due to misunderstanding of the latter. In this theory, random processes (not necessarily sampling drift) play an essential role but only as an adjunct of selection. Many of those who have referred to the theory have insisted that random drift (specifically sampling drift) had been proposed as an alternative to selection, instead of merely as a source of raw material for selection at a higher level than that provided by mutation. In order to clarify this matter, it is desirable to begin with the major premises of the theory since in fairly recent papers some of these have been asserted to have been the opposite of what they actually were.

Premises

A. Multiple Factor Theory of Quantitative Variability. The aspect of evolution that is considered primarily is that of adaptive transformation based on the cumulative effects of changes in the frequencies of multiple minor factors, apparently responsible at any given time for merely quantitative variability. Species are assumed to carry numerous isoalleles at most loci, at fairly high frequencies, instead of being almost homallelic for a single type allele at each. The occasional utilization of major mutations is by no means excluded, but it is assumed that the establishment of one in the species depends on an adaptive process in the array of modifiers.

B. Universal Pleiotropy. The ramifications from the primary effect of any gene replacement through the network of metabolic reactions and of intercellular developmental processes to the characters which have selective differences, insure that each such replacement have effects on numerous characters (cf. Wright, 1963a).

C. Multiple Selective Peaks. The occurrence of joint reactions in the above networks implies extensive interaction effects among the effects of genes on the various characters. Moreover, all characters contribute to a single one, "selective value". Because of pleiotropy and interaction, there is always the potentiality for a vast number of different more or less harmonious combinations. These correspond to different "selective peaks" in the "surface" of selective values relative to the multidimensional field of gene frequencies. This contrasts with the *single* best type which would necessarily be present if each gene were favorable or unfavorable in itself. Finally, even where there is apparently additivity with respect to a quantitatively varying character, the usual intermediacy of the optimum grade insures the potentiality for a great many selective peaks, and pleiotropy insures that these be at diverse values.

D. Multiple Partially Isolated Demes. Most species contain many small, random breeding local populations (demes) that are sufficiently isolated, if only by distance, to permit differentiation of their sets of gene

frequencies, but that are not so isolated as to prevent the gradual spreading of favorable gene complexes throughout the species from their centers of origin. This differentiation need not be associated with conspicuous phenotypic differences.

Phases of the Evolutionary Process

Change of gene frequency is treated as the elementary evolutionary process since it permits reduction of the effects of all factors to a common basis.

According to the theory built on the above premises, each significant step in the evolutionary process involves, in general, the conjunction of three phases. In principle, these would permit a continuing process as long as there is any ecological opportunity for this, with very little mutation and without necessarily involving any environmental differences among localities or any systematic environmental changes in time. In the first statement of these three phases, no such differences or changes are assumed.

1. Phase of Random Drift. In each deme the set of gene frequencies drifts at random in a multidimensional probability distribution about the equilibrium characteristic of a particular selective peak. The set of equilibrium values for each gene frequency is the resultant of three sorts of "pressures", those due to recurrent mutation, to recurrent immigration from other demes, and to selection. The fluctuations responsible for the random drift are in this special case the cumulative effects of accidents of sampling.

2. Phase of Mass Selection. From time to time, the set of gene frequencies drifts across one of the many two-factor saddles in the probability distribution in a deme. There ensues a period of relatively rapid change, dominated by selection among individuals (or families), until the set approaches the equilibrium associated with the new selective peak about which it now drifts at random, and thus returns to the first phase, but in general at a higher level.

3. Phase of Interdemic Selection. A deme that comes under control of a selective peak, superior to those controlling the neighboring demes, produces a greater surplus population and by excess dispersion systematically shifts the positions of equilibrium of these toward its own position, until the same saddle is crossed in them and they move autonomously to the same peak. This process spreads in concentric circles. Two such circles spreading from different centers may overlap and give rise to

a new center which combines the two different favorable interaction systems and becomes a still more active population source. The virtually infinite field of interaction systems may be explored in this way with only a small number of novel mutations as alleles which had been rare, largely displace the previously more abundant ones.

There is a still higher level of adaptation at which a high mean rate of reproduction becomes an inadequate criterion of success. Such a rate may lead to overpopulation which threatens the persistence of the group by overcrowding and exhaustion of resources. In the long run, the most successful portions of the species are those in which the genetic system favors reproductive rates in balance with resources.

Effects of Fluctuating Environmental Change

The preceding model is unrealistic in postulating that there are no environmental changes of sufficient duration to be significant. Long period fluctuations in conditions, occurring more or less independently in different demes, simulate the effects of accidents of sampling but differ in being independent of population size. These are best treated mathematically as a component of the random drift within each deme, even though momentarily deterministic (Wright, 1931, 1935b, 1948). The same is true of fluctuating changes in immigration either in amount or quality (Wright, 1948).

Effects of Persistent Local Differences in Conditions

Conditions usually differ systematically in different regions in the range of a species. Thus the prevailing pattern of selective peaks in the species is subject to local modifications. Sufficiently great differences tend to lead to permanent differentiation and to splitting of the species. Even at a low level, most of the adaptive differences are only of local value and do not spread. Occasionally, however, a pattern of gene frequencies, arrived at by a succession of local adaptations, may have adaptive significance everywhere else, although one that could not have been reached except by the particular chain of events at its point of origin. It then spreads throughout the species as in phase 3 (Wright, 1940, 1965). In this case there is merely deterministic change within demes (from selection pressure in the deme of origin). Local differentiation functions in this case, however, as a random process from the standpoint of the species as a whole in supplying complex genetic material for intergroup selection.

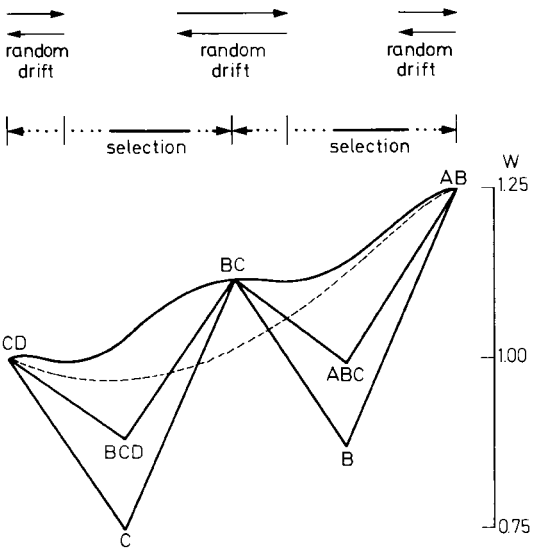

Fig. 4. Profile of mean selective values along path from lowest to highest peak through one of the four intermediate peaks (curved solid line) on same scale as Fig. 3. There is more depression along a path (broken line) avoiding all of the intermediate peaks

As the figures represent only one deme, they cannot represent the third phase of the evolutionary process, interdemic selection. This is represented in Fig. 5. Assume that there are many demes, all of which start from the lowest peak (*CD*). The species exhibits a pattern of trivial local differences due to independent random drifting in the demes.

Three are indicated as overcoming the low probability of crossing a saddle leading to establishment of control by one of the intermediate peaks. Excess growth of the population of these successful demes, followed by excess dispersion tends to carry the neighboring demes across the same saddle. All of these demes tend to shift rapidly, at first merely under immigration from the successful deme, but later under direct internal selection.

Again one may succeed in crossing the second saddle to come under control of the highest peak (*AB*). The influence of this will in turn spread in a concentric circle, but this highest combination may also be attained where two different ones such as *BC* and *AD* overlap.

At a certain stage, the species may show a pattern of strong differentiation of large areas: those still characterized by near fixation of *aabbCCDD*, those characterized by near fixation of *aaBBCCdd* and other intermediate peaks, and a few that have attained near fixation of

Mathematical Framework

For more precise definition of the concept of "random drift" and its role in evolution, it is necessary to review briefly the mathematical theory of the operation of phases 1 and 2 within demes. The role of unpredictable chances in the operation of phase 3 in the evolution of the species as a whole precludes comparable mathematical treatment of it.

As noted earlier, the systematic pressures on gene frequency are conveniently grouped in three categories: those due to recurrent change in the genetic material itself (mutation pressure), those due to introduction from without (immigration pressure), and a wastebasket category, change in gene frequency without either of these (selection pressure). Selection pressure includes effects of differential viability at any stage, whether with respect to physiology or to adaptation to the external environment, differential emigration, differential mating, differential fecundity, and asymmetrical segregation (meiotic drive, Sandler and Novitski, 1957).

These are measured by the changes, $\bar{\Delta}q$, in gene frequency, q, which they tend to bring about per generation. The total pressure, where all are so slight that order is unimportant, is the sum of the partial pressures. In the simplest cases, with mutation rates v and u to and from the gene in question, replacement of the portion m of the population by immigrants with mean gene frequency Q, and with a momentary net selective advantage, s, of the gene over its alleles, collectively, the total pressure is as follows (Wright, 1931)

$$\bar{\Delta}q = [v(1-q) - uq] - m(q-Q) + sq(1-q) \tag{1}$$

The various components have been elaborated to deal with situations more realistically. Thus mutation pressure in a system of multiple alleles can be represented by a set of equations of the type $\bar{\Delta}q_x = \sum[(u_{ix}q_i)] - (\sum u_{xi})q_x$ where u_{ix} refers to the rate of mutation of an allele to the gene, A_x, and u_{xi} is the reverse (Wright, 1949). The degree of dominance may be taken care of by expressing selection pressure in the form $(s+tq)\,q(1-q)$ (Wright, 1937). Much more general forms will be taken up later.

In most cases, some of the pressures are positive, others negative. Selection pressure by itself may involve opposed components. These give balanced polymorphism in one way or other. The net effect is to push gene frequencies toward an equilibrium value, $\hat{q}$, calculated by putting $\bar{\Delta}q = 0$.

Some random processes occur too rarely in the history of the population in question for statistical treatment and are best treated as unique events. There may be a unique introduction of a gene by migrant individuals or by an unusual hybridization. There may be a unique selective incident. The initial crossing of a particular saddle to initiate phase 2 is

a unique event. Many random intrademic processes can, however, be represented as contributions to the variance of fluctuations about the equilibrium point per generation (Wright, 1931, 1948, 1956b). Letting N be the effective population size of the deme, σ_s^2 the variance of selective values of the gene in question, σ_m^2 the variance of amounts of replacement by immigrants, and σ_Q^2 the variance of fluctuations in the gene frequency of immigrants.

$$\sigma_{\Delta q}^2 = (1/2N)\, q(1-q) + \sigma_s^2 q^2 (1-q)^2 + \sigma_m^2 (q-Q)^2 + m^2 \sigma_Q^2 \qquad (2)$$

The first term is the contribution from accidents of sampling, the second is that from local fluctuations in the selection coefficient (simplest case), and the third and fourth are those from fluctuations in the amount and quality of immigration respectively. *These fluctuations do not constitute random drift* since they refer to contributions to variance in a single generation while *random drift implies a cumulative process.*

The directed and random processes operate jointly to determine a probability distribution which describes the extent of the random drift of the gene in question about its equilibrium value. Whatever the formulae for Δq and $\sigma_{\Delta q}^2$, this distribution is given by the following (Wright, 1938a, 1945b, 1952) in which C is a constant such that the total probability is one.

$$\phi(q) = (C/\sigma_{\Delta q}^2) \exp\left[2 \int (\bar{\Delta} q/\sigma_{\Delta q}^2)\, dq\right], \qquad (3)$$

where

$$\int_0^1 \phi(q)\, dq = 1 .$$

This defines the amount of random drift under the given conditions. While the total pressure per generation on gene frequency, $\bar{\Delta} q$, and the variance of fluctuations, $\sigma_{\Delta q}^2$, also per generation, are sums which can be analyzed into contributions from the various factors; this is not true of the random drift, $\phi(q)$. This makes it impossible to define precisely the term sampling drift as a component if $\sigma_{\Delta q}^2$ is composite, but it may be defined as $\phi(q)$ in the absence of other sorts.

This one dimensional probability distribution does not, however, include the aspect of random drift which makes it of more than trivial significance in evolution: the possibility of crossing a saddle between the currently occupied selective peak and another. It is of significance only as cross-section of the total multidimensional distribution, within which the gene in question is drifting at random, defined by specified gene frequencies at all other interacting loci.

General Formulae for Selection Pressure

The symbol W has been defined as the absolute selective value of a genotype in an interaction system that is under consideration, in the sense that $\bar{W}$ ($=\sum f_i W_i$ where f_i is the frequency of the *i-th* genotype) is the ratio of effective population size, N, in one generation to that in the preceding generation under the specified conditions with respect to the rest of the genome and the environment (Wright, 1949). Random mating and Hardy-Weinberg frequencies are usually assumed within the deme, and also such weak selective differences within each locus that recombination keeps pace with changes in gene frequency sufficiently well that deviations from random combination among interacting loci may be ignored (Wright, 1942). If it is assumed that the genotypic frequencies in the population do not depart appreciably from Hardy-Weinberg ratios, then the allele frequency change is given by

$$\bar{\Delta} q_x = \frac{q_x(1-q_x)}{2\bar{W}} \left[\sum W \frac{\partial f}{\partial q_x}\right]. \tag{4}$$

Where there are multiple alleles at a locus, evaluation depends on taking

$$\frac{\partial q_i}{\partial q_x} = \frac{-q_i}{1-q_x}.$$

The appearance of this formula is deceptively simple. Its use in conjunction with other components of $\bar{\Delta} q$, and those of $\sigma^2_{\Delta q}$ in ϕ(q) is not such a gross oversimplification in principle as has sometimes been alleged. Thus in the case of four alleles at each of 100 loci, a rather simple system, the summation involves 10^{100} terms (a larger number than the number of elementary particles in the known universe). It does not, indeed, deal adequately with some types of chromosome aberration, or with such strong selective differences that the assumption of random combination is seriously invalidated, and does not take account of unique events or of cytoplasmic heredity. It is also, of course, intended to apply only to intrademic selection.

Obviously calculations can be made only from rather simple models, involving only a few loci, or simple patterns of interaction among many similarly behaving loci. In such calculations it is usually most convenient to deal with selective values that are relative to some standard, W_{st}, usually assigned to a particular genotype, $w = W/W_{st}$ (Wright, 1950). Since $w/\bar{w} = W/\bar{W}$

$$\bar{\Delta} q_x = \frac{q_x(1-q_x)}{2\bar{w}} \left[\sum w \frac{\partial f}{\partial q_x}\right]. \tag{5}$$

Apart from application to simple systems, the greatest significance of this general formula is that its form brings out properties of systems that would not be apparent otherwise. This is especially the case where it can be assumed that constant values can be attributed to all genotypes as wholes (no frequency dependence). While probably never strictly true, this should often be a good approximation with respect to competition of individuals in relation to the external environment, though not where social interactions are involved. With constant w's, Eq. (5) reduces to the following, noting that the standard may often be chosen so that $\bar{w}$ in the denominator may be treated as 1 (Wright, 1935a, 1937).

$$\bar{\Delta} q_x = \frac{q_x(1-q_x)}{2\bar{w}} \frac{\partial \bar{w}}{\partial q} = (1/2) q_x(1-q_x) \frac{\partial \log \bar{w}}{\partial q_x}. \tag{6}$$

Where this formula holds, the point in the multidimensional "surface" of mean selective values, relative to the set of gene frequencies occupied by the deme, tends to move up the gradient, $\frac{\partial \bar{w}}{\partial q_x}$ or more accurately $\frac{\partial \log \bar{w}}{\partial q_x}$ except as qualified by the term $q_x(1-q_x)$ and by other pressures, not introduced into it.

This surface may have multiple selective peaks at each of which all Δq's are zero either because at a maximum, $\frac{\partial \bar{w}}{\partial q_x} = 0$, or because the gene is lost ($q_x = 0$) or fixed ($q_x = 1$).

A population that deviates from random combination within and among loci and so is not on this surface, for example F_1 of a cross between inbred lines, rapidly moves toward it, if the conditions assumed here are met, and on reaching it, moves along it until it comes to rest at a selective peak, except as diverted by other pressures. A "determinative" peak with respect to all pressures (mutation and immigration in addition to selection) has the property that Lerner (1954) has called genetic homeostasis. The population tends to return to it after any small displacement. After a large displacement, however, it may come to rest at a different peak.

The Multidimensional Distribution of Gene Frequencies

The formula for the total multidimensional probability distribution has not been obtained in terms of values of $\bar{\Delta} q$ and $\sigma^2_{\Delta q}$ of the various genes but some fairly general formulae have been given (Wright, 1937, 1949). For example, with given effective N and m for the population, Q for

each gene and constant W for each genotype

$$\phi(q_1, q_2, \ldots, q_n) = C\bar{W}^{2N}\Pi_i[q_i^{4NmQ_i - 1}]. \quad (7)$$

The product term has a factor for each allele at each locus.

This formula brings out at a glance how the multiple peaks in the surface of mean selective values, $\bar{W}$, tend to be reflected in greatly exaggerated form in multiple peaks in the probability distribution. It is obvious that there is only a very small chance that the set of gene frequencies will drift across any but an exceedingly shallow saddle from one peak to another unless the population passes through bottlenecks of extremely small size. Moreover, there cannot be much random drift unless $4Nm$ is small. The conditions under which effective N and effective m are much smaller than their apparent values will be considered later.

In general, the distribution for an interacting set of loci is restricted over a long period of time (if conditions are constant) within a shell of extremely low probabilities to the neighborhood of a single selective peak. This portion of the total multidimensional distribution is what constitutes the random drift.

Such a definition may seem unnecessarily complicated. It should be emphasized again, however, that no appreciable evolutionary significance has been attributed to the random drifting of a single gene frequency about its equilibrium point but only to such drifting of a set of many gene frequencies under conditions that permit occasional escape across a two-factor saddle.

A Simple Illustration

The interplay of random drift and intrademic selection may perhaps be grasped most easily from a graphical representation (Wright, 1963 b). Figs. 1 to 4 give a highly simplified illustration of these processes in a single deme. It is assumed (Fig. 1) that the grade of the character in question is determined additively, without dominance, by four equivalent pairs of alleles, but that there is an optimum at the mid-value, converting this into a case of extreme factor interaction with respect to selective value. There are only six selective peaks here instead of the indefinitely large number expected if all characters are involved.

It is further assumed that there are small pleiotropic effects of two of the plus factors (A, B) which cause the peaks to be at three levels, a lowest (homallelic "CD" or, in full, $aabbCCDD$), four intermediate, and a highest (homallelic $AABBccdd$). Fig. 2 shows the relative selective values of the 16 possible homallelic populations. The system of gene frequencies is four dimensional.

This is in a continuous area. In a linear continuum; the amount of differentiation at all levels is enormously greater (Wright, 1943).

These are ideal situations which in nature would nearly always be complicated by selective differences within and among neighborhoods. The process of the building up of differences among large areas by isolation by distance is so slow that very small selective differences take precedence. It is, however, important to recognize that if extensive differentiation is brought about by temporary selective differences, a large degree of everchanging differentiation tends to be maintained indefinitely under isolation by distance.

An intermediate structure, in which there are numerous large clusters with very restricted dispersion between them, is probably more frequent than either the ideal island pattern or a uniform continuum. The effective neighborhood size here is not the population number of the cluster but the increment per generation in the size of ancestral populations based on the amount of dispersion between clusters. Sampling drift can easily play an important role with this structure (Wright, 1951 b).

Deviations from Random Combination

It was noted that formulae 4 to 6 for selection pressure in the presence of interaction, depended on the assumption of random combination. It has been shown that there are no serious departures from their validity if the interactive selection is of lower order than the amount of recombination as is usually the case for genes in different chromosomes or with loose linkage in the same chromosome (Wright, 1945a, 1952, 1965). Even where there is considerable departure from random combination, the pattern of selective values, with numerous selective peaks, holds qualitatively so that the theory is not seriously affected in qualitative terms. There is a "surface of mean selective values" but the populations on it deviate somewhat from random combination (Wright, 1967).

Mean Selective Value and Fitness

The differences in the implications of Eq. (6) for constant genotypic selective values and (4) or (5), where they do not reduce to (6) because of frequency dependent selective values, are important in the theory. The meaning in the latter case is less intuitively obvious than in the case of (6). The nature of the difference may be seen by writing the term $\sum\left(W_i \frac{\partial f_i}{\partial q_x}\right)$ in the form $\left[\frac{\partial \bar{W}}{\partial q_x} - \left(\frac{\partial \bar{W}}{\partial q_x}\right)\right]$ in which the difference from (6) is wholly in the second component. It is apparent that with frequency

dependence, the course of change is not controlled by the gradient of the surface $\bar{W}$ to the extent that it is under constancy of the genotypic selective values. The population does not in general tend to come to rest at the selective peaks of $\bar{W}$ in so far as controlled by selection pressure.

In some cases the expression $\sum\left[(W/\bar{W})\frac{\partial f}{\partial q}\right]$ can be integrated giving an expression $F(W/\bar{W})$ which defines a surface relative to the sets of gene frequencies in the same way that $\bar{W}$ (or more precisely $\log \bar{W}$) does if the W's are constant, but it may be a very different surface.

$$\overline{\Delta q_x} = (1/2)\, q_x(1-q_x)\frac{\partial F(W/\bar{W})}{\partial q_x}. \tag{8}$$

It is convenient to distinguish $\bar{W}$ and $F(W/\bar{W})$ where the latter exists at all, as surfaces of "mean selective value" and of "fitness" respectively. The latter term is appropriate because it is its slope that controls the course of mass selection according to Eq. (8).

This fitness function can always be found in the case of a mere pair of alleles. It can also be found in cases in which the *relative* selective values (w's) are constant but the *absolute* ones (W's) are not, either because the competition among individuals is of a sort that has no effect on population size ($W = k(w/\bar{w})$, $\bar{W} = k$, a constant, while $F(W/\bar{W}) = \log \bar{w}$), or because the absolute values all involve the same function, ψ, of one or more of the gene frequencies ($W = \psi w$, $\bar{W} = \psi \bar{w}$ but $F(W/\bar{W}) = \log \bar{w}$ because of cancellation of ψ in $W/\bar{W}$). Finally, if the relative selective value of each genotype is a function of its own frequency that can be expressed in powers of the latter and $\bar{w}$ in the denominator can be treated as 1, integration is possible and gives an expression for $F(w/\bar{w})$ (Wright, 1949, 1960a, 1964).

In most cases, however, there is no such function. Eq. (4) and (5) hold for all gene frequencies in the interaction system but $F(W/\bar{W})$ of Eq. (8) does not exist. Nevertheless, the population tends to move along a determinable course, often of a strongly spiral sort, in the field of gene frequencies, toward a position at which all $\overline{\Delta q}$'s are zero. There may be many such positions which may be called "selective goals" even though not peak values of any definable "surface". The situation is analogous to movement in a vector field in which there is no potential function because of a curl (Wright, 1956b).

Whether $F(W/\bar{W})$ exists or not, the points toward which selection may carry a panmictic population and the selective peaks, with respect to mean selective value may differ greatly if the genotypic selective values are frequency dependent. A genotype that parasitizes its own species may move toward fixation even though its presence is injurious to all indi-

viduals in proportion to a function, ψ, of its frequency. As it approaches fixation, the absolute mean selective value, $\bar{W}$, declines and may become less than 1, leading to extinction. Conversely a genotype that benefits the population in proportion to its frequency but at its own expense and thus of low "fitness", tends toward extinction, again with decline in absolute mean selective value (unless there is sufficient benefit to close relatives).

In R. A. Fisher's (1930) fundamental theorem of natural selection, "the rate of increase of fitness of any organism at any time is equal to its genetic variance in fitness at that time", the word "fitness" is used in two senses. In the second sense it is a property of individual genotypes W which have a "genetic" (additive) "variance". In the first sense, it is a property of the population that has a "rate of increase". This, it turns out, is $F(W/\bar{W})$ if the latter exists, and if it does not, the quantity $\left[\frac{\partial \bar{W}}{\partial t} - \left(\frac{\overline{\partial \bar{W}}}{\partial t}\right)\right]/\bar{W}$ plays the role of rate of increase of fitness in the theorem (assuming random combination, otherwise there is a residual term) (Wright, 1956b). Letting W_A be the sum of additive effects of genes,

$$\frac{\partial F(W/\bar{W}}{\partial t} = \sigma^2_{W_A}/\bar{W} \quad \text{if} \quad F(W/\bar{W}) \text{ exists.} \tag{9}$$

In any case

$$\left[\frac{\partial \bar{W}}{\partial t} - \left(\frac{\overline{\partial \bar{W}}}{\partial t}\right)\right]/\bar{W} = \sigma^2_{W_A}/\bar{W}. \tag{10}$$

It has been generally recognized that "fittest" in the expression "the survival of the fittest" has only a tantologous meaning. In this sense it is appropriate to designate the property of the population that automatically increases under selection as the "fitness function." It seems desirable, however, to use a different term for $\bar{W}$, "mean selective value", a property of the population that may decrease under selection, in order to avoid ambiguity. This implies use of "selective value" rather than "fitness" for the property of individuals of which $\bar{W}$ is the population mean. This involves the paradox, however, that increase in the fitness function of a population may imply decrease in population size ($\partial N/\partial t = (\bar{W} - 1)$ under given conditions) and may even lead to extinction.

Complications in Phase 3

Phase 3 depends on the shifting balance between local selection and immigration as far as each deme is concerned. In the simplest case $\Delta q = sq(1-q) - m(q-Q)$ with equilibrium frequency of the gene, $\hat{q}$. This

is related to the values of $s(=\bar{W}-1)$, m and Q approximately as below (Wright, 1931):

	$\lvert s\rvert \gg m$	$\lvert s\rvert = m$	$\lvert s\rvert \ll m$
Favorable selection ($s>0$)	$1-\frac{m}{s}(1-Q)$	$\sqrt{Q}$	$Q\left[1+\frac{s}{m}(1-Q)\right]$
Unfavorable selection ($s<0$)	$\frac{mQ}{(-s)}$	$1-\sqrt{1-Q}$	$Q\left[1-\frac{(-s)}{m}(1-Q)\right]$

If a particular deme reaches a high selective peak and becomes a much greater source of emigration than before, gene frequencies in neighboring demes tend to shift from left to right to come under control of the gene frequencies, Q's, in the source.

Much more material for evolutionary change is to be expected in an array of partially isolated demes than in an equally large panmictic population. Various types of balance occur, indeed, in panmictic populations: balancing of adverse selection by recurrent mutation (Haldane, 1927), selective advantage of heterozygotes over both homozygotes (Fisher, 1922), opposition between alleles that are superior in different aspects of selective value if superiority is associated with more than semidominance (Haldane, 1962), selective advantage of whichever allele falls below a critical level in frequency, likely to occur in a region with diverse niches (Wright and Dobzhansky, 1946) and even mutation pressure in the case of almost neutral alleles (Wright, 1931, 1966). These are all somewhat special cases, however, in comparison with the situation in a large array of partially isolated demes. In the latter, selection is practically certain to be occurring in somewhat different directions in different demes, because their environments are somewhat different or, if not, because they have come to occupy different selective peaks. This insures that the species as a whole have more than one allele at high frequencies, while dispersion insures that this be the case in each deme.

These considerations make it probable that population growth will occur unequally throughout the range. There should be an evershifting pattern of population sources and sinks that will insure continual change in composition of the population as a whole and of the selective peaks that predominate. There has, however, been no adequate mathematical theory for the operation of this third phase as a whole and none can be developed because of the role played by unique events. Even a rather small number of strongly heterallelic loci provide the basis for a virtually infinite number of combinations and a very large and changing array of selective peaks. The times and places at which there is a primary shift

from control by one to control by another, and what this other will be, are wholly unpredictable matters.

There is a complication in the fact that the selective peaks that are of significance in phase 2 are those with a high fitness function $F(W/\bar{W})$ while those that are of significance in phase 3 are those characterized by rapid population growth and high dispersive and invasive capacities. This depends on more than high mean selective value $\bar{W}$, but the latter is a direct measure of rate of population growth and much more of an indicator of the whole set than is $F(W/\bar{W})$ where there is a difference.

There is little conflict unless selection is strongly frequency dependent. Where there is conflict the course of evolution is presumably a compromise of some sort. In phase 3 there is interference with the spreading through the species of types of individual "fitness" that are deleterious to the group and promotion of the spreading of types of behavior that are beneficial to the group at the expense of the individual, but not necessarily with full success (Wright, 1956b, 1964).

Major Mutations

The local shifts from control by one selective peak to control by another on which phase 3 depends, are likely to occur only across extremely shallow saddles and thus where selective differences are very slight. This accounts for the emphasis (in premise A) on multifactorial quantitative variability. This, however, by no means precludes an important role in evolution of mutations that by themselves present the opportunity for a major step.

It is unlikely that such a mutation will be free from side effects which put it at a net selective disadvantage. Its usefulness depends on a process of domestication in which these side effects are overcome by a suitable combination of modifiers. If this mutation is continually recurring in demes throughout the range of the species, it may encounter somewhere, at some time, a set of modifiers that puts it above the critical line of net selective advantage, whereupon the whole interaction system, major gene and modifiers, starts spreading slowly throughout the species (Wright, 1952, 1963b).

Selection Among Clones

There is an extreme form of the shifting balance theory which should be mentioned. This is the process that occurs in a species with prevailing uniparental reproduction but with an occasional crossing of clones. Crossing gives rise to an enormous variety of recombinant clones. Selection among these, necessarily according to genotypes as wholes, rapidly