaxed, as the gametic array returns to random. By contrast, the gains from changes in gene frequency are permanent unless and until counter-selection restores the original gene frequency."

Kempthorne (1957, p. 361), when discussing Fisher's "Fundamental Theorem of Natural Selection", also makes an interesting statement which is more explicit with regard to the contribution of specific epistatic variance components. The statement is:

> "It is interesting to speculate on the possible extension of the result to the case of more than one locus. It is likely that, if the appropriate λ quantities remain constant, the rate of increase in fitness will involve both additive and additive $\times$ additive components of genotypic variance of fitness."

* Division of Plant Industry, C.S.I.R.O., Canberra.

Starting with these intuitive notions, it is now desirable to provide a more rigorous and detailed development of the theoretical responses of a population to artificial selection.

More exactly, the objectives of this study are to discuss some aspects of the general problem of description and prediction associated with truncation selection based on the individual phenotype. The argument will be developed for increasingly complex genetic situations until the generalization is reached which includes any number of alleles at each of an arbitrary number of loci associated in an arbitrary system of linkages. The genes may exhibit any set of dominance and epistatic values.

The generalization of results is made easier by a generalization of the notion of hereditary units to include not only the gene but also units of higher levels of organization. Because of the emphasis which is placed on the notion of generalizing the unit of inheritance, the following points will be discussed in the next three sections:

(i) The problem posed by the modern concept of the gene and the possibility of considering units of higher levels of genetic organization.

(ii) The characterization of a random-mating population in equilibrium by different units of inheritance.

(iii) The generalization of definitions which have been developed for the gene analysis in order that they may be applied to higher-order units.

After these introductory sections, the consequences of truncation selection will be examined when selection is applied to the following genetic populations:

(i) Genotypes which are generated at a single gene locus—the argument is based on the usual gene analysis.

(ii) Genotypes which are generated at two gene loci which are linked—the argument is based on a gametic analysis with a gene interpretation.

(iii) Genotypes which are generated by a completely arbitrary gene system—the argument is based primarily on an individual analysis.

The importance of this subject is considerable for at least two reasons. Firstly, mass selection (i.e. selection based on the individual phenotype) is undoubtedly the most extensively used method of selection in plant and animal breeding. It is, therefore, important to know what are the theoretical consequences of such a selection programme, and to know how predictions of genetic gains may be made.

Secondly, a recent trend in quantitative genetics is to make inferences regarding the phenomenon of "genetic homeostasis" (Lerner 1954), from controlled selection experiments, which are usually conducted with a convenient experimental organism such as *Drosophila*. In these experiments it is often observed that the mean of a population, which has been subject to unidirectional artificial selection, regresses, on relaxation of selection, toward its original position. This phenomenon has been termed genetic homeostasis by Lerner (1954), and it is assumed that this regression is due to the effects of natural selection which act antagonistically to artificial selection.

It is clear that to properly evaluate the effects of natural selection from selection experiments alone (i.e. without fitness tests), it is essential to understand the theoretical consequences of artificial selection and relaxation *in the absence of natural selection.* For example, it will be shown that the contributions of non-zero additive × additive × etc. components of variance to the responses of selection and relaxation following selection mimic those due to natural selection. Thus, unless the effects from at least one source can be measured, the effects of both are hopelessly confounded and inferences about the contribution of natural selection cannot be made.

(*a*) *Units of Inheritance*

It appears that the modern concept of the gene, which is evolving from intensive studies of complex loci in the entire range of organisms from bacteriophage to man, differs radically from the classical notion of the gene as a single indivisible unit capable of being described unambiguously in terms of recombination, mutation, and physiological activity. It now appears that the chromosomes may be divided, first, into fundamental loci (i.e. limited regions) each of which specifically controls a biological activity. It is probable that each locus contains many mutational and recombinational sites, and, in many instances, linear linkage maps may be obtained for the locus from intralocus recombination data. In some cases, in which pairs of mutants within the same locus can be tested for complementarity, maps of functional regions (cistrons) may be obtained. However, anomalies may arise with the complementation criterion. For example, when mutants have pleiotropic effects, complementation tests may lead to cistrons which are physically discontinuous (Carlson 1959). A particularly lucid summary of the modern concept of the complexities which may exist at a locus is given by Fincham (1959):

> "The picture which seems to be emerging, at least from the *Neurospora* work, is of chromosomes segmented into small and apparently quite sharply distinct regions, each concerned, though almost certainly indirectly, in the formation of a particular kind of protein molecule. Within these regions, which I have been calling loci, mutations can occur at many different sites. Different mutant derivatives of the same locus, that is to say alleles, can often interact at meiosis, either by crossing-over in the orthodox sense or by "conversions", to give a wild-type allele, and their cytoplasmic products can sometimes interact to give a wild or semi-wild phenotype in a heterocaryon. Loci of this kind conform to none of the usual definitions of the gene. Yet the most striking and incontrovertible fact about the chromosome as a genetic structure has surely always been its segmentation into regions of highly specific and differentiated function. It is this fact, rather than any segmentation of the chromosome with respect to crossing-over, which has given solidity to the idea of the gene, and which still does so. While the recon becomes vanishingly small, and the cistron tends to fall apart, the gene locus, regarded as a physiologically differentiated segment, still retains a semblance of reality."

The question is how does this modern concept of the gene affect the treatment of quantitative inheritance? More explicity, the issue is how to characterize the genetic complexity at a locus in order to facilitate the analysis of quantitative inheritance and theoretical problems in plant and animal breeding.

There are at least two methods of representing the genetic situation at a complex locus. To illustrate, consider a locus which has a simplified structure

consisting of only two genetic conditions (mutant and normal) at each of two mutational sites. In the first method, the locus can be subdivided into two subloci, one for each of the mutational sites. This approach yields two sets of alleles, each set being the genetic alternatives at each sublocus. In this case, the gene model for quantitative inheritance must be extended to accommodate position effect which may occur between alleles at different subloci. This, so far, has never been done.

The alternative method is to consider the overall locus as the basic entity, and to regard all possible genetic structures at this locus as the set of multiple alleles. Thus, in the simplified example, the four possible gene states are $(++)$, (m_1+), $(+m_2)$, and (m_1m_2). These, then, would be regarded as the alleles of the locus. Such a representation avoids the introduction of intralocus position effect because complexities such as the *cis–trans* relations would be absorbed in the dominance parameters. However, a resultant complication of this approach is that mutation of alleles as defined above includes both point mutation in its conventional sense and intralocus recombination. For example, recombination between mutational sites arranged in a *trans* configuration, $m_1+/+m_2$, results in non-parental locus types, $(++)$ and (m_1m_2). It is of course clear that the frequency of such intralocus recombination is low compared with the frequency of recombination between genes at different loci. Hence, it would appear that with the alleles defined as above, the contribution of locus mutation (point mutation and intralocus recombination) would be negligible in most theoretical plant and animal breeding studies.

Assuming that this representation of a locus is satisfactory, it is possible and desirable to extend the notion of hereditary units to higher levels of genetic organization; that is, to the chromosome, gamete, and individual. It will be shown that such an extension is valuable for certain aspects of selection theory.

In a given population there exists a finite number of different configurations for a given set of homologous chromosomes. Each configuration can be considered as an "allele": a macrogene with multiple effects. These alleles are unstable since mutation now includes point mutation, all forms of chromosomal aberrations, and recombination within and between loci along the entire length of the chromosome. To further extend the analogy with the gene concept, each set of homologous chromosomes may be regarded as a multiple allele series at one locus; there being n loci in all, where n is the haploid chromosome number. The average effect for a given chromosome can be defined as well as the interactions between homologous chromosomes and the interactions between non-homologous pairs of chromosomes.

In a similar manner, gametes represent a higher level of genetic organization. In this case individual gametes are analogous to alleles and the entire array of gametes in a population is analogous to the array of multiple alleles at a single locus. Gametes are extremely unstable. Mutation now embraces point mutation, chromosomal aberrations, recombination, and chromosomal segregation.

Finally, individuals comprise a single array, analogous to a multiple allele series at a single locus. As a unit of heredity, the individual is clearly the least stable, as mutation now includes all factors listed for gametes plus variation which is generated by the union of gametes.

In summary, then, it is clear that there are different levels of genetic organization and that the hereditary units for each level are amenable to genetic analysis. The gene locus is an organized chromosomal segment which contains many different mutational and recombinational sites. It is in some respects, comparable to a minute chromosome. The chromosome is composed of a collection of gene loci. Since it is a morphological entity, there is no ambiguity in its definition. The gamete is a collection of chromosomes such that one chromosome of each homologous set is included. Finally, the diploid individual is a combination of two gametes.

(*b*) *Characterization of a Random-mating Population by Different Units of Inheritance*

A random-mating system is one in which the frequencies of matings between the various classes of genotypes are equal to the product of the frequencies of the genotypes themselves. A random-mating population in equilibrium is one in which the frequencies of the genotypes do not change from one generation to the next. Thus, if the genotypic array of a population is $\Sigma f_i G_i$, where G_i is the ith genotype and f_i its frequency, then the system of random matings may be generated by squaring this array, i.e.

$$(\Sigma f_i G_i)^2 = \sum_{ij} f_i f_j G_i G_j,$$

where $G_i G_j$ represents the mating between the ith and jth genotypes. The results of these matings produces another population, the array of which may be denoted as $\Sigma f_i' G_i$. If $f_i' = f_i$, then the population is said to be in equilibrium.

It is now useful to consider how a representation of a random-mating population in equilibrium can be generated by the various basic units of heredity, i.e. genes, chromosomes, gametes, and individuals. The basic principle is that an equilibrium population for genotypes at a single locus may be obtained by "squaring" the array of multiple alleles for the locus. This, of course, assumes that the allelic array has been derived from the equilibrium population without selection. This principle holds for any unit of inheritance and for any system of linkages. Thus, if $\Sigma f_i H_i$ represents the array of multiple alleles at a single locus for any system of hereditary units, the equilibrium population of genotypes at the locus may be generated as

$$(\Sigma f_i H_i)^2 = \sum_{ij} f_i f_j H_i H_j.$$

If the units of inheritance are diploid genotypes, then the combination $H_i H_j$ represents the full-sib array which results from the mating of the ith and the jth genotypes.

If genes or chromosomes are considered as units of inheritance then more than one locus must eventually be considered. In this case, let $\Sigma f_i^r H_i^r$ represent the array of alleles at the rth locus. The equilibrium population for all loci is then obtained by multiplying together the genotypic arrays produced at each locus, i.e.

$$\prod_{r=1}^{n} [\sum_i f_i^r H_i^r]^2.$$

Confining attention now to a single locus (for any hereditary unit), it is convenient to represent the operation of squaring by forming a two-way multiplication table. Thus $(\Sigma f_i H_i)^2$ can be set out as follows:

	H_1 (f_1)	H_2 (f_2)	. . .	H_m (f_m)
H_1 (f_1)	H_1H_1 $(f_1)^2$	H_1H_2 (f_1f_2)	. . .	H_1H_m (f_1f_m)
.	.	.	.	.
.	.	.	.	.
.	.	.	.	.
H_m (f_m)	H_mH_1 (f_mf_1)	H_mH_2 (f_mf_2)	. . .	H_mH_m $(f_m)^2$

The usefulness of this representation is that it provides a pattern which is clearly amenable to all of the ramifications of the analysis of variance for a two-way classification with proportional subclass frequencies. Therefore, effects and interactions can be defined and a mathematical model constructed from an identity of means. Also an identity in sums of squares can be used to define an orthogonal partitioning of the total variance into component parts associated with the various classes of effects.

Fisher (1918) laid the foundations for such an analysis using "genes" as the hereditary units. This early pioneering work has been extended by Kempthorne (1957, for general reference). However, it is obvious that this Fisher–Kempthorne approach can be generalized to include any level of hereditary unit.

(c) *Definitions*

Referring, now, to the two-way table, generalized definitions can be made as follows:

Let

H_i = hereditary unit (gene, chromosome, gamete, or individual),

f_i = frequency of H_i,

h_{ij} = genotypic deviation associated with the H_iH_j combination, such that $\sum_{ij} f_i f_j h_{ij} = 0$.

Any genotypic value, h_{ij}, may be represented by the following identity,

$$h_{ij} \equiv h_{i.} + h_{.j} + (h_{ij} - h_{i.} - h_{.j}),$$

which may be recast as

$$h_{ij} = \gamma_i + \gamma_j + \theta_{ij},$$

where

$\gamma_i = \sum_j f_j h_{ij}$ = general combining ability (g.c.a.) effect of H_i,

$\gamma_j = \sum_i f_i h_{ij}$ = g.c.a. effect of H_j,

and

$\theta_{ij} = h_{ij} - h_{i.} - h_{.j}$ = specific combining ability (s.c.a.) effect for the combination H_iH_j.

The total variance may be partitioned as follows:

$$\sum_{ij} f_i f_j h_{ij}^2 \equiv 2\sum f_i \gamma_i^2 + \sum_{ij} f_i f_j \theta_{ij}^2,$$

which may be recast as

$$\sigma_H^2 = \sigma_{\text{g.c.a.}}^2 + \sigma_{\text{s.c.a.}}^2,$$

where

$\sigma_{\text{g.c.a.}}^2$ = g.c.a. variance,

and

$\sigma_{\text{s.c.a.}}^2$ = s.c.a. variance.

The usual analysis based on genes may be regarded as a special case of the above more general representation. If H_i ($i = 1, \ldots, m$) are genes (i.e. multiple alleles at a single locus), then the symbolization may be converted to the more usual gene notation as follows:

$\gamma_k = \alpha_k$ = additive effect of A_k,

$\theta_{ij} = \delta_{ij}$ = non-additive (dominance) effect of A_iA_j,

$\sigma_{\text{g.c.a.}}^2 = \sigma_A^2$ = additive genetic variance,

and

$\sigma_{\text{s.c.a.}}^2 = \sigma_D^2$ = non-additive (dominance) variance.

It may be noted that the terms general and specific combining ability effects and variances are introduced to apply to all units of inheritance and in the case of genes they are synonymous with the well-established terms, additive and non-additive effects and variances. This has been done to avoid confusion which would possibly otherwise exist if one were to apply the words additive and non-additive to effects and variances of higher units than the gene. For example, in the case where genotypes involve genes at more than one gene locus, the g.c.a. effects of higher units than the gene are a function not only of additive but also of certain non-additive gene effects.

In the more generalized argument of this study, and others to follow, it is convenient to use the individual as the unit of inheritance and to use certain covariances between relatives as the genetic parameters of particular interest.

The following defines three covariances and relates them to the "individual" general and specific combining ability variances.

To characterize the random-mating population with the individual as the unit of inheritance, let $\Sigma f_i H_i$ designate the array of parent individuals undergoing random mating, and let $\Sigma f_i h_i = 0$ denote the corresponding array of genotypic values. The cross between the ith and the jth parents yields a full-sib array the mean of which may be designated as $h_{ij.} = \sum_k p_{ijk} h_{ijk}$. Note that the ijkth progeny has an arbitrary frequency p_{ijk} (such that $\sum_k p_{ijk} = 1$), and hence any system of linkage may occur.

The full-sib means may be set out in the usual two-way table as follows:

	H_1 (f_1)	H_2 (f_2)	. . .	H_m (f_m)	
H_1 (f_1)	$h_{11.}$ $(f_1)^2$	$h_{12.}$ $(f_1 f_2)$	. . .	$h_{1m.}$ $(f_1 f_m)$	$h_{1..}$
.	.	.	.	.	.
.	.	.	.	.	.
.	.	.	.	.	.
H_m (f_m)	$h_{m1.}$ $(f_m f_1)$	$h_{m2.}$ $(f_m f_2)$	. . .	$h_{mm.}$ (f_m^2)	$h_{m..}$
					$h_{...} = 0$

The parent–offspring covariance (designated as Cov (PO)) may be defined as the expected value of the cross-product of the genotypic deviation of an arbitrary parent individual and the mean genotypic deviation of the half-sib array associated with the parent individual. If h_i is the genotypic deviation of the parent genotype H_i, then

$$\begin{aligned} \text{Cov(PO)} &= E(h_i \, . \, h_{i..}) \\ &= \Sigma f_i h_i \, . \, h_{i..} \, . \end{aligned}$$

The covariance of full-sibs (designated as Cov (FS)) may be defined as the expected value of the cross-product of the genotypic deviation of an arbitrary individual and the mean genotypic deviation of the full-sib array of which it is a member. Thus,

$$\begin{aligned} \text{Cov(FS)} &= E(h_{ijk} \, . \, h_{ij.}) \\ &= \sum_{ij} f_i f_j \sum_k p_{ijk} h_{ijk} \, . \, h_{ij.} \\ &= \sum_{ij} f_i f_j (h_{ij.})^2 . \end{aligned}$$

The covariance of half-sibs (designated as Cov (HS)) may be defined as the expected value of the cross-product of the genotypic deviation of an arbitrary individual and the mean genotypic deviation of the half-sib array of which it is a member. Thus

$$\begin{aligned}\text{Cov(HS)} &= E(h_{ijk} \cdot h_{i..}) \\ &= \sum_{ij} f_i f_j \sum_k p_{ijk} h_{ijk} \cdot h_{i..} \\ &= \sum f_i (h_{i..})^2.\end{aligned}$$

Interpretation of the general and specific combining ability variance components may be made in terms of covariances of full-sibs and half-sibs as follows:

$$\begin{aligned}\sigma^2_H &= \sum_{ij} f_i f_j (h_{ij.})^2 \\ &= \text{Cov(FS)}, \\ \sigma^2_{\text{g.c.a.}} &= 2\sum f_i (\gamma_i)^2 \\ &= 2\sum f_i (h_{i..})^2 \\ &= 2\ \text{Cov(HS)},\end{aligned}$$

and

$$\begin{aligned}\sigma^2_{\text{s.c.a.}} &= \sum_{ij} f_i f_j \theta^2_{ij} \\ &= \text{Cov(FS)} - 2\ \text{Cov(HS)}.\end{aligned}$$

The above definitions apply to a completely general genetic situation. In terms of genes this means a genetic situation which is completely arbitrary for (i) number of alleles at any locus, (ii) number of loci, (iii) system of linkages, and (iv) dominance and epistatic relationships.

It may be noted that not all of the above definitions are used in the present paper. However, this study is the first of a series which will include a treatment of full-sib and half-sib selection, and, collectively, these studies will make use of the entire range of definitions. Hence, in this first paper, it seems worth while to completely set out the notion of higher-order units of inheritance and their associated definitions.

II. Consequences of Truncation Selection Based on Individual Phenotype

This study is concerned with individual selection within the framework of a breeding programme which consists of cycles. In each cycle, selection is applied to members of a random-mating population and the selected individuals are then mated at random to provide the population for the next cycle. The original unselected population, with which the selection programme starts, is assumed to be in equilibrium.

The arguments to be developed are formulated for an idealized situation in which the populations are infinite in size and, therefore, can be characterized by continuous distributions. The method of defining selection values is that due to

Kimura (1958) and some parts of the more generalized argument are found in the work of Kimura (1958).

In the remainder of the paper the consequences of selection are examined for three levels of complexity in terms of gene structure: (i) a single locus level, (ii) a level involving two linked loci, and (iii) a generalized level. These studies, fundamentally, represent three different approaches to the problem of describing the response to selection by utilizing different units of inheritance. In the first analysis, the gene is considered as the basic unit and the consequences are examined when selection is applied to genotypes at a single gene locus. The total response is then obtained by summing over all gene loci. The gamete is considered as the basic unit in the second analysis with, however, a gene interpretation so that the detailed results can be compared with those of the gene analysis.

Finally, in the last section, generalizations are made by using analyses in which the individual is considered as the basic unit of inheritance. However, the frequency of an individual is necessarily specified in terms of the frequencies of the gametes which united to form the individual. In order to compare the results with the previous analyses, the generalized results are interpreted in terms of the example consisting of two loci which are linked.

(*a*) *Selection of Genotypes Generated by Alleles at One Locus*

(i) *Definitions*

(1) *Parameters of the Random-mating Population in Equilibrium.*—The random-mating population generated by m alleles at one locus may be set out in the following two-way table:

	A_1	A_2	. . .	A_m	
	(p_1)	(p_2)		(p_m)	
A_1	d_{11}	d_{12}	. . .	d_{1m}	α_1
(p_1)	$(p_1)^2$	(p_1p_2)		(p_1p_m)	
	w_{11}	w_{12}		w_{1m}	
.	.	.	.	.	.
.	.	.	.	.	.
.	.	.	.	.	.
A_m	d_{m1}	d_{m2}	. . .	d_{mm}	α_m
(p_m)	(p_mp_1)	(p_mp_2)		$(p_m)^2$	
	w_{m1}	w_{m2}		w_{mm}	
					0

In this table,

(*a*) $A_1, A_2, \ldots, A_m$ represent the m alleles,

(*b*) p_i = frequency of A_i,

(*c*) d_{ij} = genotypic value of A_iA_j, such that

$$\mu_0 = \sum_{ij} p_i p_j d_{ij} = 0,$$

and

(*d*) w_{ij} = selection value of A_iA_j (defined later).

The genotypic value, d_{ij}, may be characterized by the following gene model,

$$d_{ij} = \alpha_i + \alpha_j + \delta_{ij},$$

where

$$\alpha_i = \sum_j p_j d_{ij} = \text{additive effect of the } A_i \text{ allele},$$

and

$$\delta_{ij} = d_{ij} - \alpha_i - \alpha_j = \text{dominance effect associated with } A_iA_j.$$

The total genotypic variance may be partitioned as follows:

$$\sum_{ij} p_i p_j d_{ij}^2 = 2\sum p_i \alpha_i^2 + \sum_{ij} p_i p_j \delta_{ij}^2,$$

which may be represented symbolically as

$$\sigma_G^2 = \sigma_A^2 + \sigma_D^2,$$

where

$$\sigma_G^2 = \sum_{ij} p_i p_j d_{ij}^2 = \text{genotypic variance},$$

$$\sigma_A^2 = 2\sum p_i \alpha_i^2 \quad = \text{additive genetic variance},$$

and

$$\sigma_D^2 = \sum_{ij} p_i p_j \delta_{ij}^2 = \text{dominance variance}.$$

(2) *Selection Values.*—The assumptions in the following argument may be listed as follows:

(i) The genotypic variability of the characteristic which is being studied is controlled by genes, each of small effect, at many loci.

(ii) The phenotypic variability, due to environmental effects together with that due to the segregation at the numerous loci, is normally distributed with mean zero and variance σ^2.

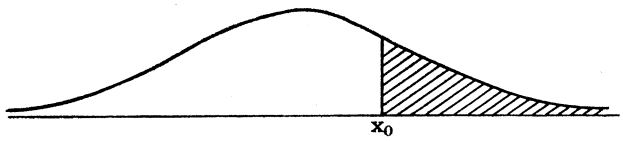
(iii) The initial random-mating population is in equilibrium for genes at all loci.

With regard to the particular locus in question, it is conceptually possible to subdivide the entire populations of individuals into groups corresponding to the various genotypes $A_iA_j (i, j = 1, \ldots, m)$. The relative frequencies of these groups are p_ip_j $(i, j = 1, \ldots, m)$. From the above assumptions, it is clear that the subpopulation of individuals having a given genotype, A_iA_j, is normally distributed with genotypic mean, d_{ij}, and variance, σ_{ij}^2. That is to say, different members of

this population all have the genotype A_iA_j, for the locus under study, but may have different genes for the other loci, as well as different environmental conditions. These differences generate the normal population with genotypic mean, d_{ij}, and variance, σ^2_{ij}. With regard to the definition of selection values, there are two further assumptions which need to be made concerning the magnitudes of d_{ij} and σ^2_{ij}. These are: (i) d_{ij} is small in relation to σ so that the quantities $(d_{ij}/\sigma)^2$ and $(d_{ij}/\sigma^2)^2$ may be neglected, and (ii) the genotypic variance generated by the locus in question is small, relative to the total phenotypic variance, so that $\sigma^2_{ij} \cong \sigma^2$.

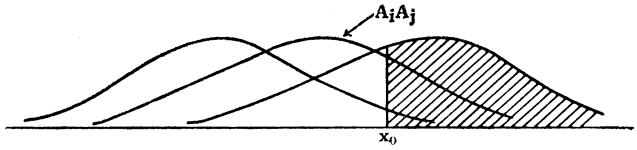
The "truncation" selection programme is such that all members of the entire population which have a greater phenotypic value than a given value, say x_0, will be selected for mating at random to produce the next generation of individuals. This selection programme may be diagrammed as follows:

(i) Selection programme depicted for the entire population:



Individuals represented by shaded area are mated at random to produce the next population.

(ii) Selection programme depicted in terms of subpopulations:



The selection value, w_{ij}, for the genotype A_iA_j is defined to be proportional to the probability that an individual of the genotype A_iA_j survives selection. This probability is

$$\Pr(x>x_0) = \frac{1}{\sigma_{ij}\sqrt{(2\pi)}}\int_{x_0}^{\infty} \exp\{-[(x-d_{ij})^2/2\sigma^2_{ij}]\}\mathrm{d}x$$

$$\cong \frac{1}{\sigma\sqrt{(2\pi)}}\int_{x_0}^{\infty} \exp\{-[(x^2-2xd_{ij}+d^2_{ij})/2\sigma^2]\mathrm{d}x$$

$$\cong \frac{1}{\sigma\sqrt{(2\pi)}}\int_{x_0}^{\infty} \exp[-(x^2/2\sigma^2)]\,.\,\exp(x\,d_{ij}/\sigma^2)\mathrm{d}x$$

$$\cong \frac{1}{\sigma\sqrt{(2\pi)}}\int_{x_0}^{\infty} \exp[-(x^2/2\sigma^2)][1+(x\,d_{ij}/\sigma^2)]\mathrm{d}x$$

$$\cong \frac{1}{\sigma\sqrt{(2\pi)}}\int_{x_0}^{\infty}\exp[-(x^2/2\sigma^2)]\mathrm{d}x+(d_{ij}/\sigma^2).\frac{1}{\sigma\sqrt{(2\pi)}}\int_{x_0}^{\infty}x.\exp[-(x^2/2\sigma^2)]\mathrm{d}x$$

$$= v+(d_{ij}/\sigma^2)iv$$

$$\propto 1+(d_{ij}/\sigma^2)i,$$

where v is the proportion of the original population which is selected and i is the selection differential, i.e.

$$i = \left\{\frac{1}{\sigma\sqrt{(2\pi)}}\int_{x_0}^{\infty}x.\exp[-(x^2/2\sigma^2)]\mathrm{d}x\right\}\Big/v.$$

The selection value for A_iA_j is then defined to be

$$w_{ij} = 1+(i/\sigma^2)d_{ij},$$

or

$$w_{ij} = 1+\bar{\imath}(d_{ij}/\sigma),$$

where $\bar{\imath} = i/\sigma$ = standardized form of the selection differential.

(ii) *Consequences of One Cycle of Selection*

The problem for review in this section is that of determining the change in population parameters due to a single cycle of truncation selection. The cycle starts with a random-mating population in equilibrium as described in the previous section. This population is designated as Π_0 and the parameters associated with this population are designated with the superscript "0". The progeny population produced by the first cycle of selection is designated as Π_1, and its parameters are designated with superscript "1". The elements and variances of the gene model are always assumed to be those associated with Π_0.

The frequency of A_iA_j following selection is

$$p_i^0p_j^0w_{ij}^0 = p_i^0p_j^0+(i/\sigma^2)p_i^0p_j^0d_{ij}^0.$$

The total frequency of all selected genotypes is

$$\sum_{ij}[p_i^0p_j^0+(i/\sigma^2)p_i^0p_j^0d_{ij}^0] = 1.$$

The genotypic mean of the selected parents is

$$\mu_s = \sum_{ij}[p_i^0p_j^0+(i/\sigma^2)p_i^0p_j^0d_{ij}^0]d_{ij}^0$$

$$= i(\sigma_G^2/\sigma^2)$$

$$= i(\text{heritability in the broad sense}).$$

The gene frequency for the A_i allele in the selected population is

$$p_i^1 = \sum_j[p_i^0p_j^0+(i/\sigma^2)p_i^0p_j^0d_{ij}^0]$$

$$= p_i^0+\bar{\imath}\,p_i^0(\alpha_i/\sigma)$$

$$= p_i^0+\Delta p_i.$$

The total gene array produced by the selected parents is

$$\Sigma p_i^1 A_i = \Sigma (p_i^0 + \Delta p_i) A_i.$$

Hence, the progeny genotypic array which results from random mating the selected parents is obtained by squaring the gene array as follows:

$$(\Sigma p_i^1 A_i)^2 = \sum_{ij} p_i^0 p_j^0 A_i A_j + (i/\sigma) \sum_{ij} p_i^0 p_j^0 (\alpha_i + \alpha_j) A_i A_j + i^2 \sum_{ij} p_i^0 p_j^0 (\alpha_i/\sigma)(\alpha_j/\sigma) A_i A_j.$$

The progeny mean is obtained by substituting d_{ij}^0 for $A_i A_j$. Thus

$$\mu_1 = (i/\sigma)\sigma_A^2 + i^2 \sum_{ij} p_i^0 p_j^0 (\alpha_i/\sigma)(\alpha_j/\sigma)\delta_{ij}.$$

This last equation can be simplified by assuming that (α/σ) is small so that the square or product of two such quantities can be neglected. Assumptions of this sort will be made throughout this study. In this case

$$\mu_1 = i(\sigma_A^2/\sigma^2).$$

For a single locus, the increment advance in the genotypic mean due to selection is equal to the difference between the genotypic means of Π_1 and Π_0, i.e.

$$\begin{aligned} \Delta\mu_{10} &= \mu_1 - \mu_0 \\ &= i(\sigma_A^2/\sigma^2) \\ &= i(\text{heritability in the narrow sense}). \end{aligned}$$

For individual loci these quantities are negligible, but the sum of such effects over a large number of loci is assumed to be appreciable.

This increment change in means may be predicted from the difference between the phenotypic means (which are equal to genotypic means when infinite populations are considered) of the selected parents and the unselected original population. This difference is defined to be the value i. The prediction equation is

$$\Delta\mu_{10} = Gi.$$

Hence $G = \sigma_A^2/\sigma^2 =$ heritability in the narrow sense.

Thus, prediction of the genotypic advance can be made for the case of a single cycle of selection operating in a genetic system composed of an arbitrary number of alleles at a single locus.

If the cycle of selection is followed by random mating without selection (either artificial or natural) the population structure remains unchanged and the population mean remains at $\mu = i(\sigma_A^2/\sigma^2)$, i.e. the population is in equilibrium. This assumes that the gene has negligible mutation rate in relation to the time span concerned. That is, point mutation together with recombination within a locus yield a low total mutation rate.

(iii) *Consequences of Two or More Cycles of Continuous Selection*

The problem in this section is to describe the changes in parameters which occur with two or more cycles of continuous selection.*

In the previous section it was shown that the progeny resulting from the first cycle of selection constitutes a random-mating population in equilibrium which may be characterized as

$$\Pi_1 = \sum_{ij} p_i^1 p_j^1 A_i A_j,$$

with mean

$$\mu_1 = \sum_{ij} p_i^1 p_j^1 d_{ij}^0$$

$$= i(\sigma_A^2/\sigma^2).$$

Assuming that the selection differential i remains the same and that the phenotypic variance is essentially the same as in Π_0, the frequency of A_iA_j following selection in Π_1 is

$$\begin{aligned} p_i^1 p_j^1 w_{ij}^1 &= p_i^1 p_j^1[1+(i/\sigma)d_{ij}^1] \\ &= p_i^1 p_j^1[1+(i/\sigma)(d_{ij}^0-\mu_1)] \\ &= p_i^1 p_j^1[1+(i/\sigma)d_{ij}^0-(i/\sigma)(i\,\sigma_A^2/\sigma)] \\ &= p_i^1 p_j^1\{1+(i/\sigma)d_{ij}^0-i^2[2\textstyle\sum p_i^0(\alpha_i/\sigma)^2]\} \\ &\cong p_i^1 p_j^1\{1+(i/\sigma)d_{ij}^0\}. \end{aligned}$$

It may be noted that when more than one locus is considered, the relation

$$d_{ij}^1 = d_{ij}^0 - i(\sigma_A^2/\sigma^2),$$

(where σ_A^2 is the additive variance for the particular locus in question) still holds. The sum of these frequencies is

$$\sum_{ij} p_i^1 p_j^1[1+(i/\sigma)d_{ij}^0] = 1.$$

The frequency of A_i becomes

$$\begin{aligned} p_i^2 &= \sum_j p_i^1 p_j^1[1+(i/\sigma)d_{ij}^0] \\ &\cong p_i^0[1+2i(\alpha_i/\sigma)]. \end{aligned}$$

Hence

$$\begin{aligned} \Pi_2 &= (\textstyle\sum p_i^2 A_i)^2 \\ &= \sum_{ij} p_i^2 p_j^2 A_i A_j, \end{aligned}$$

and

$$\begin{aligned} \mu_2 &= \sum_{ij} p_i^2 p_j^2 d_{ij}^0 \\ &\cong 2i(\sigma_A^2/\sigma^2). \end{aligned}$$

* The phrase "continuous selection" means that selection occurs in each and every cycle under consideration.

The total increment change in the population mean due to the two cycles of selection is then

$$\Delta\mu_{20} = \mu_2 - \mu_0$$
$$\cong 2i(\sigma_A^2/\sigma^2).$$

More generally, after n generations of continuous selection,

$$p_i^n \cong p_i^0 + ni\bar{p}_i^0(\alpha_i/\sigma),$$

and

$$\Delta\mu_{n0} \cong ni(\sigma_A^2/\sigma^2).$$

These responses refer to the responses due to artificial selection unopposed by natural selection. This assumption will always be made unless stated otherwise.

It is clear from these results that the *predicted* response to selection is linear when plotted against the number of selection cycles. Actually, however, the response to selection results in an asymptotic approach to the goal of selection whether it is that of homozygosity or a stable equilibrium. Hence the basis of prediction becomes more subject to error as the mean of the selected population becomes farther removed from its original position. This is primarily due to the increasing magnitude of the neglected quantities in the analysis. Thus, starting with the basic assumption that the square and products of the quantities (α/σ) are negligible, it is assumed that

$$(\bar{\imath}/\sigma)d_{ij}^n = (\bar{\imath}/\sigma)(d_{ij}^0 - \mu_n)$$
$$\cong (\bar{\imath}/\sigma)d_{ij}^0,$$

that is

$$(\bar{\imath}/\sigma)\mu_n \cong 0,$$

where μ_n is the increment change in the population mean due to n cycles of selection operating on the single locus. Clearly, as n increases this approximation becomes worse. Hence the linear predicted response holds for only a relatively short segment of the total response curve.

A general discussion of the attainment of the selection goal follows in the next section.

(iv) *Attainment of Selection Goal*

Selection operating on individuals which are subject to random mating leads to either a homozygous population or to a polymorphic population in equilibrium. The following discusses the attainment of either one of the two possible selection goals for the situation of constant selection values applied to genotypes generated by only two alleles at a single locus. In this case selection results in a stable polymorphic equilibrium if overdominance exists, and if overdominance does not exist selection results in a population homozygous for the most desirable allele. A more detailed argument follows.

Assume that as a result of selection the ratio of the three genotypes surviving selection is

$$A_1A_1 : A_1A_2 : A_2A_2 = (1-s_1) : 1 : (1-s_2) = (w_{11}/w_{12}) : 1 : (w_{22}/w_{12}).$$

Clearly then

$$s_1 \cong -(i/\sigma^2)(d_{11}-d_{12}) = -(i/\sigma^2)[(\alpha_1-\alpha_2)+(\delta_{11}-\delta_{12})],$$

and

$$s_2 \cong -(i/\sigma^2)(d_{22}-d_{12}) = -(i/\sigma^2)[(\alpha_2-\alpha_1)+(\delta_{22}-\delta_{12})].$$

From these equations it appears that the selection coefficients, and hence the selection values, are a function of both additive and non-additive effects.

The increment changes in gene frequencies, as before, are

$$\Delta p_1 \cong (i/\sigma^2)p_1\alpha_1,$$

and

$$\Delta p_2 \cong (i/\sigma^2)p_2\alpha_2.$$

Thus, changes in gene frequencies are functions of only additive gene effects.

It is obvious that the values for α's and δ's change slightly with every cycle of selection. As the goal of selection is approached,

$$\Delta p_i \to 0,$$

$$\alpha\text{'s} \to 0,$$

and

$$\sigma_A^2 \to 0.$$

The specific goal of selection depends on the degree of dominance:

(1) If partial or no dominance exists, and if A_1 is the most favoured allele, then s_1 is negative and s_2 is positive, and, therefore, the order of selection preference is $A_1A_1 > A_1A_2 > A_2A_2$. The changes in gene frequencies are: $\Delta p_1 > 0$ and $\Delta p_2 < 0$ for all values of p_1 and p_2. Thus, the population tends to homozygosity of the A_1A_1 genotype.

(2) If overdominance exists, both s_1 and s_2 are positive, irrespective of gene frequencies. Therefore, the heterozygote will be preferred over both homozygotes at all times. A stable equilibrium is reached when the gene frequencies become

$$p_1 = s_2/(s_1+s_2),$$

and

$$p_2 = s_1/(s_1+s_2).$$

Hence, the increment change in gene frequency of the A_1 allele will be positive or negative depending on the value of p_1 in the population undergoing selection relative to the equilibrium frequency of p_1.

The trend to the selection goal can be examined from the point of view of the change in the genotypic mean of the population due to selection. The increment change for a cycle of selection has been shown to be

$$\Delta\mu = i(\sigma_A^2/\sigma^2).$$

Since σ_A^2 is necessarily positive or zero, selection continuously increases the population mean until the maximum mean value is attained. This value occurs when $\Delta\mu = 0$, i.e. when $\sigma_A^2 = 0$. This is true for any degree of dominance. Thus, when partial dominance exists, the population mean is a maximum when the population is homozygous for A_1A_1, and it is only at this composition of the population that $\sigma_A^2 = 0$ and $\Delta\mu = 0$. When overdominance exists $\sigma_A^2 = 0$ and, hence, $\Delta\mu = 0$ when the stable equilibrium is reached. At this point the population has a maximum value.

When more than two alleles are considered, the equilibrium conditions are more complicated. All that needs to be mentioned in this study is that selection again may result in either a homozygous or a polymorphic population. The necessary and sufficient conditions for the maintenance of all alleles in a stable equilibrium have been given by Owen (1953), Kimura (1956), and Mandel (1959).

(*b*) *Selection of Genotypes Generated by Alleles at Two Loci which may be Linked*

This section is concerned with the consequences of selection which operates on genotypes generated by an arbitrary number of alleles at each of two linked loci. The argument holds for any recombination value and for arbitrary sets of dominance and epistatic values.

(i) *Definitions.*—In extending the considerations from one to two loci, it is useful to employ the *gamete* as the unit of inheritance rather than the gene. However, an interpretation of the gametic analysis will be made in terms of gene effects and variances.

With more than one locus to consider, the notation necessarily becomes more complicated since both loci and genes need to be identifiable. For convenience, the Kempthorne (1957) notation is used. Let $\sum_{i=1}^{m} p_i^1 A_i^1$ represent the array of alleles at the first locus and $\sum_{k=1}^{n} p_k^2 A_k^2$ represent the array of alleles at the second locus. The two loci may exhibit linkage with a recombination frequency whose value is y. Let the frequency of the gamete $(A_i^1 A_k^2)$ be $f_{ik} = p_i^1 p_k^2$. The gametic array is then $\sum_{ik} f_{ik}(A_i^1 A_k^2)$.

The random-mating population in equilibrium may be generated by squaring the gametic array, i.e.

$$[\sum_{ik} f_{ik}(A_i^1 A_k^2)]^2 = \sum_{ijkl} f_{ik} f_{jl}(A_i^1 A_k^2)(A_j^1 A_l^2).$$

This representation is set out in the following two-way table in which the genotypic value of $(A_i^1 A_k^2)(A_j^1 A_l^2)$ is $d_{ik.jl}$ whose value is chosen such that

$$\sum_{ijkl} f_{ik} f_{jl}\, d_{ik.jl} = 0.$$

	$A_1^1A_1^2$	$A_1^1A_2^2$	. . .	$A_m^1A_n^2$	
	(f_{11})	(f_{12})		(f_{mn})	
$A_1^1A_1^2$	$d_{11.11}$	$d_{11.12}$		$d_{11.mn}$	
(f_{11})	$(f_{11})^2$	$(f_{11}f_{12})$	. . .	$(f_{11}f_{mn})$	
	$w_{11.11}$	$w_{11.12}$		$w_{11.mn}$	
.	.	.	.	.	
.	.	.	.	.	
.	.	.	.	.	
$A_m^1A_n^2$	$d_{mn.11}$	$d_{mn.12}$		$d_{mn.mn}$	
(f_{mn})	$(f_{mn}f_{11})$	$(f_{mn}f_{12})$	. . .	$(f_{mn})^2$	
	$w_{mn.11}$	$w_{mn.12}$		$w_{mn.mn}$	

The genotypic value, $d_{ik.jl}$, is characterized by the Kempthorne gene model as follows:

$$d_{ik.jl} = \alpha_i^1+\alpha_j^1+\alpha_k^2+\alpha_l^2+\delta_{ij}^1+\delta_{kl}^2+(\alpha\alpha)_{ik}+(\alpha\alpha)_{il}+(\alpha\alpha)_{jk}+(\alpha\alpha)_{jl}$$
$$+(\alpha\delta)_{ikl}+(\alpha\delta)_{jkl}+(\delta\alpha)_{ijk}+(\delta\alpha)_{ijl}+(\delta\delta)_{ijkl},$$

where

α_u^a = additive genetic effect of the A_u^a allele,

δ_{uv}^a = dominance effect for the $A_u^aA_v^a$ genotype,

$(\alpha\alpha)_{ik}$ = additive × additive epistatic effect associated with genes A_i^1 and A_k^2,

$(\alpha\delta)_{ikl}$ = additive × dominance epistatic effect associated with the gene A_i^1 and the genotype $A_k^2A_l^2$, and

$(\delta\delta)_{ijkl}$ = dominance × dominance epistatic effect associated with the genotypes $A_i^1A_j^1$ and $A_k^2A_l^2$.

The total genotypic variance may be partitioned as

$$\sigma_G^2 = \sigma_A^2+\sigma_D^2+\sigma_{AA}^2+\sigma_{AD}^2+\sigma_{DD}^2,$$

where

σ_G^2 = total genotypic variance generated by the two loci,

σ_A^2 = additive genetic variance,

σ_D^2 = dominance variance,

σ_{AA}^2 = additive × additive variance,

σ_{AD}^2 = additive × dominance variance,

and

σ_{DD}^2 = dominance × dominance variance.

The selection value $w_{ik.jl}$ for the genotype $(A_i^1A_k^2)(A_j^1A_l^2)$ is defined to be proportional to the probability that an individual of the genotype $(A_i^1A_k^2)(A_j^1A_l^2)$ survives selection. Following the same argument as given for the single locus case, the selection value is

$$w_{ik.jl} = 1+(i/\sigma^2)d_{ik.jl}.$$

(ii) *Consequences of One Cycle of Selection.*—The objective of this section is to determine the changes in population parameters due to one cycle of truncation selection which is then followed by an indefinite number of cycles of random mating without selection. The programme starts with a random-mating population in equilibrium, which is designated as Π_0. As before, to simplify notation all parameters of the gene model are assumed to be those associated with Π_0 and therefore will not have a superscript notation.

The frequency of the genotype $(A_i^1A_k^2)(A_j^1A_l^2)$ following selection is

$$f_{ik}^0 f_{jl}^0 w_{ik.jl}^0 = f_{ik}^0 f_{jl}^0[1+(i/\sigma^2)d_{ik.jl}^0].$$

The total frequency over all selected genotypes is

$$\sum_{ijkl} f_{ik}^0 f_{jl}^0[1+(i/\sigma^2)d_{ik.jl}^0] = 1.$$

The genotypic mean of the selected parents is

$$\mu_s = \sum_{ijkl} f_{ik}^0 f_{jl}^0[1+(i/\sigma^2)d_{ik.jl}^0]d_{ik.jl}^0.$$

The progeny population resulting from random mating the selected parents can be generated by squaring the gametic array produced by the selected parents. To obtain this array it is first necessary to consider the gametic array produced by an arbitrary genotype, $(A_i^1A_k^2)(A_j^1A_l^2)$, which is

$$\{[(1-y)/2](A_i^1A_k^2+A_j^1A_l^2)+(y/2)(A_i^1A_l^2+A_j^1A_k^2)\}.$$

The gametic array for all selected parents is then,

$$\sum_{ijkl} f_{ik}^0 f_{jl}^0 w_{ik.jl}^0\{[(1-y)/2](A_i^1A_k^2+A_j^1A_l^2)+(y/2)(A_i^1A_l^2+A_j^1A_k^2)\},$$

which, on using a summation device illustrated by Kempthorne (1957), is equal to

$$\sum_{ijkl}\{f_{ik}^0 f_{jl}^0 w_{ik.jl}^0(1-y)/2+f_{jl}^0 f_{ik}^0 w_{jl.ik}^0(1-y)/2+f_{il}^0 f_{jk}^0 w_{il.jk}^0(y/2)+f_{jk}^0 f_{il}^0 w_{jk.il}^0(y/2)\}(A_i^1A_k^2)$$

$$= \sum_{ijkl}\{f_{ik}^0 f_{jl}^0 w_{ik.jl}^0(1-y)+f_{il}^0 f_{jk}^0 w_{il.jk}^0(y)\}(A_i^1A_k^2)$$

$$= \sum_{ik} f_{ik}^1(A_i^1A_k^2),$$

where

$$f_{ik}^1 = f_{ik}^0 \sum_{jl} f_{jl}^0[1+(i/\sigma^2)d_{ik.jl}^0]$$

$$= f_{ik}^0+(i/\sigma^2)f_{ik}^0[\alpha_i^1+\alpha_k^2+(\alpha\alpha)_{ik}].$$

The frequency of the progeny genotype $(A_i^1A_k^2)(A_j^1A_l^2)$ is

$$f_{ik}^1 f_{jl}^1 = \{f_{ik}^0+(i/\sigma^2)f_{ik}^0[\alpha_i^1+\alpha_k^2+(\alpha\alpha)_{ik}]\}\{f_{jl}^0+(i/\sigma^2)f_{jl}^0[\alpha_j^1+\alpha_l^2+(\alpha\alpha)_{jl}]\}$$

$$\cong f_{ik}^0 f_{jl}^0+(i/\sigma^2)f_{ik}^0 f_{jl}^0[\alpha_i^1+\alpha_j^1+\alpha_k^2+\alpha_l^2+(\alpha\alpha)_{ik}+(\alpha\alpha)_{jl}].$$

The genotypic mean of the progeny population, then, is

$$\mu_1 = \sum_{ijkl} f_{ik}^1 f_{jl}^1 d_{ik.jl}^0$$

$$\cong (i/\sigma^2)[\sigma_A^2+\tfrac{1}{2}\sigma_{AA}^2].$$

It is immediately apparent that this mean value for Π_1 is not the same as that predicted with the gene analysis. Thus, when it is considered that selection operates on genotypes at each locus separately, one cycle of selection results in an increment change of $(i/\sigma^2)\sigma_{A(1)}^2$ for the first locus and $(i/\sigma^2)\sigma_{A(2)}^2$ for the second locus. The total increment change due to selection operating separately on the two loci is, then,

$$\mu_1 = (i/\sigma^2)[\sigma_{A(1)}^2+\sigma_{A(2)}^2]$$

$$= (i/\sigma^2)\sigma_A^2.$$

Although it is clear that the more accurate prediction of the *immediate* results of one cycle of selection is that obtained by using the gamete rather than the gene analysis, the question remains as to what happens to the predicted mean value when selection is relaxed and mating is continued at random.

Briefly, the answer is as follows; if epistasis occurs, the progeny population, Π_1, is not in gene equilibrium, i.e.

$$\sum_{ijkl} f_{ik}^1 f_{jl}^1 (A_i^1A_k^2)(A_j^1A_l^2) \neq [\sum_{ij} (p_i^1)^1 (p_j^1)^1 A_i^1A_j^1] \cdot [\sum_{kl} (p_k^2)^1 (p_l^2)^1 A_k^2A_l^2],$$

or more simply

$$f_{uv}^1 \neq (p_u^1)^1 (p_v^2)^1,$$

where $(p_u^1)^1$ is the frequency of A_u^1 in Π_1.

Since the progeny population is not in gene equilibrium and since the gamete is a highly mutable unit of inheritance (i.e. $(A_i^1A_k^2)(A_j^1A_l^2)$ produces not only parental but also a relatively high frequency of non-parental gametes) continued random mating in the absence of selection causes the population structure to continually change until equilibrium is reached. In the case of two linked loci the speed of this change depends on the magnitude of the recombination frequency. As the structure of the population changes, the mean of the population decays until finally, at equilibrium, the population mean equals that which is predicted on the basis of the gene as a unit of inheritance. Then, assuming that the gene is stable and that natural selection is not operating, the population mean will remain at this value. The following develops the argument more rigorously.

Starting with the progeny population which results from one cycle of selection, the objective is to show what happens to the population structure and the population mean value when random mating is continued without selection. Again,

consider the parameters associated with the gene model as those defined for the population Π_0 and, therefore, the superscript "0" will not be used. However, the gamete frequencies will have a more complicated superscript notation, i.e. let $f_{ik}^{1,r}$ denote the frequency of the gamete $(A_i^1 A_k^2)$ in the rth generation of random mating without selection, after one cycle of selection.

The progeny population following one cycle of selection may be designated as

$$\Pi_{1,0} = \sum_{ijkl} f_{ik}^{1,0} f_{jl}^{1,0} (A_i^1 A_k^2)(A_j^1 A_l^2).$$

The total gametic array from $\Pi_{1,0}$, in the absence of selection, is

$$\begin{aligned}
&\sum_{ijkl} f_{ik}^{1,0} f_{jl}^{1,0} \{[(1-y)/2](A_i^1 A_k^2 + A_j^1 A_l^2) + (y/2)(A_i^1 A_l^2 + A_j^1 A_k^2)\} \\
&\quad = \sum_{ijkl} [(1-y) f_{ik}^{1,0} f_{jl}^{1,0} + y f_{il}^{1,0} f_{jk}^{1,0}](A_i^1 A_k^2) \\
&\quad = \sum_{ik} f_{ik}^{1,1} (A_i^1 A_k^2),
\end{aligned}$$

where

$$\begin{aligned}
f_{ik}^{1,1} &= \sum_{jl} \{(1-y) f_{ik}^{1,0} f_{jl}^{1,0} + y f_{il}^{1,0} f_{jk}^{1,0}\} \\
&= (1-y) f_{ik}^{1,0} + y \sum_{jl} f_{il}^{1,0} f_{jk}^{1,0} \qquad \text{.....(1)} \\
&= (1-y)\{f_{ik}^{0,0} + (i/\sigma^2) f_{ik}^{0,0} [\alpha_i^1 + \alpha_k^2 + (\alpha\alpha)_{ik}]\} \\
&\quad + y \sum_{jl} \{f_{il}^{0,0} + (i/\sigma^2) f_{il}^{0,0} [\alpha_i^1 + \alpha_l^2 + (\alpha\alpha)_{il}]\}\{f_{jk}^{0,0} + (i/\sigma^2) f_{jk}^{0,0} [\alpha_j^1 + \alpha_k^2 + (\alpha\alpha)_{jk}]\} \\
&\cong f_{ik}^{0,0} + (i/\sigma^2) f_{ik}^{0,0} [\alpha_i^1 + \alpha_k^2 + (1-y)(\alpha\alpha)_{ik}].
\end{aligned}$$

The mean of the population $\Pi_{1,1}$ is then

$$\begin{aligned}
\mu_{1,1} &= \sum_{ijkl} f_{ik}^{1,1} f_{jl}^{1,1} d_{ik.jl}^0 \\
&= \sum_{ijkl} \{f_{ik}^{0,0} + (i/\sigma^2) f_{ik}^{0,0} [\alpha_i^1 + \alpha_k^2 + (1-y)(\alpha\alpha)_{ik}]\} \\
&\qquad \times \{f_{jl}^{0,0} + (i/\sigma^2) f_{jl}^{0,0} [\alpha_j^1 + \alpha_l^2 + (1-y)(\alpha\alpha)_{jl}]\} d_{ik.jl}^0 \\
&\cong (i/\sigma^2)[\sigma_A^2 + (1-y)\tfrac{1}{2}\sigma_{AA}^2].
\end{aligned}$$

An argument used by Kempthorne (1957) may be employed to predict the mean after an arbitrary number m of generations of random mating without selection.

Equation (1) may be rewritten as

$$f_{ik}^{1,1} = (1-y) f_{ik}^{1,0} + y \sum_l f_{il}^{1,0} \sum_j f_{jk}^{1,0},$$

where

$$\sum_l f_{il}^{1,0} = f_{i.}^{1,0} = \text{frequency of } A_i^1 \text{ in } \Pi_{1,0},$$

and

$$\sum_j f_{jk}^{1,0} = f_{.k}^{1,0} = \text{frequency of } A_k^2 \text{ in } \Pi_{1,0}.$$

In the absence of selection gene frequencies do not change, i.e. $f_{i.}^{1,1} = f_{i.}^{1,0}$ etc. Therefore, the quantity $(f_{i.}^{1,1}.f_{.k}^{1,1})$ may be subtracted from the right-hand side of (**1**) and $(f_{.i}^{1,0}.f_{.k}^{1,0})$ may be subtracted from the left-hand side of the same equation. Thus,

$$f_{ik}^{1,1} - f_{i.}^{1,1} f_{.k}^{1,1} = (1-y) f_{ik}^{1,0} + y f_{i.}^{1,0} f_{.k}^{1,0} - f_{i.}^{1,0} f_{.k}^{1,0}$$

$$= (1-y)(f_{ik}^{1,0} - f_{i.}^{1,0} f_{.k}^{1,0}),$$

or

$$\Delta_{ik}^{1,1} = (1-y)\,\Delta_{ik}^{1,0}.$$

Likewise

$$\Delta_{ik}^{1,2} = (1-y)\,\Delta_{ik}^{1,1}.$$

$$= (1-y)^2 \Delta_{ik}^{1,0},$$

and more generally

$$\Delta_{ik}^{1,m} = (1-y)^m \Delta_{ik}^{1,0},$$

or

$$f_{ik}^{1,m} - f_{i.}^{1,m} f_{.k}^{1,m} = (1-y)^m (f_{ik}^{1,0} - f_{i.}^{1,0} f_{.k}^{1,0}).$$

Since $f_{i.}^{1,m} = f_{i.}^{1,0}$, etc.

$$f_{ik}^{1,m} = f_{i.}^{1,0} f_{.k}^{1,0} + (1-y)^m (f_{ik}^{1,0} - f_{i.}^{1,0} f_{.k}^{1,0}). \qquad \ldots\ldots\ldots (2)$$

Recalling that

$$f_{i.}^{1,0} = p_i^1[1 + (i/\sigma^2)\alpha_i^1],$$

$$f_{.k}^{1,0} = p_k^2[1 + (i/\sigma^2)\alpha_k^2],$$

and

$$f_{ik}^{1,0} = f_{ik}^{0,0}\{1 + (i/\sigma^2)[\alpha_i^1 + \alpha_k^2 + (\alpha\alpha)_{ik}]\},$$

equation (**2**) becomes,

$$f_{ik}^{1,m} \cong f_{ik}^{0,0}\{1 + (i/\sigma^2)[\alpha_i^1 + \alpha_k^2 + (1-y)^m (\alpha\alpha)_{ik}]\}.$$

The mean of the population which is submitted to one cycle of selection and then to m generations of random mating without selection is

$$\mu_{1,m} = \sum_{ijkl} f_{ik}^{1,m} f_{jl}^{1,m} d_{ik.jl}^{0}$$

$$\cong (i/\sigma^2)[\sigma_A^2 + (1-y)^m \tfrac{1}{2}\sigma_{AA}^2].$$

Thus, with random mating without selection, the mean of the population $\Pi_{1,0}$ decays toward the lower asymptote which is

$$\lim_{m\to\infty} (\mu_{1,m}) \to (i/\sigma^2)\sigma_A^2.$$

This is the value predicted by the gene analysis.

The change in population mean may also be described by the use of the increment mean values. Thus, if the increment change for means in the $(m-1)$th

and mth populations is defined as

$$ {}_1\Delta_{(m-1),m} = \mu_{1,(m-1)} - \mu_{1,m}, $$

then

$$ {}_1\Delta_{(m-1),m} = (i/\sigma^2)\{(1-y)^{m-1}[1-(1-y)]\}\tfrac{1}{2}\sigma^2_{AA} $$

$$ = (i/\sigma^2)[y(1-y)^{m-1}]\tfrac{1}{2}\sigma^2_{AA}. $$

Hence

$$ \lim_{m\to\infty}[{}_1\Delta_{(m-1),m}] \to 0. $$

(iii) *Consequences of Two or More Cycles of Continuous Selection.*—The objective in this section is to describe the changes in parameters which occur with an arbitrary number of continuous cycles of selection. The procedure will be to outline briefly the normal method of obtaining Π_2 by selecting in Π_1. Then the problem of generalizing to n generations of continuous selection will be attacked.

In the previous section it was shown that one generation of selection yielded the following population

$$ \Pi_1 = \sum_{ijkl} f^1_{ik} f^1_{jl} (A^1_i A^2_k)(A^1_j A^2_l). $$

After selection, the frequency of $(A^1_i A^2_k)(A^1_j A^2_l)$ is

$$ f^1_{ik} f^1_{jl} w^1_{ik.jl} \cong f^1_{ik} f^1_{jl} w^0_{ik.jl} $$

$$ = f^1_{ik} f^1_{jl}[1 + (i/\sigma^2) d^0_{ik.jl}]. $$

The total array of gametes from the selected genotypes is

$$ \sum_{ijkl} f^1_{ik} f^1_{jl} w^0_{ik.jl}\{[(1-y)/2](A^1_i A^2_k + A^1_j A^2_l) + (y/2)(A^1_i A^2_l + A^1_j A^2_k)\} $$

$$ = \sum_{ik} f^2_{ik}(A^1_i A^2_k), $$

where

$$ f^2_{ik} = \sum_{jl}[(1-y) f^1_{ik} f^1_{jl} w^0_{ik.jl} + y f^1_{il} f^1_{jk} w^0_{il.jk}] $$

$$ = A + B. $$

The A term may be evaluated as follows:

$$ A = (1-y)\sum_{jl}\{f^0_{ik} f^0_{jl} + (i/\sigma^2) f^0_{ik} f^0_{jl}[\alpha^1_i + \alpha^1_j + \alpha^2_k + \alpha^2_l + (\alpha\alpha)_{ik} + (\alpha\alpha)_{jl}] + (i/\sigma^2) f^0_{ik} f^0_{jl} d^0_{ik.jl}\} $$

$$ = (1-y)\{f^0_{ik} + 2(i/\sigma^2) f^0_{ik}[\alpha^1_i + \alpha^2_k + (\alpha\alpha)_{ik}]. $$

The B term yields

$$ B = y\sum_{jl}\{f^0_{il} f^0_{jk} + (i/\sigma^2) f^0_{il} f^0_{jk}[\alpha^1_i + \alpha^1_j + \alpha^2_k + \alpha^2_l + (\alpha\alpha)_{il} + (\alpha\alpha)_{jk}] + (i/\sigma^2) f^0_{il} f^0_{jk} d^0_{il.jk}\} $$

$$ = y\{f^0_{ik} + (i/\sigma^2) f^0_{ik}(\alpha^1_i + \alpha^2_k) + (i/\sigma^2) f^0_{ik}[\alpha^1_i + \alpha^2_k + (\alpha\alpha)_{ik}]\}. $$

Hence

$$f_{ik}^2 = f_{ik}^0 + 2(i/\sigma^2) f_{ik}^0[\alpha_i^1 + \alpha_k^2 + (\alpha\alpha)_{ik}] - y(i/\sigma^2) f_{ik}^0 (\alpha\alpha)_{ik}.$$

The mean of Π_2 is, then,

$$\begin{aligned}
\mu_2 &= \sum_{ijkl} f_{ik}^2 f_{jl}^2 d_{ik.jl}^0 \\
&\cong \sum_{ijkl} \{f_{ik}^0 f_{jl}^0 + 2(i/\sigma^2) f_{ik}^0 f_{jl}^0 [\alpha_i^1 + \alpha_j^1 + \alpha_k^2 + \alpha_l^2 + (\alpha\alpha)_{ik} + (\alpha\alpha)_{jl}] \\
&\qquad - y(i/\sigma^2) f_{ik}^0 f_{jl}^0 [(\alpha\alpha)_{ik} + (\alpha\alpha)_{jl}]\} d_{ik.jl}^0 \\
&= 2(i/\sigma^2)(\sigma_A^2 + \tfrac{1}{2}\sigma_{AA}^2) - y(i/\sigma^2)\tfrac{1}{2}\sigma_{AA}^2 \\
&= (i/\sigma^2)[\sigma_A^2 + \tfrac{1}{2}\sigma_{AA}^2] + (i/\sigma^2)[\sigma_A^2 + (1-y)\tfrac{1}{2}\sigma_{AA}^2].
\end{aligned}$$

The final problem is to generalize the results to n generations of continuous selection. Thus, it is required to give the approximate value for the mean of Π_n in terms of the parameters of Π_0. To do this it is necessary to express the frequency of the gamete $(A_i^1 A_k^2)$ in the nth generation in terms of the frequency of the same gamete in Π_0.

The first step is to obtain a recurrence relation involving f_{ik}^n and f_{ik}^{n-1}. Consider, then, the $(n-1)th$ generation, i.e.

$$\Pi_{(n-1)} = \sum_{ijkl} f_{ik}^{n-1} f_{jl}^{n-1} (A_i^1 A_k^2)(A_j^1 A_l^2).$$

Following selection, the frequency of $(A_i^1 A_k^2)(A_j^1 A_l^2)$ is

$$f_{ik}^{n-1} f_{jl}^{n-1} w_{ik.jl}^{n-1} \cong f_{ik}^{n-1} f_{jl}^{n-1} w_{ik.jl}^0.$$

The total array of gametes from the selected parents is

$$\begin{aligned}
&\sum_{ijkl} f_{ik}^{n-1} f_{jl}^{n-1} w_{ik.jl}^0 \{[(1-y)/2](A_i^1 A_k^2 + A_j^1 A_l^2) + (y/2)(A_i^1 A_l^2 + A_j^1 A_k^2)\} \\
&\qquad = \sum_{ik} f_{ik}^n (A_i^1 A_k^2),
\end{aligned}$$

where

$$\begin{aligned}
f_{ik}^n &= \sum_{jl} [(1-y) f_{ik}^{n-1} f_{jl}^{n-1} w_{ik.jl}^0 + y f_{il}^{n-1} f_{jk}^{n-1} w_{il.jk}^0] \\
&= A + B.
\end{aligned}$$

The terms A and B may be evaluated as follows:

$$A = (1-y) f_{ik}^{n-1} + (1-y)(i/\sigma^2) f_{ik}^{n-1} \sum_{jl} f_{jl}^{n-1} d_{ik.jl}^0,$$

and

$$B = y f_{i.}^{n-1} f_{.k}^{n-1} + y(i/\sigma^2) \sum_{jl} f_{il}^{n-1} f_{jk}^{n-1} d_{il.jk}^0.$$

Hence

$$f_{ik}^n = (1-y) f_{ik}^{n-1} + y f_{i.}^{n-1} f_{.k}^{n-1} + (1-y)(i/\sigma^2) f_{ik}^{n-1} \sum_{jl} f_{jl}^{n-1} d_{ik.jl}^0 + y(i/\sigma^2) \sum_{jl} f_{il}^{n-1} f_{jk}^{n-1} d_{il.jk}^0.$$

In order to evaluate f_{ik}^n in terms of the parameters of Π_0, consider, first, the frequencies of f_{ik} for the first few cycles:

(i) $n = 1$

$$f_{ik}^1 = (1-y)f_{ik}^0+(i/\sigma^2)f_{ik}^0[\alpha_i^1+\alpha_k^2+(\alpha\alpha)_{ik}]+yf_{ik}^0.$$

(ii) $n = 2$

$$f_{ik}^2 = (1-y)^2f_{ik}^0+[1+(1-y)](i/\sigma^2)f_{ik}^0[\alpha_i^1+\alpha_k^2+(\alpha\alpha)_{ik}]$$
$$+[1+(1-y)]yf_{ik}^0+y(i/\sigma^2)f_{ik}^0(\alpha_i^1+\alpha_k^2).$$

(iii) $n = 3$

$$f_{ik}^3 = (1-y)^3f_{ik}^0+[1+(1-y)+(1-y)^2](i/\sigma^2)f_{ik}^0[\alpha_i^1+\alpha_k^2+(\alpha\alpha)_{ik}]$$
$$+[1+(1-y)+(1-y)^2]yf_{ik}^0+[2+(1-y)]y(i/\sigma^2)f_{ik}^0(\alpha_i^1+\alpha_k^2).$$

(iv) $n = 4$

$$f_{ik}^4 = (1-y)^4f_{ik}^0+[1+(1-y)+(1-y)^2+(1-y)^3](i/\sigma^2)f_{ik}^0[\alpha_i^1+\alpha_k^2+(\alpha\alpha)_{ik}]$$
$$+[1+(1-y)+(1-y)^2+(1-y)^3]yf_{ik}^0+[3+2(1-y)+(1-y)^2]y(i/\sigma^2)f_{ik}^0(\alpha_i^1+\alpha_k^2).$$

It appears that, in general,

$$f_{ik}^n = (1-y)^nf_{ik}^0+[\sum_{r=1}^{n}(1-y)^{r-1}]yf_{ik}^0+[\sum_{r=1}^{n}(1-y)^{r-1}](i/\sigma^2)f_{ik}^0[\alpha_i^1+\alpha_k^2+(\alpha\alpha)_{ik}]$$
$$+\{\sum_{t=1}^{n-1}[\sum_{r=1}^{t}(1-y)^{r-1}]y\}(i/\sigma^2)f_{ik}^0(\alpha_i^1+\alpha_k^2)$$
$$=\{(1-y)^n+y[(1-(1-y)^n)/y]\}f_{ik}^0+[(1-(1-y)^n)/y](i/\sigma^2)f_{ik}^0[\alpha_i^1+\alpha_k^2+(\alpha\alpha)_{ik}]$$
$$+\{\sum_{t=1}^{n-1}[(1-(1-y)^t)/y]y\}(i/\sigma^2)f_{ik}^0(\alpha_i^1+\alpha_k^2)$$
$$=f_{ik}^0+[(1-(1-y)^n)/y](i/\sigma^2)f_{ik}^0[\alpha_i^1+\alpha_k^2+(\alpha\alpha)_{ik}]+\{n-[(1-(1-y)^n)/y]\}(i/\sigma^2)f_{ik}^0(\alpha_i^1+\alpha_k^2)$$
$$=f_{ik}^0+n(i/\sigma^2)f_{ik}^0(\alpha_i^1+\alpha_k^2)+[(1-(1-y)^n)/y](i/\sigma^2)f_{ik}^0[(\alpha\alpha)_{ik}].$$

Having obtained an expression relating the frequency of the gamete $(A_i^1A_k^2)$ in the nth generation to parameters in Π_0, it is possible to evaluate the mean of Π_n in terms of the parameters of Π_0. Thus,

$$\mu_n = \sum_{ijkl} f_{ik}^n f_{jl}^n d_{ik.jl}^0$$
$$= \sum_{ijkl}\{f_{ik}^0+n(i/\sigma^2)f_{ik}^0(\alpha_i^1+\alpha_k^2)+[(1-(1-y)^n)/y](i/\sigma^2)f_{ik}^0[(\alpha\alpha)_{ik}]\}$$
$$\times\{f_{jl}^0+n(i/\sigma^2)f_{jl}^0(\alpha_j^1+\alpha_l^2)+[(1-(1-y)^n)/y](i/\sigma^2)f_{jl}^0[(\alpha\alpha)_{jl}]\}\times d_{ik.jl}^0$$
$$\cong \sum_{ijkl}\{f_{ik}^0f_{jl}^0+n(i/\sigma^2)f_{ik}^0f_{jl}^0(\alpha_i^1+\alpha_j^1+\alpha_k^2+\alpha_l^2)+[(1-(1-y)^n)/y]$$
$$\times(i/\sigma^2)f_{ik}^0f_{jl}^0[(\alpha\alpha)_{ik}+(\alpha\alpha)_{jl}]\}\times d_{ik.jl}^0$$
$$= n(i/\sigma^2)(\sigma_A^2)+[(1-(1-y)^n)/y](i/\sigma^2)\tfrac{1}{2}\sigma_{AA}^2,$$

or

$$\mu_n = (i/\sigma^2)[n\,\sigma_A^2 + \sum_{r=1}^{n} (1-y)^{r-1}\tfrac{1}{2}\sigma_{AA}^2]$$

$$= (i/\sigma^2)[\sigma_A^2+\tfrac{1}{2}\sigma_{AA}^2]+(i/\sigma^2)[\sigma_A^2+(1-y)\tfrac{1}{2}\sigma_{AA}^2]+ \ldots$$

$$+ \ldots +(i/\sigma^2)[\sigma_A^2+(1-y)^{n-1}\tfrac{1}{2}\sigma_{AA}^2].$$

It is clear that the extent of the influence of σ_{AA}^2 is largely determined by the magnitude of the recombination value which has the range $0 \leqslant y \leqslant \frac{1}{2}$. Thus if $y=0$ (i.e. no recombination),

$$\mu_n = (i/\sigma^2)[n\,\sigma_A^2+n(\tfrac{1}{2}\sigma_{AA}^2)],$$

and if $y = \frac{1}{2}$ (loci independent),

$$\mu_n = (i/\sigma^2)\{n\,\sigma_A^2+[2-(\tfrac{1}{2})^{n-1}]\tfrac{1}{2}\sigma_{AA}^2\}.$$

Therefore, if the loci exhibit a low recombination value, considerable effect can be generated by σ_{AA}^2, and if the loci are independent the maximum contribution after n generations of selection is approximately σ_{AA}^2 (with large n).

It is also clear that even with constant selection differential and quite apart from the disturbance due to approximations, the increment changes between consecutive cycles of selection are not equal (assuming $y \neq 0$). Thus, if $\Delta\mu_{n.n-1} = \mu_n - \mu_{n-1}$, then

$$\Delta\mu_{1,0} = (i/\sigma^2)[\sigma_A^2+\tfrac{1}{2}\sigma_{AA}^2],$$

$$\Delta\mu_{2,1} = (i/\sigma^2)[\sigma_A^2+(1-y)\tfrac{1}{2}\sigma_{AA}^2],$$

and more generally

$$\Delta\mu_{n,n-1} = (i/\sigma^2)[\sigma_A^2+(1-y)^{n-1}\tfrac{1}{2}\sigma_{AA}^2].$$

Hence, the influence of σ_{AA}^2 diminishes as the number of cycles in the selection programme increases. This causes a departure from linearity of the response of selection with time.

(iv) *Consequences of Relaxation of Selection after* n *Cycles of Continuous Selection.*—The objective in this last part of the section dealing with the consequences of selection operating on genotypes generated by alleles at two loci is to develop the prediction equation for the mean of a population which is submitted to n generations of continuous selection and then to m generations of random mating without selection.

In the last section it was shown that the population after n continuous cycles of selection had the following structure

$$\Pi_{n,0} = \sum_{tjkl} f_{tk}^{n,0} f_{jl}^{n,0} (A_t^1 A_k^2)(A_j^1 A_l^2).$$

If, now, mating is at random, in the absence of selection, the frequency of the gamete $(A_i^1 A_k^2)$ in the next generation is

$$f_{ik}^{n,1} = (1-y) f_{ik}^{n,0} + y f_{i.}^{n,0} f_{.k}^{n,0}.$$

Since gene frequencies do not change, this equation may be rewritten as

$$f_{ik}^{n,1} - f_{i.}^{n,1} f_{.k}^{n,1} = (1-y)(f_{ik}^{n,0} - f_{i.}^{n,0} f_{.k}^{n,0}),$$

which may be symbolized as

$$\Delta_{ik}^{n,1} = (1-y)\,\Delta_{ik}^{n,0}.$$

More generally

$$\Delta_{ik}^{n,m} = (1-y)^m \Delta_{ik}^{n,0},$$

or

$$f_{ik}^{n,m} = f_{i.}^{n,0} f_{.k}^{n,0} + (1-y)^m (f_{ik}^{n,0} - f_{i.}^{n,0} f_{.k}^{n,0}). \quad \ldots(3)$$

Recalling that

$$f_{i.}^{n,0} = p_i^1 + n(i/\sigma^2) p_i^1 \alpha_i^1,$$

$$f_{.k}^{n,0} = p_k^2 + n(i/\sigma^2) p_k^2 \alpha_k^2,$$

and

$$f_{ik}^{n,0} = f_{jk}^{0,0} + a(i/\sigma^2) f_{ik}^{0,0}[\alpha_i^1 + \alpha_k^2 + (\alpha\alpha)_{ik}] + b(i/\sigma^2) f_{ik}^{0,0}(\alpha_i^1 + \alpha_k^2),$$

where

$$a = [(1-(1-y)^n)/y],$$

and

$$b = \{n - [(1-(1-y)^n)/y]\},$$

equation (3) becomes

$$f_{ik}^{n,m} = f_{ik}^{0,0} + n(i/\sigma^2) f_{ik}^{0,0}(\alpha_i^1 + \alpha_k^2) + (1-y)^m \{a(i/\sigma^2) f_{ik}^{0,0}[\alpha_i^1 + \alpha_k^2 + (\alpha\alpha)_{ik}] + (b-n)(i/\sigma^2) f_{ik}^{0,0}(\alpha_i^1 + \alpha_k^2)\}.$$

It is now possible to obtain the mean of the population that has had a history of n generations of selection followed by m generations of random mating without selection. This mean is

$$\begin{aligned}
\mu_{n,m} &= \sum_{ijkl} f_{ik}^{n,m} f_{jl}^{n,m} d_{ik.jl}^{0} \\
&\cong \sum_{ijkl} \{f_{ik}^{0,0} f_{jl}^{0,0} + n(i/\sigma^2) f_{ik}^{0,0} f_{jl}^{0,0}(\alpha_i^1 + \alpha_j^1 + \alpha_k^2 + \alpha_l^2) + (1-y)^m a(i/\sigma^2) \\
&\quad \times f_{ik}^{0,0} f_{jl}^{0,0}[\alpha_i^1 + \alpha_j^1 + \alpha_k^2 + \alpha_l^2 + (\alpha\alpha)_{ik} + (\alpha\alpha)_{jl}] \\
&\quad + (1-y)^m (b-n)(i/\sigma^2) f_{ik}^{0,0} f_{jl}^{0,0}(\alpha_i^1 + \alpha_j^1 + \alpha_k^2 + \alpha_l^2)\} \times d_{ik.jl}^{0} \\
&= n(i/\sigma^2)\sigma_A^2 + (1-y)^m a(i/\sigma^2)(\sigma_A^2 + \tfrac{1}{2}\sigma_{AA}^2) + (1-y)^m (b-n)(i/\sigma^2)\sigma_A^2 \\
&= n(i/\sigma^2)\sigma_A^2 + [(1-(1-y)^n)/y](1-y)^m (i/\sigma^2)\tfrac{1}{2}\sigma_{AA}^2,
\end{aligned}$$

or

$$\begin{aligned}
\mu_{n,m} &= n(i/\sigma^2)\sigma_A^2 + (1-y)^m [\sum_{r=1}^{n} (1-y)^{r-1}](i/\sigma^2)\tfrac{1}{2}\sigma_{AA}^2 \\
&= (i/\sigma^2)[\sigma_A^2 + (1-y)^m \tfrac{1}{2}\sigma_{AA}^2] + (i/\sigma^2)[\sigma_A^2 + (1-y)^m (1-y)\tfrac{1}{2}\sigma_{AA}^2] \\
&\quad + \ldots + (i/\sigma^2)[\sigma_A^2 + (1-y)^m (1-y)^{n-1} \tfrac{1}{2}\sigma_{AA}^2].
\end{aligned}$$

If the increment change in means in the $(m-1)$th and mth populations is defined as

$$ {}_n\Delta\mu_{(m-1),m} = \mu_{n,m-1} - \mu_{n,m}, $$

then

$$ \begin{aligned} {}_n\Delta\mu_{(m-1),m} &= \{[(1-(1-y)^n)/y](1-y)^{m-1} - [(1-(1-y)^n)/y](1-y)^m\}(i/\sigma^2)\tfrac{1}{2}\sigma^2_{AA} \\ &= [(1-(1-y)^n)/y](1-y)^{m-1}[1-(1-y)](i/\sigma^2)\tfrac{1}{2}\sigma^2_{AA} \\ &= (1-y)^{m-1}[1-(1-y)^n](i/\sigma^2)\tfrac{1}{2}\sigma^2_{AA}. \end{aligned} $$

When $n = 1$,

$$ {}_1\Delta\mu_{(m-1),m} = (1-y)^{m-1}y(i/\sigma^2)\tfrac{1}{2}\sigma^2_{AA}, $$

as found in a previous section.

It is quite clear that for any value of n,

$$ \lim_{m\to\infty} ({}_n\Delta\mu_{(m-1),m}) \to 0. $$

Thus, the mean of the population $\Pi_{n,0}$ decays to

$$ \lim_{m\to\infty} (\mu_{n,m}) \to n(i/\sigma^2)\sigma^2_A. $$

Again it must be pointed out that in this analysis it is assumed that natural selection is not operating.

(c) *Generalizations*

The approach which utilizes a gamete analysis with a gene interpretation, as set out for the two-locus case, can be extended to include more loci. However, the problem becomes immensely difficult due, primarily, to the increase in the number of linkage parameters. For example, with three loci there are three recombination values which must be considered. It is for this reason that a somewhat different approach is used.

By introducing the notion of the individual as a unit of inheritance and utilizing certain elements of the gamete analysis, complete generalization can be obtained for at least some descriptive aspects of the response to truncation selection. Clearly, however, a generalized analysis based on individuals and gametes as units of inheritance cannot yield a detailed description such as that developed in the previous sections, unless, of course, a gene interpretation is made. This requires that the genetic structure is specified in terms of genes, gene loci, and linkage parameters.

In the following, the first step is to briefly set out the generalized analysis. Then an interpretation of this analysis is made in terms of the gene system which involves two linked loci, the system which has been treated in detail in Section II(*b*). This gene interpretation is made for two reasons, (i) to illustrate the versatility of methods which may be employed by utilizing different levels of genetic organization as units of inheritance, and (ii) to show that the generalized analysis does give detailed results if the gene structure is specified.

An attack on the generalized description of the change in the population mean, due to selection, is made by using the individual as the basic unit of inheritance and specifying the frequency of the individual in terms of the frequencies of the gametes which united to form the individual. The argument starts with definitions which apply to the elements in the original random-mating population in equilibrium, Π_0.

Let

$\sum f_i G_i$ = gametic array,

H_{ij} = genotype which results from the union of G_i and G_j,

$\sum_{ij} f_i^0 f_j^0 H_{ij}$ = genotypic array,

and

h_{ij} = genotypic value of H_{ij}, such that $\sum_{ij} f_i^0 f_j^0 h_{ij} = 0$.

To define the mean of a full-sib array, further definitions are required.

Let

$\sum_k p_{ijk} G_{ijk}$ = gametic array produced by H_{ij},

$\sum_n p_{lmn} G_{lmn}$ = gametic array produced by H_{lm},

$H_{ijk.lmn}$ = genotype resulting from the union of gametes G_{ijk} and G_{lmn},

and

$h_{ijk.lmn}$ = genotypic value of $H_{ijk.lmn}$, such that

$$\sum_{ijklmn} f_i^0 f_j^0 f_l^0 f_m^0 p_{ijk} p_{lmn} h_{ijk.lmn} = 0.$$

The full-sib array which results from the cross between an arbitrary sire, H_{ij}, and an arbitrary dam, H_{lm}, is, then,

$$H_{(ij.)(lm.)} = \sum_{kn} p_{ijk} p_{lmn} H_{ijk.lmn},$$

and the mean of this array is

$$h_{(ij.)(lm.)} = \sum_{kn} p_{ijk} p_{lmn} h_{ijk.lmn}.$$

Thus, the random mating-population in equilibrium, Π_0, can be generated entirely in terms of the individual as a unit of inheritance as follows:

$$\Pi_0 = \sum_{ijlm} (f_i^0 f_j^0)(f_l^0 f_m^0) H_{(ij.)(lm.)}.$$

The mean of Π_0 is then

$$\mu_0 = \sum_{ijlm} (f_i^0 f_j^0)(f_l^0 f_m^0) h^0_{(ij.)(lm.)} = 0.$$

The consequences of selection may now be considered. First, denote the frequency of H_{ij} in the selected parents from Π_0 as

$$\begin{aligned} P^1_{ij} &= (f_i^0 f_j^0) w^0_{ij} \\ &= f_i^0 f_j^0 + (i/\sigma^2) f_i^0 f_j^0 h^0_{ij}. \end{aligned}$$

The mean of the selected parents is then,

$$\begin{aligned}\mu_s &= \sum_{ij} P^1_{ij} h^0_{ij} \\ &= \sum_{ij} [f^0_i f^0_j + (i/\sigma^2) f^0_i f^0_j h^0_{ij}] h^0_{ij} \\ &= i(\sigma^2_G/\sigma^2).\end{aligned}$$

The mean of the progeny population, Π_1, may be determined as follows:

$$\begin{aligned}\mu_{1,0} &= \sum_{ijlm} P^1_{ij} P^1_{lm} h^0_{(ij.)(lm.)} \\ &\cong \sum_{ijlm} \{(f^0_i f^0_j)(f^0_l f^0_m) + (i/\sigma^2)(f^0_i f^0_j)(f^0_l f^0_m)(h^0_{ij} + h^0_{lm})\} h^0_{(ij.)(lm.)} \\ &= \sum_{ijlm} (f^0_i f^0_j)(f^0_l f^0_m) h^0_{(ij.)(lm.)} + (i/\sigma^2) \sum_{ijlm} (f^0_i f^0_j)(f^0_l f^0_m)(h^0_{ij} + h^0_{lm}) h^0_{(ij.)(lm.)} \\ &= i\{[2\ \mathrm{Cov(PO)}]/\sigma^2\}.\end{aligned}$$

If epistasis occurs, this predicted mean value is not the same as that predicted on the basis of a gene analysis, i.e.

$$\mu_1 = i(\sigma^2_A/\sigma^2).$$

However, if random mating is imposed without selection, then the mean, $i\{[2\ \mathrm{Cov(PO)}]/\sigma^2\}$, regresses to

$$\lim_{m\to\infty} (\mu_{1,m}) \to i(\sigma^2_A/\sigma^2).$$

The means, $\mu_{1,0}$ and $\lim_{m\to\infty} (\mu_{1,m})$, may be predicted as follows:

$$\mu_{1,0} = i\{[2\ \mathrm{Cov(PO)}]/\sigma^2\},$$

and

$$\lim_{m\to\infty} (\mu_{1,m}) = i(\sigma^2_A/\sigma^2) = i \text{ (heritability in the narrow sense).}$$

Consider, now, a second cycle of selection. The population Π_1 may be generated as

$$\sum_{ijlm} P^1_{ij} P^1_{lm} H_{(ij.)(lm.)}.$$

However, this representation, involving only individual genotypes and their frequencies, does not specify the frequency of a given genotype, H_{ij}, in Π_1. This frequency must be specified by the frequency of gametes which unite to form H_{ij}, i.e. $(f^1_i f^1_j)$. Hence, if P^2_{ij} denotes the frequency of H_{ij} in the population selected from Π_1, then

$$\begin{aligned}P^2_{ij} &= (f^1_i f^1_j) w^1_{ij} \\ &\cong f^1_i f^1_j [1 + (i/\sigma^2) h^0_{ij}].\end{aligned}$$

The mean of the progeny population, Π_2, is then

$$\mu_2 = \sum_{ijlm} P_{ij}^2 P_{lm}^2 h^0_{(ij.)(lm.)}$$

$$\cong \sum_{ijlm} (f_i^1 f_j^1)(f_l^1 f_m^1)[1+(i/\sigma^2)(h^0_{ij}+h^0_{lm})]h^0_{(ij.)(lm.)}$$

$$= \sum_{ijlm} (f_i^1 f_j^1)(f_l^1 f_m^1)h^0_{(ij.)(lm.)} + (i/\sigma^2)\sum_{ijlm} (f_i^1 f_j^1)(f_l^1 f_m^1)(h^0_{ij}+h^0_{lm})h^0_{(ij.)(lm.)}$$

$$= A + B.$$

The A term is, by definition, the mean of a population which is subjected to one cycle of selection and then to one generation of random mating without selection. Thus

$$A = \mu_{1,1}.$$

Since

$$f_i^1 = f_i^0 + (i/\sigma^2)K_i,$$

where K_i is a constant, the B term is approximately equal to

$$(i/\sigma^2)\sum_{ijlm} (f_i^0 f_j^0)(f_l^0 f_m^0)(h_{ij}+h_{lm})h^0_{(ij.)(lm.)}$$

$$= i\{[2\ \mathrm{Cov(PO)}]/\sigma^2\}.$$

Thus

$$\mu_{2,0} = \mu_{1,1} + i\{[2\ \mathrm{Cov(PO)}]/\sigma^2\}.$$

The mean of the population which has undergone n cycles of selection may be obtained by an extension of the above argument. If P_{ij}^n is the frequency of H_{ij} in the selected population from Π_{n-1}, then the mean of Π_n is

$$\mu_{n,0} = \sum_{ijlm} P_{ij}^n P_{lm}^n h^0_{(ij.)(lm.)},$$

where

$$P_{ij}^n \cong (f_i^{n-1} f_j^{n-1}) w_{ij}^0.$$

Hence

$$\mu_n \cong \sum_{ijlm} [(f_i^{n-1} f_j^{n-1}) w_{ij}^0][(f_l^{n-1} f_m^{n-1}) w_{lm}^0] h^0_{(ij.)(lm.)}$$

$$= \sum_{ijlm} (f_i^{n-1} f_j^{n-1})(f_l^{n-1} f_m^{n-1})[1+(i/\sigma^2)(h^0_{ij}+h^0_{lm})]h^0_{(ij.)(lm.)}$$

$$= \mu_{(n-1),1} + i\{[2\ \mathrm{Cov(PO)}]/\sigma^2\}.$$

The increment difference between the means for the $(n-1)$th and the nth generation is

$$\Delta\mu_{n,n-1} = \mu_n - \mu_{n-1}$$
$$= \mu_{(n-1),1} - \mu_{(n-2),1}.$$

Generally speaking, then, the mean of the progeny population which results from random mating selected parents from the previous population is equal to

the summation of two parts: (i) the mean of the previous population after it has been allowed to mate at random without selection for one generation, plus (ii) the increment $i\{[2\ \mathrm{Cov}(PO)]/\sigma^2\}$. If estimation is desired, both of these quantities are easily estimated and do not require a gene interpretation.

The consequences of relaxation of selection cannot be carried very far in a generalized formulation since it is not possible to obtain a recurrence relation for gamete frequencies in consecutive generations without specifying the gene constitution. However, the following general statements can be made.

The mean of the population that has had a history of n consecutive cycles of selection, followed by m generations of random mating without selection is

$$\mu_{n,m} = \sum_{ijlm} (f_i^{n,m-1} f_j^{n,m-1})(f_l^{n,m-1} f_m^{n,m-1}) h^0_{(ij.)(lm.)}.$$

If

$$n\Delta\mu_{(m-1),m} = \mu_{n,m-1} - \mu_{n,m},$$

then

$$\begin{aligned} n\Delta\mu_{(m-1),m} = \sum_{ijlm} \{&[(f_i^{n,m-2} f_j^{n,m-2})(f_l^{n,m-2} f_m^{n,m-2})] \\ &-[f_i^{n,m-1} f_j^{n,m-1})(f_l^{n,m-1} f_m^{n,m-1})]\} h^0_{(ij.)(lm.)} \\ = \Sigma\{&{}_n\Delta(\text{mating frequency})\} h^0_{(ij.)(lm.)}. \end{aligned}$$

As m increases, the gamete frequency tends to the product of the component gene frequencies, and

$${}_n\Delta(\text{mating frequency}) \to 0,$$

and

$$n\Delta\mu_{(m-1),m} \to 0,$$

$$\mu_{n,m} \to i(\sigma_A^2/\sigma^2).$$

All of the results so far presented are valid for a completely general situation including any number of alleles at each of any number of loci which are associated in an arbitrary system of linkages. Also any system of dominance and epistatic values may be involved.

These generalized results will now be evaluated for the specific two-locus case.

For two loci, the mean of a population submitted to n cycles of selection was found to be

$$\mu_{n,0} = n(i/\sigma^2)\sigma_A^2 + [\sum_{r=1}^{n} (1-y)^{r-1}](i/\sigma^2)\tfrac{1}{2}\sigma_{AA}^2.$$

In generalized terms the same mean is represented as

$$\mu_{n,0} = (i/\sigma^2)[2\ \mathrm{Cov}(\mathrm{PO})] + \mu_{(n-1),1},$$

where, for two loci,

$$2\ \mathrm{Cov}(\mathrm{PO}) = \sigma_A^2 + \tfrac{1}{2}\sigma_{AA}^2,$$

and

$$\mu_{(n-1),1} = (n-1)(i/\sigma^2)\sigma_A^2 + (1-y)[\sum_{r=1}^{n-1} (1-y)^{r-1}](i/\sigma^2)\tfrac{1}{2}\sigma_{AA}^2.$$

Hence

$$\mu_{n,0} = (i/\sigma^2)(\sigma_A^2+\tfrac{1}{2}\sigma_{AA}^2)+(n-1)(i/\sigma^2)\sigma_A^2+(1-y)[\sum_{r=1}^{n-1}(1-y)^{r-1}](i/\sigma^2)\tfrac{1}{2}\sigma_{AA}^2.$$

But this is clearly equal to

$$n(i/\sigma^2)\sigma_A^2+[\sum_{r=1}^{n}(1-y)^{r-1}](i/\sigma^2)\tfrac{1}{2}\sigma_{AA}^2.$$

Thus, the generalized representation yields the required specific result for two loci.

Next, the general analysis yields the following equation for the increment change, due to selection, in the means of the $(n-1)$th and nth populations:

$$\Delta\mu_{n,n-1} = \mu_{(n-1),1}-\mu_{(n-2),1}.$$

Evaluation of this equation for the two-locus case may be made as follows:

$$\begin{aligned}\Delta\mu_{n,n-1} &= \{(n-1)(i/\sigma^2)\sigma_A^2+(1-y)[(1-(1-y)^{n-1})/y](i/\sigma^2)\tfrac{1}{2}\sigma_{AA}^2\}\\ &\quad-\{(n-2)(i/\sigma^2)\sigma_A^2+(1-y)[(1-(1-y)^{n-2})/y](i/\sigma^2)\tfrac{1}{2}\sigma_{AA}^2\}\\ &= (i/\sigma^2)\sigma_A^2+(1-y)(\{[(1-y)^{n-2}]/y\}-\{[(1-y)^{n-1}]/y\})(i/\sigma^2)\tfrac{1}{2}\sigma_{AA}^2\\ &= (i/\sigma^2)[\sigma_A^2+(1-y)^{n-1}\tfrac{1}{2}\sigma_{AA}^2],\end{aligned}$$

which is the expression previously found for the two-locus case.

Finally, it is necessary to evaluate the generalized term for differences in means on relaxation of selection, ${}_n\Delta\mu_{(m-1),m}$, in terms of the two-locus example. To do this it is necessary to recast the general expression as follows:

$$\begin{aligned}{}_n\Delta\mu_{(m-1),m} &= \sum_{ijklrstu}(f_{ik}^{n,m-2}f_{jl}^{n,m-2})(f_{rt}^{n,m-2}f_{su}^{n,m-2})h_{(ik.jl)(rt.su)}\\ &\quad-\sum_{ijklrstu}(f_{ik}^{n,m-1}f_{jl}^{n,m-1})(f_{rt}^{n,m-1}f_{su}^{n,m-1})h_{(ik.jl)(rt.su)}\\ &= A-B.\end{aligned}$$

where

$(f_{ik}^{n,m-2}f_{jl}^{n,m-2})$ = frequency of the arbitrary sire $(A_i^1A_k^2)(A_j^1A_l^2)$ in $\Pi_{n,m-2}$,

$(f_{rt}^{n,m-2}f_{su}^{n,m-2})$ = frequency of the arbitrary dam $(A_r^1A_t^2)(A_s^1A_u^2)$ in $\Pi_{n,m-2}$,

and

$h_{(ik.jl)(rt.su)}$ = mean of the full-sib array resulting from the cross

$$[(A_i^1A_k^2)(A_j^1A_l^2)\times(A_r^1A_t^2)(A_s^1A_u^2)].$$

The mean of the full-sib array may be expanded as follows:

$$\begin{aligned}h_{(ik.jl)(rt.su)} &= [(1-y)/2]^2(d_{ik.rt}^0+d_{ik.su}^0+d_{jl.rt}+d_{jl.su}^0)\\ &\quad+\tfrac{1}{2}y[(1-y)/2](d_{ik.ru}^0+d_{ik.st}^0+d_{jl.ru}^0+d_{jl.st}^0)\\ &\quad+\tfrac{1}{2}y[(1-y)/2](d_{il.rt}^0+d_{il.su}^0+d_{jk.rt}^0+d_{jk.su}^0)\\ &\quad+(y/2)^2(d_{il.ru}^0+d_{il.st}^0+d_{jk.ru}^0+d_{jk.st}^0).\end{aligned}$$

The A term becomes,

$$A = \sum_{ijklrstu} \{f_{ik}^{0,0} f_{jl}^{0,0} f_{rt}^{0,0} f_{su}^{0,0} + n(i/\sigma^2) f_{ik}^{0,0} f_{jl}^{0,0} f_{rt}^{0,0} f_{su}^{0,0} (\alpha_i^1 + \alpha_j^1 + \alpha_r^1 + \alpha_s^1 + \alpha_k^2 + \alpha_l^2 + \alpha_t^2 + \alpha_u^2)$$

$$+ (1-y)^{m-2} a(i/\sigma^2) f_{ik}^{0,0} f_{jl}^{0,0} f_{rt}^{0,0} f_{su}^{0,0} [\alpha_i^1 + \alpha_j^1 + \alpha_r^1 + \alpha_s^1 + \alpha_k^2 + \alpha_l^2 + \alpha_t^2 + \alpha_u^2$$

$$+ (\alpha\alpha)_{ik} + (\alpha\alpha)_{jl} + (\alpha\alpha)_{rt} + (\alpha\alpha)_{su}] + (1-y)^{m-2} (b-n)(i/\sigma^2) f_{ik}^{0,0} f_{jl}^{0,0} f_{rt}^{0,0} f_{su}^{0,0}$$

$$\times (\alpha_i^1 + \alpha_j^1 + \alpha_r^1 + \alpha_s^1 + \alpha_k^2 + \alpha_l^2 + \alpha_t^2 + \alpha_u^2)\} h_{(ik.jl)(rt.su)}^0,$$

where

$$a = [(1-(1-y)^n)/y],$$

and

$$b = \{n - [(1-(1-y)^n)/y]\}.$$

Hence

$$A = [n + (1-y)^{m-2}(b-n) + (1-y)^{m-2} a](i/\sigma^2)\sigma_A^2 + [a(1-y)^{m-1}](i/\sigma^2)\tfrac{1}{2}\sigma_{AA}^2.$$

Likewise

$$B = [n + (1-y)^{m-1}(b-n) + (1-y)^{m-1} a](i/\sigma^2)\sigma_A^2 + [a(1-y)^m](i/\sigma^2)\tfrac{1}{2}\sigma_{AA}^2.$$

Then

$$\begin{aligned} {}_n\Delta\mu_{(m-1),m} &= A - B \\ &= (1-y)^{m-1}[1-(1-y)^n](i/\sigma^2)\sigma_{AA}^2, \end{aligned}$$

as previously found.

In this way it is clear that the generalized analysis yields detailed results when the gene structure of the situation is specified.

III. Discussion

The main objective of this study is to attempt a generalized descriptive treatment of the consequences of truncation selection based on the individual phenotype. The generalization is possible by broadening the concept of the unit of inheritance to include not only genes but also gametes and individuals.

Analyses utilizing the notion of higher-order hereditary units with a gene interpretation based on the generalized Kempthorne gene model allow a detailed examination of the consequences of selection and relaxation following selection for a two-locus case. These analyses show that the immediate response to selection may be different from that predicted on the basis of the gene analysis if additive $\times$ additive type of epistasis occurs. However, due to the "mutability" of these higher-order inheritance units, the population mean, on relaxation of selection, decays to that predicted by the gene analysis.

Some of the assumptions underlying the theory presented in this study should be emphasized because it is on the fulfilment of these assumptions that the accuracy of the analytical description of the response to selection rests.

First, it is assumed that the populations are infinite in size. In actual experiments, if *small* samples are taken to represent the populations, genetic "drift" will undoubtedly affect the reliability of the prediction procedure.

Second, it is assumed that the effects of individual genes are small so that the square and products of the quantities (gene effect/total phenotypic standard deviation) can be neglected. When more than one gene locus is involved it is assumed that the analysis deals, separately, with only small sub-sets of the total set of loci. In this way the approximations still hold. The total response is then obtained by an appropriate summing of responses over all such small sub-sets. However, as pointed out before, the errors introduced by the approximations tend to accumulate so that the basis of prediction becomes more subject to error as the mean of the selected population becomes farther removed from its original position.

The third point is that the theory developed in this study assumes that the reproductive value is the same for all selected genotypes. That is, natural selection is not operating differentially on the various genotypes. In this connection, probably the most interesting outcome of the study is that even if the assumption is true, the response to selection and relaxation of selection mimics the response which would occur if natural selection *were* operating antagonistically to artificial selection. For example, for the two-locus case in which natural selection is *not* operating and σ^2_{AA} is *not* equal to zero, it is found that the increment change due to selection in successive generations yields successively smaller increments. More explicitly, in the expression

$$\Delta\mu_{n,n-1} = (i/\sigma^2)[\sigma^2_A + (1-y)^{n-1}\tfrac{1}{2}\sigma^2_{AA}],$$

it is clear that the value of the increment decreases as n increases. This diminishing of increments is somewhat similar to the effect that one would expect on the assumption that the intensity of natural selection increases as the cumulative change in the population mean due to artificial selection increases.

Likewise, the decay of the mean on relaxation from

$$\mu_{n,0} = (i/\sigma^2)[n\sigma^2_A + \sum_{r=1}^{n}(1-y)^{r-1}\tfrac{1}{2}\sigma^2_{AA}]$$

to

$$\lim_{m\to\infty}(\mu_{n,m}) \to (i/\sigma^2)n\sigma^2_A$$

simulates the response which would occur if natural selection were operating in the absence of artificial selection to regress the mean toward the original unselected value. Thus, it would appear that in order to establish that natural selection is operating antagonistically to artificial selection, it would be advantageous to use criteria other than those mentioned above.

Finally, in the detailed case involving two linked loci, it is assumed that the recombination frequency is the same for the two sexes. This simplification often does not exist. For example, an extreme case occurs in *Drosophila* where crossing over does not occur in the male. Thus, a somewhat more complicated analysis is required to accommodate different recombination values in the two sexes. However, such a complication does not change the general picture; it merely alters the speed of the response to selection and response to relaxation following selection.

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