Behavior of Pairs of Loci in Finite Monoecious Populations*

B. S. Weir† and C. Clark Cockerham

Department of Statistics, North Carolina State University, Raleigh, North Carolina 27607

Received March 15, 1974

Transition equations are established for descent measures for pairs of loci in finite randomly mating monoecious populations. The two special cases of equal chance gamete formation and two gametes per parent are considered in detail. The descent measures allow genotypic frequencies to be found but are used mainly to evaluate three quadrigenic moments, including the variance of the linkage disequilibrium. Numerical properties of these moments are compared to previously reported values.

We present an exact treatment of the behavior of pairs of loci in finite randomly mating monoecious populations with distinct generations and in the absence of any disturbing forces such as selection. In the first place this work rests on our earlier work on two-locus inbreeding coefficients in finite populations (Weir and Cockerham, 1969). Although similar notation and expansion procedures are used, this paper is more limited in scope in that it does not consider independent gametic sampling or dioecious mating. Such extensions would be straightforward to make. Secondly, this paper is concerned with the evaluation and use of two-locus descent measures (Cockerham and Weir, 1973). Many of the details involving the measures are taken straight from that paper. Finally, this paper is intended as a sequel to our recent treatment of digenic descent measures in finite populations (Cockerham and Weir, 1974). As well as details of the digenic measures in a variety of finite mating schemes, that paper discussed the behavior of the expected value of linkage disequilibrium.

The descent measures evaluated in this paper, in conjunction with initial conditions, provide exact frequencies for all possible categories of two, three and four genes involving at the most two alleles at each of the two loci. This does not imply that the population has only two alleles per locus. From these measures and frequencies are deduced various disequilibrium functions, the variance of

* Paper No. 4300 of the Journal Series of the North Carolina State University Agricultural Experiment Station, Raleigh, NC. This investigation was supported in part by NIH research grant number GM 11546 from the National Institute of General Medical Sciences.
† On leave from the Department of Mathematics, Massey University, Palmerston North, New Zealand.
linkage disequilibria and related moments, and the rates of approach to equilibrium conditions for monoecious populations.

There have been several other papers recently on this topic, and we shall point out the differences and similarities between them and the present paper as the occasions arise.

One of the main differences between the various approaches is that of random union of gametes (e.g. (Hill and Robertson, 1968; Karlin and McGregor, 1968)) and random union of zygotes (e.g. (Watterson, 1970; Serant and Villard, 1972; Littler, 1973)). All of these last authors have commented on the differences of the two approaches. Our model is that of random union of zygotes, but we give numerical values calculated by the random union of gametes models to point out the magnitudes of the differences.

The other main departure of our work from that of other workers is in our use of descent measures with their attendant simple probability arguments. Ohta and Kimura (1969a) use diffusion approximations. Hill and Robertson (1968) present a "moment matrix." Watterson (1970) and Littler (1973) use Markov chains, as do Serant and Villard (1972) who apply a "linearization" technique to nonlinear recurrence formulae. It is an indication of the complexity of the algebra involved that several of these papers contain slight errors. These errors will be corrected where appropriate in this discussion.

**Descent Measures**

For a given set of genes, descent measures give the probabilities of the various arrangements of the genes from which the set is descended on an initial set of gametes. For two loci we define the summary descent measures as the eight elements of a vector $X^\ast(ab, a'b')$ where $a, a'$ are two genes at one locus and $b, b'$ are two genes at another locus. If we use the equivalence relation, denoted by $\equiv$, to mean that equivalent genes are descended from genes on one initial gamete, the measures are written as $X^\ast(ab, a'b')$

$$
\begin{align*}
X^1(ab, a'b') = & \begin{pmatrix}
X^1_{11}(ab, a'b') & \text{prob}(a = a' = b = b') \\
X^1_{1i}(ab, a'b') & \text{prob}(a = a', b = b') \\
X^1_{ii}(ab, a'b') & \text{prob}(a = b, a' = b') \\
X^1_{ij}(ab, a'b') & \text{prob}(a = b', a' = b) \\
\end{pmatrix} \\
& \begin{pmatrix}
\frac{1}{4}[\text{prob}(a = a = b) + \text{prob}(a = a' = b') + \text{prob}(a' = b = b') + \text{prob}(a = b = b')] \\
\frac{1}{4}[\text{prob}(a = a') + \text{prob}(b = b')] \\
\frac{1}{4}[\text{prob}(a = b) + \text{prob}(a' = b')] \\
\frac{1}{4}[\text{prob}(a = b') + \text{prob}(a' = b)] \\
\end{pmatrix}
\end{align*}
$$
Joint equivalence relations such as \((a \equiv a', b \equiv b')\) refer to descension from either one or two gametes. Either all four genes descended from one gamete or the two \(a\) genes descended from one gamete and the two \(b\) genes from another gamete. The quantities averaged in the last four components are generally equal when the genes \(a, b, a', b'\) are located on two or four gametes but fall into two classes when the genes are on three gametes. A more general formulation was given earlier (Cockerham and Weir, 1973).

Within each class of summary component, the descent measures are distinguished according to the number and origin of the gametes on which the genes of interest are located, just as were the two-locus inbreeding coefficients (Weir and Cockerham, 1969). We note first that four genes can be carried on two, three or four gametes so that digametic, trigametic and quadrigametic measures are needed. The gametes are then identified according either to the individuals from which they came (average individual measures) or to the set of gametes to which they belong (gametic set measures).

The eight component digametic average individual measure is written as

\[
\theta_{BC} = \mathbf{X}^*(ab, a'b': ab \text{ and } a'b' \text{ are on two gametes from individuals } B \text{ and } C, \text{ respectively}).
\]

While we could quite consistently define eight component trigametic and quadrigametic measures, we find it more convenient to work with just four components:

\[
\gamma_{B,DE} = \mathbf{X}_{4}^*(ab, a'b': ab, a' \text{ and } b' \text{ are on three gametes from individuals } B, D \text{ and } E, \text{ respectively}),
\]

\[
\delta_{BC,DE} = \mathbf{X}_{4}^*(ab, a'b': a, b, a', b' \text{ are on four gametes from individuals } B, C, D \text{ and } E, \text{ respectively}),
\]

where

\[
\mathbf{X}_{4}^* = [X_{11}^{11}, X_{11}, X_{11}^{11}, X_{11}]'.
\]

The only other average individual measure needed is \(\gamma_{1,BC,D}^*\) which is the probability of equivalence of two genes at one locus from individuals \(B\) and \(C\) and a gene at the other locus from individual \(D\). We are assuming symmetry between loci.

Each of the average individual measures is an average quantity. The digametic measure \(\theta_{BC}\), for example, is averaged over all individuals in the groups of individuals to which \(B\) and \(C\) belong. If these groups are of size one, then \(\theta_{BC} = \theta_{BC}\), the usual individual descent measure (Cockerham and Weir, 1973).

In this paper we are concerned only with monoecious mating so that there is only one group of individuals in each generation. Furthermore we confine
attention to "combined gametic sampling." In other words, the male and female gametes from a group are chosen at random from the entire gametic output of that group. Descent relations between gametes will not be affected by whether those gametes are male or female so that, as far as descent measures are concerned, we need consider only one set of gametes between generations. This situation is to be contrasted to the more general treatment given to inbreeding coefficients (Weir and Cockerham, 1969).

With one set of gametes then, we distinguish gametic set measures according only to the number of gametes involved. The eight component digametic set measure is written as

\[ \Theta_B = X^*(ab, a'b': ab \text{ and } a'b' \text{ are on two gametes belonging to the set of gametes from group } B) \]

and the four component trigametic and quadrigametic set measures are written as

\[ \Gamma_B = X_4^*(ab, a'b': ab, a' \text{ and } b' \text{ are on three gametes belonging to the set of gametes from group } B), \]
\[ \Delta_B = X_4^*(ab, a'b': a, b, a', b' \text{ are on four gametes belonging to the set of gametes from group } B). \]

We also need to define \( r_{1B} \) as the probability of equivalence of two genes at one locus and one gene at the other locus located on three gametes belonging to the set of gametes from group \( B \).

The quantity to be determined for any group is the average of the individual descent measures for members of that group. For group \( A \), following earlier notation (Cockerham and Weir, 1973), we would write this as \( \bar{F}_A \), but if the parent group of \( A \) is group \( B \), then evidently \( \bar{F}_A = \Theta_B \) and we use the symbol \( \Theta \) only in this paper.

This last relation shows that the descent measure of a group in any generation is just a gametic set measure defined on the output gametic set of the previous generation. We have previously discussed the evaluation of the two components \( \bar{F}_{1A} \) and \( \bar{F}_{1A} \) of \( \bar{F}_A \) (Weir and Cockerham, 1969).

To evaluate \( \Theta_B \) we set up one-step transition equations for each summary component. This involves tracing genes on two gametes of the output gametes from \( B \) back one generation to the output gametes from \( C \), the parental group of \( B \). To take proper account of equivalences that may be imposed when two gametes originate from a single individual in group \( B \), we first express the gametic set measure \( \Theta_B \) as a linear combination of average individual measures \( \bar{r} \) defined for group \( B \). It is the genes referred to in these average individual measures which are then traced to gametes in the output set of group \( C \). The argument between successive gametic set measures involves an intermediate argument on average individual measures then. Because the four genes referred
to in \( \Theta_B \) may descend from two, three or four gametes in the previous generation, we need to establish transition equations for the trigametic and quadrigametic set measures also.

To express set measures in terms of average individual measures, we make use of the following gametic sampling probabilities defined on the output set of gametes from a group.

- \( Q_{B}^{2} \), \( Q_{B}^{21} \) are the probabilities that any two gametes came from one or two individuals, respectively, in group \( B \);
- \( Q_{B}^{3} \), \( Q_{B}^{21} \), \( Q_{B}^{111} \) are the probabilities that any three gametes came from one, two, or three individuals, respectively, in group \( B \);
- \( Q_{B}^{4} \), \( Q_{B}^{31} \), \( Q_{B}^{211} \), \( Q_{B}^{1111} \) are the probabilities that any four gametes came from one, three, or four individuals, respectively, in group \( B \);
- \( Q_{B}^{21} \) is the probability that of any four gametes, three were from one individual and the fourth from a different individual in group \( B \);
- \( Q_{B}^{22} \) is the probability that of any four gametes, two were from one individual and the other two from a different individual in group \( B \).

General expressions and particular values for these probabilities have been given previously (\( P \)'s in (Weir and Cockerham, 1969)).

With all of these quantities defined we can proceed to the evaluation of descent measures in a randomly mating monoecious population of size \( N \) each generation.

### Transition Equations and Behavior of the Descent Measures

For convenience we imagine that groups \( A, B, C \) comprise generations \( t + 1 \), \( t \), \( t - 1 \), respectively. The descent measure for group \( A \) can then be written as \( \bar{F}_A = \Theta_B \) or \( \bar{F}_{(t+1)} = \Theta_{(t+1)} \). We consider each of the eight summary components in turn.

The three digenic components have already been discussed at some length (Cockerham and Weir, 1974). We have shown that their behavior over time is governed by the transition equations:

\[
\Theta_{1(t+1)} = \frac{1}{2} Q^2 + \left(1 - \frac{1}{2} Q^2\right) \Theta_{1(t)} ,
\]

\[
\Theta_{1(t+1)} = \left[\frac{(1 + \lambda)/2}{\Theta_{1(t)}} + \frac{(1 - \lambda)/2}{\Theta_{1(t)}}\right] ,
\]

\[
\Theta_{1(t+1)} = \frac{1}{2} Q^2 \Theta_{1(t)} + \left(1 - \frac{1}{2} Q^2\right) \Theta_{1(t)} ,
\]

where \( \lambda \) is the linkage parameter (one minus twice the recombination fraction) between the two loci. Since gametic sampling scheme and population size remain constant over time, the subscripts on the gametic sampling probabilities have been omitted. This will usually be the case.
Writing the reciprocal of $Q^2$ as $N_e$, the gametic variance effective number, these equations have solutions

\[ \theta_{1(t)} = 1 - ((2N_e - 1)/2N_e) \theta_t, \]  
\[ \theta_{1(t)} = \left[ 1 + N_e (1 - \lambda) \left( \frac{1 + \lambda}{2} - \frac{1}{2N_e} \right) \right] / [1 + N_e (1 - \lambda)], \]  
\[ \theta_{1(t)} = \left[ 1 - \left( \frac{1 + \lambda}{2} - \frac{1}{2N_e} \right) \right] / [1 + N_e (1 - \lambda)], \]

where as usual we have assumed that the initial population is noninbred and unrelated so that $\theta_{1(0)} = \theta_{1(t)} = 1$ and all other descent measures are zero initially.

For the trigenic components we have digametic and trigametic classes for both gametic set and average individual measures. Expressing the gametic set measures in terms of average individual measures involves little more than applying the definitions of the gametic sampling probabilities, and gives

\[ \theta_{1B} = Q^2 \bar{\theta}_{BB} + Q^{11} \bar{\theta}_{BB'}, \]  
\[ \theta_{1B} = Q^2 \bar{y}_{BB,B} + \frac{1}{2} Q^{11} (\bar{y}_{BB,B'} + 2 \bar{y}_{BB',B}) + Q^{111} \bar{y}_{BB',B'}, \]

where distinct members of group $B$ are denoted by primes ($B, B', B''$). The expansions of average individual measures back to gametic set measures of the previous generation involves taking account of whether gametes carrying two genes of interest are parental or recombinant. Details have been given earlier (Cockerham and Weir, 1973) and lead to

\[ \bar{\theta}_{BB} = \frac{1 + \lambda}{4} \theta_{1C} + \frac{1}{2} \bar{\theta}_{1C} + \frac{1 - \lambda}{4} \bar{\theta}_{1C}, \]  
\[ \bar{y}_{BB,B} = \frac{1}{2} \theta_{1C} + \frac{1}{2} \bar{\theta}_{1C} + \frac{1}{2} \bar{\theta}_{1C}, \]  
\[ \bar{y}_{BB,B'} = \frac{1}{2} \theta_{1C} + \frac{1}{2} \bar{\theta}_{1C} + \frac{1}{2} \bar{\theta}_{1C}, \]  
\[ \bar{y}_{BB',B'} = \frac{1}{2} \theta_{1C} + \frac{1}{2} \bar{\theta}_{1C} + \frac{1}{2} \bar{\theta}_{1C}. \]

Combining these two sets of equations provides the required transition equations

\[ \theta_{1(t+1)} = \left[ \frac{1}{2} + \frac{\lambda}{2} \right] \theta_{1(t)} + \frac{1 - \lambda}{2} (1 - Q^2) \theta_{1(t)} \]  
\[ + Q^2 \left( \frac{1 + \lambda}{4} \theta_{1(t)} + \frac{1 - \lambda}{4} \theta_{1(t)} \right), \]
\[ \theta_{1(t+1)} = \left( \frac{1}{2} Q^3 + \frac{1}{2} Q^{111} \right) \theta_{1(t)} + \left( \frac{1}{2} Q^{21} + Q^{11} \right) \theta_{1(t)} \]  
\[ + \frac{1}{2} Q^3 \theta_{1(t)} + \frac{1}{2} Q^{111} \theta_{1(t)} \theta_{1(t)} \theta_{1(t)}, \]
Within each of the digametic, trigametic and quadrigametic classes, the relation between gametic set and average individual measures is the same for each of the four quadrigametic components. The structure of these equations is

\[
\Theta_B = Q_B^{00} + Q_B^{11}, \\
\Gamma_B = Q_B^{00} + 2Q_B^{11} + Q_B^{11}, \\
\Delta_B = \frac{1}{3}Q_B^{00} + \frac{1}{3}Q_B^{11} + \delta_B + \delta_B' + \delta_B'' + \delta_B''', \\
\phi_B = \frac{1}{3}Q_B^{00} + \frac{1}{3}Q_B^{11} + \delta_B + \delta_B' + \delta_B'' + \delta_B'''.
\]

Each of these equations holds if every measure \(X (\Theta, \Gamma, A, \theta, \gamma, \phi, \delta, \bar{\gamma})\) is indexed as \(X_{11}, X_{11}, X_{11}\), or \(X_{11}\).

The establishment of transition equations between gametic set measures will be illustrated here for three components of the digametic measure, but details for all quadrigametic components are given in Appendix A. We find it convenient to use

\[
\mathbf{X} = \begin{bmatrix} X_{11} \\ X_{11} \\ X_{11} \\ X_{11} \end{bmatrix}, \quad \mathbf{V} = \begin{bmatrix} 1 & 0 & 0 \\ 0 & 0 & 1 \\ 0 & 1 & 0 \\ 1 & 1 & 1 \end{bmatrix}, \quad \mathbf{U} = \begin{bmatrix} 1 \\ 1 \\ 1 \end{bmatrix}.
\]

From earlier work (Cockerham and Weir, 1973) we have the following expansions.

\[
\tilde{\theta}_{BB'} = \frac{(1 + \lambda)^2}{4} \tilde{\Theta}_C + \frac{1 - \lambda^2}{2} \tilde{\Theta}_C + \frac{(1 - \lambda)^2}{4} \tilde{\Delta}_C,
\]

\[
\tilde{\phi}_{BB} = \left[\frac{(1 + \lambda)^2}{8} I + \frac{(1 - \lambda)^2}{8} V\right] \tilde{\Theta}_C + \frac{1 - \lambda^2}{2} \tilde{\Theta}_1 C + \frac{(1 - \lambda)^2}{8} \tilde{\Theta}_1 C U,
\]

where \(I\) is the 3 \(\times\) 3 identity matrix. From Eq. (9) then

\[
\tilde{\Theta}_{(u+1)} = \left[ (2 - Q^2) \frac{(1 + \lambda)^2}{8} I + Q^2 \frac{(1 - \lambda)^2}{8} V \right] \tilde{\Theta}_{(u)} + (1 - Q^2) \frac{1 - \lambda^2}{2} \tilde{\Theta}_{(u)} + (1 - Q^2) \frac{1}{2} \tilde{\Theta}_{(u)} + \frac{(1 - \lambda^2)}{8} \tilde{\Theta}_{(u)} U.
\]
In this paper we will be concerned with two gametic sampling plans: equal gametic formation and two gametes per parent. For the first case every output gamete from a group is equally likely to have come from every member of the group, and for the second case each member of a group is constrained to give exactly two gametes to the total output of that group. The gametic sampling probabilities for each case have been given previously (Weir and Cockerham, 1969).

For equal chance, \( Q^2 = 1/N \) and for two gametes per parent, \( Q^2 = 1/(2N - 1) \).

The values \( N \) or \( 2N - 1 \) may be substituted for \( N \) in Eqs. (4)-(6) to give the behavior of the digenic measures in each sampling scheme.

For convenience we list the complete set of trigenic and quadrigenic transition equations for each gametic sampling scheme in Appendix B. It will be seen there that the three-by-three transition equations \( \Omega_{EC} \) and \( \Omega_{TG} \) given previously (Weir and Cockerham, 1969, Eqs. 27 and 29) for the two-locus panmictic coefficients are again used. These matrices are also given in Appendix B.

The behavior over time of each of the eight components of the group descent measure \( \Theta \) may now be discussed.

From Eqs. (4)-(6) we see that the one-locus inbreeding coefficient increases monotonically from zero to one, while \( \theta^1 \) and \( \theta^0 \) approach a limiting value of

\[
\theta^{i(\infty)} = 1/((1 + N_s(l - \lambda)) \tag{13}
\]

from above and below, respectively. We have also noted (Cockerham and Weir, 1973) that, in general, \( \theta^{2(\infty)} = \theta^{1(\infty)} \) and all other measures have the same final value as does \( \theta^{1(\infty)} \). In this sense then the final structure of the population has been found. It is completely inbred and has descent status given by (13).

An explicit solution can also be found for the trigenic measure. For the equal chance case,

\[
1\theta_{1(t)} = \frac{1}{N(1-\lambda) + 1} + \frac{N(1-\lambda) - 1}{2[N(1-\lambda) + 1]} \left( \frac{1 + \lambda}{2} - \frac{1}{2N} \right)^t - \frac{1}{2[(2N - 1) + N(N - 1)(1 - \lambda)]} \left( (2N - 1) \left( \frac{2N - 1}{2N} \right)^t \right) + N(N - 1)(1 - \lambda) \left[ \frac{N - 1}{N} \left( \frac{1 + \lambda}{2} - \frac{1}{2N} \right) \right]^t,
\]

confirming that \( \theta^{i(\infty)} = \theta^{i(\infty)} \).

We do not attempt explicit solutions for the quadrigenic components but can indicate their behavior. Although simultaneous transition equations have been given, equations linking values over several successive generations for a single measure can be found. The number of generations such recurrence formulae span will be called the order of that measure. By solving this equation (or directly from the simultaneous equations) we can then express a measure in
the $t$th generation as a linear combination of the $t$th powers of the characteristic roots of the recurrence formula. The number of such roots is the order of the equation. For the equal chance case, the eight group measures have the following orders and characteristic roots.

$$\Theta_1: \text{order 1: root } \left(1 - \frac{1}{2N}\right),$$

$$\Theta_1^1, \Theta_1^2: \text{order 1: root } \left(\frac{1 + \lambda}{2} - \frac{1}{2N}\right),$$

$$\Theta_1^3: \text{order 3: roots } \left(1 - \frac{1}{2N}\right) \geq \left(\frac{1 + \lambda}{2} - \frac{1}{2N}\right) > \frac{N - 1}{N} \left(\frac{1 + \lambda}{2} - \frac{1}{2N}\right),$$

$$\Theta_{11}: \text{order 4: roots } \left(1 - \frac{1}{2N}\right) \geq r_1 > r_2 > r_3,$$

$$\Theta_{11}^2: \text{order 6: roots } \left(1 - \frac{1}{2N}\right) \geq r_1 \geq \left(\frac{1 + \lambda}{2} - \frac{1}{2N}\right) > \frac{N - 1}{N} \times \left(\frac{1 + \lambda}{2} - \frac{1}{2N}\right) \geq r_2 > r_3,$$

$$\Theta_{11}^3, \Theta_{11}^4: \text{order 7: roots } \left(1 - \frac{1}{2N}\right) \geq r_1 \geq \left(\frac{1 + \lambda}{2} - \frac{1}{2N}\right) > \frac{N - 1}{N} \times \left(\frac{1 + \lambda}{2} - \frac{1}{2N}\right) \geq r_2 \geq \frac{N - 1}{N} \left[\left(\frac{1 + \lambda}{2}\right)^2 - \frac{1}{2N}\right] > r_3,$$

where $r_1$, $r_2$, $r_3$ are the eigenvalues of $\Omega_{EC}$. The largest of them, $r_1$, has been tabulated previously (Weir and Cockerham, 1969). It should be mentioned that $r_1$, $r_2$, $r_3$ do not appear to be rational functions of $N$ and $\lambda$. Quite a good "approximation" to $r_1$ for $\lambda = 0$ is $(1 - (1/2N))^2$, so that

$$1 - (1/2N) \geq r_1 > (1 - (1/2N))^2 \quad \text{for all } \lambda.$$

Apart from $\Theta_1$ and $\Theta$ then, all group descent measures approach their final value at the rate of $(1 - (1/2N))$.

We now turn to a discussion of the use of the descent measures.

**Frequencies of Gene Functions**

We retain our earlier (Cockerham and Weir, 1973) notation for quadrigenic frequencies. In generation $t$ the frequency with which a random pair of gametes carry $a_i\delta_j$ and $a_k\delta_l$ is $P_{kl(i)}^{ij}$, the frequency with which a random triplet of
gametes carry \( a_i, b_j, a_k \), and \( b_l \) is \( P^{i,j}_{k,l(t)} \) and the frequency with which a random quartet of genes carry \( a_i, b_j, a_k \) and \( b_l \) is \( P^{i,j}_{k,l(t)} \). Various marginal sums of these quantities give digenic and trigenic frequencies. The frequency of a gamete carrying genes \( a_i \) and \( b_j \), for example, is just

\[
P^{i,j}_{..(t)} = \sum_k \sum_l P^{i,j}_{k,l(t)} = \sum_k \sum_l P^{i,j}_{k,l(t)}.
\]

As we have seen (Cockerham and Weir, 1973), these \( t \)th generation frequencies may be expressed in terms of initial frequencies (denoted by script letters) and the \( t \)th generation (group) descent measures. Before enlarging on this we again (Cockerham and Weir, 1974) distinguish between two types of initial generations.

One type is supposed to be formed by the random union of a specific set of \( 2N \) gametes. This specific set has \( m_{ij} \) gametes carrying genes \( a_i, b_j \) and is characterized by the following exact frequencies.

\[
\rho^{i,j} = \frac{m_{ij}}{2N} = \hat{p}_i \hat{q}_j + \mathcal{D}_{ij}, \quad \hat{p}_i = \frac{1}{2N} \sum_i m_{ij}, \quad \hat{q}_j = \frac{1}{2N} \sum_i m_{ij}.
\]

Initial ancestors are considered to be a randomization of these gametes into pairs so that calculated frequencies in later generations are averages over all arrangements.

The other type of initial generation we consider is when the initial set of gametes is considered to be a random sample from an infinite randomly mating population characterized by

\[
\rho^{i,j} = p_i q_j + \mathcal{D}_{ij}
\]

and an average or expectation \( (\mathbb{E}) \) is taken over all samples so that

\[
\mathbb{E}(\mathcal{D}) = p_i, \quad \mathbb{E}(q_j) = q_j, \quad \mathbb{E}(\rho^{i,j}) = \rho^{i,j},
\]

\[
\mathbb{E}(\mathcal{D}_{ij}) = [(2N - 1)/2N] \mathcal{D}_{ij}, \quad \mathbb{E}(\hat{p}_i \hat{q}_j) = p_i q_j + \mathcal{D}_{ij}/2N.
\]

This will be referred to as the population composed of a random set of \( 2N \) gametes.

To illustrate the construction of frequencies in an arbitrary generation and to show the differences between the two initial generations, we consider \( P^{i,j}_{i,(t)} \). This digametic frequency refers to one gamete carrying genes \( a_i \) and \( b_j \), and the second gamete carrying gene \( a_i \). As usual a dot indicates summation. These three genes are descended from either two or three initial genes. They are descended from two genes on one initial gamete with probability \( \Theta_{1(t)}^{i,j} \) or on two initial gametes with probability \( \Theta_{2(t)}^{i,j} - \Theta_{1(t)}^{i,j} \). They are descended from three
BEHAVIOR OF PAIRS OF LOCI IN FINITE MONOECIOUS POPULATIONS

333
genes on two or three initial gametes with probabilities \((\Theta_{1(t)} + \Theta_{2(t)} - 2_1\Theta_{11(t)})\)
and \((1 - \Theta_{1(t)} - \Theta_{11(t)} - 1\Theta_{2(t)} + 2_1\Theta_{11(t)})\), respectively. This gives

\[
P_{ij}^{i(t)} = \Theta_{1(t)}^2 \Phi_{ij}^{i(t)} + (\Theta_{1(t)} - \Theta_{11(t)} \Phi_{ij}^{i(t)} + (\Theta_{2(t)} + \Theta_{21(t)}) \Phi_{ij}^{i(t)}
\]

\[
+ (1 - \Theta_{1(t)} - \Theta_{11(t)} - 1\Theta_{2(t)} + 2_1\Theta_{11(t)} \Phi_{ij}^{i(t)} .
\]

Now the initial frequencies \(\Phi_{ij}^{i(t)}\), \(\Phi_{ij}^{i(t)}\), \(\Phi_{ij}^{i(t)}\) have previously (Cockerham and
Weir, 1973, Table 3) been expressed in terms of \(\hat{p}_i\), \(\hat{q}_i\), \(\Phi_{ij}\) so that this expression becomes

\[
P_{ij}^{i(t)} = \left[\frac{2N}{(2N - 1)}\right] [\hat{p}_i^2 \hat{q}_j + \hat{p}_i \hat{q}_j \Theta_{1(t)} + \hat{p}_i \Phi_{ij} \Theta_{1(t)} + \Theta_{1(t)}(1 - 2\hat{p}_i) \Phi_{ij}]
\]

\[
+ (1 - 2\hat{p}_i) \Phi_{ij} \Theta_{1(t)} - (\hat{p}_i \hat{q}_j + \Phi_{ij}))(2N - 1)
\]

\[
+ (2N/(2N - 1)(2N - 2))(1 - 2\hat{p}_i) \Phi_{ij}(1 - \Theta_{1(t)}
\]

\[
- \Theta_{1(t)} - 1\Theta_{2(t)} + 2_1\Theta_{11(t)}) .
\]

(14)

| TABLE I |
| Frequencies of Gene Functions in Terms of Descent Measures |

| Digenic Frequencies for a Random Initial Population |
| \(P_{1(t)}^{i(t)} = p_i q_j + \Theta_{1(t)} \Phi_{ij}\) |

| Trigenic Frequencies |
| \(P_{1(t)}^{i(t)} = p_i q_j + \Theta_{1(t)} \Phi_{ij}\) |

| Quadrigenic Frequencies |
| \(P_{1(t)}^{i(t)} = p_i q_j + \Theta_{1(t)} \Phi_{ij}\) |

TABLE I

Frequencies of Gene Functions in Terms of Descent Measures

Digenic Frequencies

\[
P_{1(t)}^{i(t)} = p_i q_j + \Theta_{1(t)} \Phi_{ij}
\]

Trigenic Frequencies

\[
P_{1(t)}^{i(t)} = p_i q_j + \Theta_{1(t)} \Phi_{ij}
\]

Quadrigenic Frequencies

\[
P_{1(t)}^{i(t)} = p_i q_j + \Theta_{1(t)} \Phi_{ij}
\]
By taking expectations in (14), as outlined above, we obtain the result for random initial gametes. The result also follows by letting \( N \to \infty \) and removing the hats in (14). It is the random population with which we will be mainly concerned in this paper, and all the frequencies involving two alleles at each locus which we use here are listed in Table I. They may all be deduced from earlier work (Cockerham and Weir, 1973, Tables 3 and 4; letting \( N \to \infty \) in Table 3).

It is well to remember that these frequencies are expected values. Because the descent measures take proper account of all possible paths of descent from the initial to the present generation, the frequencies given for generation \( t \) supply expected values over all sets of \( N \) individuals in generation \( t \) descending from a random initial population.

**MOMENTS OF GENE FUNCTIONS**

The frequencies for various gene functions are of direct use in evaluating moments such as the mean and variance of linkage disequilibrium in a generation.

We first introduce a set of indicator variables for each locus for the \( 2N \) gametes which unite to form generation \( t \):

\[
x_{im} = 1, \quad \text{if the } m\text{th gamete carries gene } a_i ,
\]

\[
= 0, \quad \text{otherwise},
\]

\[
y_{jn} = 1, \quad \text{if the } n\text{th gamete carries gene } b_j ,
\]

\[
= 0, \quad \text{otherwise}.
\]

The range of \( m \) and \( n \) is over the integers 1, 2, ..., \( 2N \). The range of \( i \) and \( j \) will be left arbitrary. Note that \( x_{im}^\circ = x_{im} \), \( y_{jn}^\circ = y_{jn} \).

Expected values of these indicator variables provide gene frequencies

\[
\mathbb{E}(x_{im}) = p_i, \quad \mathbb{E}(y_{jn}) = q_j
\]

and expectation can be regarded as being over all possible sets of \( 2N \) gametes. Recall that the absence of disturbing forces provides gene frequencies which are constant over time.

Now suppose that the \( 2N \) gametes contain \( n_{ij} \) gametes carrying genes \( a_i b_j \). Then,

\[
n_{ij} = \sum_m x_{im} y_{jm},
\]

and the expected value of \( n_{ij} \) is \( 2NP_{ij}^{(t)} \), so that the sample gametic frequency \( \hat{P}_{ij}^{(t)} = n_{ij}/2N \) is unbiased for the population frequency \( P_{ij}^{(t)} \).
To illustrate the use of indicator variables we consider the sample linkage 

disequilibrium $\hat{D}_{ij}(t)$ for genes $a_i$ and $b_j$ in generation $t$:

$$\hat{D}_{ij}(t) = \hat{P}_{ij}(t) - \hat{P}_{i+}(t)\hat{P}_{j+}(t) = \frac{2N - 1}{4N^2} \sum_m x_{im}y_{jm} - \frac{1}{4N^2} \sum_{m,n} x_{im}y_{jn},$$

so that

$$\delta(\hat{D}_{ij}(t)) = \frac{2N - 1}{2N} (P_{ij}^{t+}(t) - P_{i+}^{t+}(t)) = (\Theta^1_{(t)} - 1\Theta_{(t)}) \Omega_{ij},$$

for populations constituted from a specific set of initial gametes, and

$$\delta(\hat{D}_{ij}(t)) = [(2N - 1)/2N](\Theta^1_{(t)} - 1\Theta_{(t)}) \Omega_{ij},$$

for populations constituted from a random set of initial gametes, as found previously (Cockerham and Weir, 1974). From Eqs. (5) and (6),

$$((\Theta^1_{(t)} - 1\Theta_{(t)}) = [(1 + \lambda)/2] - (1/2N_e))(\Theta^1_{(t-1)} - 1\Theta_{(t-1)}),$$

so that

$$\delta(\hat{D}_{ij}(t)) = [(1 + \lambda)/2] - (1/2N_e)) \delta(\hat{D}_{ij}(t-1))$$

(15)

for both types of initial population. We have already discussed (Cockerham and Weir, 1974) the difference between this result and that used by Hill and Robertson (1966) and Karlin and McGregor (1968).

To find the variance of $D_{ij}$ we work with $\delta(\hat{D}_{ij}^2(t))$ and, following Ohta and Kimura (1969a), write it as $y_3$.

$$y_3 = \delta(\hat{D}_{ij}^2(t))$$

$$= \frac{1}{4N^2} \delta \left[ \left( \frac{2N - 1}{2N} \right)^2 \sum_m x_{im}^2y_{jm} + \left( \frac{1}{2N} \right)^2 \sum_{m,n} x_{im}y_{jn}^2 \right]$$

$$+ \frac{2N^2 - 2N + 1}{2N^2} \sum_m x_{im}y_{jm}x_{in}y_{jn}$$

$$- \frac{2N - 1}{2N^2} \sum_{m,n} (x_{im}^2y_{jm}y_{jn} + x_{im}x_{in}y_{jn}^2)$$

$$- \frac{N}{2N^2} \sum_{m,n,p,r} x_{im}y_{jm}x_{in}y_{jn} + \frac{1}{4N^2} \sum_{m,n,p,r} (x_{im}x_{in}y_{jm}^2 + x_{im}y_{jm}y_{jr})$$

$$+ \frac{1}{4N^2} \sum_{m,n,p,r} x_{im}x_{in}y_{jr}y_{js} \right]$$

$$= \frac{2N - 1}{2N} \left[ \frac{2N - 1}{4N^2} P_{ij}^{t+}(t) + \frac{1}{4N^2} P_{i+}^{t+}(t) + \frac{2N^2 - 2N + 1}{2N^2} P_{ij}^{t+}(t) \right]$$

$$- \frac{2N - 1}{2N^2} (P_{ij}^{t+}(t) + P_{i+}^{t+}(t)) - \frac{2(N - 1)^2}{N^2} P_{ij}^{t+}(t)$$

$$+ \frac{N - 1}{2N^2} (P_{i+}^{t+}(t) + P_{i+}^{t+}(t)) + \frac{(N - 1)(2N - 3)}{2N^2} P_{ij}^{t+}(t).$$
Using the expressions in Table I, each of these frequencies is replaced by a function of descent measures and we find that

\[ y_3(t) = [(2N - 1)/2N]c_1 + (1/2N)c_2 + (1/4N^2)c_3, \]

where, for example,

\[
c_1 = (\Theta_{11}(t) - 2\Gamma_{11}(t) + 4_1(t)) Y_1 + (\Theta^2_{11}(t) - 2\Gamma^2_{11}(t) + 4^2_{11}(t)) Y_2
+ [(\Theta^1_{11}(t) + 2\Theta^2_{11}(t)) - 2(\Gamma^1_{11}(t) + 1\Gamma_{11}(t) - 2\Gamma^2_{11}(t))
+ (4^1_{11}(t) + 1\Gamma_{11}(t) - 2\Gamma^2_{11}(t))] Y_3
\]

and

\[
Y_1 = \hat{p}_i(1 - \hat{p}_i) q_i(1 - q_i), \quad Y_2 = (1 - 2\hat{p}_i)(1 - 2q_i) \Theta_{ij}, \quad Y_3 = \Theta_{ij}^2.
\]

The problem of finding \( y_3(t) \) is formally solved. For large \( N \),

\[ \varepsilon(\hat{D}^3_{ij}(t)) \approx c_1, \]

and for zero initial linkage disequilibrium in this case

\[ \varepsilon(\hat{D}^3_{ij}(t)) \approx (\Theta_{11}(t) - 2\Gamma_{11}(t) + 4_1(t)) \hat{p}_i(1 - \hat{p}_i) q_i(1 - q_i). \]

Expressions for the variance of \( \hat{D}_{ij}(t) \) follow immediately.

It is more instructive however to consider two further quadrigenic moments:

\[
y_2(t) = \varepsilon[(1 - 2\hat{p}_{ij}(t))(1 - 2q_{ij}(t)) \hat{D}_{ij}(t)],
\]

\[
y_1(t) = \varepsilon[\hat{p}_{ij}(1 - \hat{p}_{ij}(t)) \hat{q}_{ij}(1 - \hat{q}_{ij}(t))],
\]

where the notation of Ohta and Kimura (1969a) is again used. The same process of taking expectations of functions of indicator variables and expressing the resulting frequencies (see Appendix C) in terms of descent measures leads to

\[ y(t) = \frac{2N - 1}{2N} \Lambda \sum_{i=1}^{3} Y_i u_i(t), \quad (16) \]

where

\[
y(t) = \begin{bmatrix} y_1(t) \\ y_2(t) \\ y_3(t) \end{bmatrix}, \quad u_1(t) = \begin{bmatrix} \Theta_{11}(t) - 2\Theta_{11}(t) + 1 \\ \Gamma_{11}(t) - 2\Theta_{11}(t) + 1 \\ 4_1(t) - 2\Theta_{11}(t) + 1 \end{bmatrix},
\]

\[
u_2(t) = \begin{bmatrix} \Theta^2_{11}(t) - 2\Theta^2_{11}(t) + 4 \Theta^2_{11}(t) + \frac{1}{2} \Theta(t) \\ \Gamma^2_{11}(t) - 2\Theta^2_{11}(t) + 4 \Theta^2_{11}(t) + \frac{1}{2} \Theta(t) \\ 4^2_{11}(t) - 2\Theta^2_{11}(t) + \Theta(t) \end{bmatrix},
\]

\[
u_3(t) = \begin{bmatrix} \Theta^3_{11}(t) - 2\Theta^2_{11}(t) + 4 \Theta^2_{11}(t) + \frac{3}{2} \Theta(t) \\ \Gamma^3_{11}(t) - 2\Theta^2_{11}(t) + 4 \Theta^2_{11}(t) + \frac{3}{2} \Theta(t) \\ 4^3_{11}(t) - 2\Theta^2_{11}(t) + \Theta(t) \end{bmatrix}.
\]
BEHAVIOR OF PAIRS OF LOCI IN FINITE MONOEIOCIOUS POPULATIONS

\[ u_{3}(t) = \begin{bmatrix} \Theta_{11}^{(t)} + 11\Theta_{1(1)} - 2\Theta_{11}^{(t)} \\ \Gamma_{11}^{(t)} + 11\Gamma_{1(1)} - 2\Gamma_{11}^{(t)} \\ 4\Gamma_{11}^{(t)} + 14\Gamma_{1(1)} - 24\Gamma_{11}^{(t)} \end{bmatrix}, \]

\[ A = \begin{bmatrix} 1 & \frac{2(N - 1)}{N^2} & \frac{(N - 1)(2N - 3)}{2N^2} \\ \frac{2(N - 1)}{N^2} & \frac{4(N - 1)(N - 2)}{N^2} & \frac{2(N - 1)(2N - 3)}{N^2} \\ \frac{2N^2 - 2N + 1}{2N^2} & \frac{2(N - 1)^2}{N^2} & \frac{(N - 1)(2N - 3)}{2N^2} \end{bmatrix}. \]

From the transition equations for the descent measures in the equal chance case,

\[ u_{i}(t+1) = \Omega_{EC}u_{i}(t), \quad i = 1, 2, 3. \]

From Eq. (16) then,

\[ y(t+1) = \Lambda_{EC}A^{-1}y(t), \quad (17) \]

and replacing \( \Omega_{EC} \) by \( \Omega_{TO} \) gives the result for two gametes per parent.

The transition matrix \( \Lambda_{EC}A^{-1} \) corresponds to several other reported matrices. Watterson (1970) in his Eqs. (3.1)–(3.3) gave a matrix for the vector

\[ [2y_1 + y_2 + 2y_3, y_3, y_1]^T. \]

Serant and Villard (1972) gave a matrix \( [(2N - 1)/2N] AB \) for the vector \( [y_1, y_2, y_3]^T \) (Note that the 3,1 element of \( B \) should be \( \alpha[1 - 4\alpha] \).) Littler (1973) gave a matrix \( A_2 \) for the vector \( y \) [note that the 2,3 element of \( A_2 \) should be \( (2/N)[((N - 1)/N][(2N - 1)/2N] - \alpha) \). Each of these three matrices has the same eigenvalues as, but is not equivalent to, \( \Lambda_{EC}A^{-1} \). For the random union of gametes model, Hill and Robertson (1968) gave matrix \( M \) for the vector \( y \). When \( \lambda = 1 \) and gametes do not undergo recombination, the two models are the same and \( M \) is equal to \( \Lambda_{EC}A^{-1} \).

A consequence of Eq. (17) is that in the \( t \)th generation, the three moments may be written as linear combinations of the \( t \)th powers of the eigenvalues of \( \Omega_{EC} \):

\[ y(t) = v_1 r_1^t + v_2 r_2^t + v_3 r_3^t, \quad (18) \]

where, for example, if \( I \) is the \( 3 \times 3 \) identity matrix,

\[ v_1 = A \left[ \frac{\Omega_{EC}^2 - (r_2 + r_3)\Omega_{EC} + r_2r_3I}{(r_1 - r_2)(r_1 - r_3)} \right] A^{-1}y(0), \]

\[ = Y_1^*y(0), \]
with similar expressions for the eigenvectors $v_2$ and $v_3$. Equation (18) can now be written

$$y(t) = \left( \sum_{s=1}^{3} \Psi_s s^t \right) y(0).$$

(19)

Again, $\Omega_{TG}$ may be substituted for $\Omega_{EC}$.

Evidently the eigenvalues $\tau_i$ correspond to those, $\lambda_i$, given by Ohta and Kimura (1969a). These writers used diffusion approximations and obtained similar results, especially for the largest eigenvalue. The proper quantities to compare are $\tau_i$ and $1 + \lambda_i/N$ [or if $s_i$ are eigenvalues of $\Omega_{TG}$: $s_i$ and $1 + \lambda_i/(2N - 1)$]. Another cubic equation for the eigenvalues for the random union of gametes model has been given by Karlin and McGregor (1968). They state that their largest root, $\mu$, also gives the limiting rate of change of $\text{var}(D_{ij})$ and so should correspond to $\tau_1$. (Note that in their formula (17) the last term in the expression for $F$ should be $N - 2$ rather than $N$). The cubic they give also follows as the characteristic equation for the matrix $M$ on page 145 of Karlin (1969), with $N$ replaced by $2N$.

A numerical comparison of the three eigenvalues for $N = 4, 16, 64$ and $\lambda = 0.0, 0.5, 0.9$ and 1.0 in the equal chance case as calculated by the methods of descent measures (or Watterson, 1970; Serant and Villard, 1972; Littler, 1973), Hill and Robertson (1968), Karlin and McGregor (1968), and Ohta and Kimura (1969a) is given in Table II. Again for the equal chance case the maximum values and generation of attainment of $\mathcal{E}(\hat{D}_{ij}^2)$, for $N = 4, 8, 16; \lambda = 0.0, 0.5, 0.9, 1.0; p_i = q_i = 0.5; D_{ij} = 0$ as calculated by the methods of descent measures (or Serant and Villard, 1972), Hill and Robertson (1968), and Ohta and Kimura (1969a) are given in Table III. For $D_{ij} = 0.25$, $\mathcal{E}(\hat{D}_{ij}^2)$ has its maximum value at $t = 0$ for all $\lambda$. For $D_{ij} = 0.125$, only for $\lambda > 0.9$ is the maximum value not at $t = 0$.

There has been interest in various correlation-like quantities. One such quantity is

$$\sigma^2_{D_{ij}(t)} = \mathcal{E}[\hat{D}_{ij}^2(t)] - \mathcal{E}[\hat{D}_{ij}^2(0)]$$

which was termed the “squared standard linkage deviation” by Ohta and Kimura (1969b). We will use their notation and will be particularly concerned with the final value of this quantity. From (19) the final value is

$$\sigma^2_{D_{ij}(t_0)} = y_3(\omega)/y_1(\omega),$$

$$= [001] \Psi_1 y(\omega)/[100] \Psi_1 y(\omega),$$
<table>
<thead>
<tr>
<th>$N = 4$</th>
<th>$N = 16$</th>
<th>$N = 64$</th>
</tr>
</thead>
<tbody>
<tr>
<td>$\lambda = 0.0$</td>
<td>$\lambda = 0.5$</td>
<td>$\lambda = 0.9$</td>
</tr>
<tr>
<td>$r_0$</td>
<td>$r_2$</td>
<td>$r_1$</td>
</tr>
<tr>
<td>Descent Measures</td>
<td>0.1317</td>
<td>0.2277</td>
</tr>
<tr>
<td>Hill and Robertson</td>
<td>0.1052</td>
<td>0.2297</td>
</tr>
<tr>
<td>Karlin and McGregor</td>
<td>0.1394</td>
<td>0.2750</td>
</tr>
<tr>
<td>Ohta and Kimura</td>
<td>-0.5183</td>
<td>0.0099</td>
</tr>
</tbody>
</table>

*Table II: Eigenvalues for Behavior of Quadrigenic Moments in Equal Chance Case Calculated by Four Different Methods*
TABLE III

Maximum Value of $\delta(D_{ij}^2)$ and Generation of Attainment in Equal Chance Case, with $p_i = q_j = 0.5$, $\delta_{ij} = 0$, as Calculated by Three Methods

<table>
<thead>
<tr>
<th>$\lambda$</th>
<th>0.0</th>
<th>0.5</th>
<th>0.9</th>
<th>1.0</th>
</tr>
</thead>
<tbody>
<tr>
<td>$N = 4$</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Descent Measures</td>
<td>0.0072(1)</td>
<td>0.0079(1)</td>
<td>0.0099(2)</td>
<td>0.0111(3)</td>
</tr>
<tr>
<td>Hill and Robertson</td>
<td>0.0068(1)</td>
<td>0.0079(2)</td>
<td>0.0100(3)</td>
<td>0.0111(4)</td>
</tr>
<tr>
<td>Ohta and Kimura</td>
<td>0.0039(2)</td>
<td>0.0056(2)</td>
<td>0.0087(3)</td>
<td>0.0103(4)</td>
</tr>
<tr>
<td>$N = 8$</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Descent Measures</td>
<td>0.0046(1)</td>
<td>0.0053(2)</td>
<td>0.0083(4)</td>
<td>0.0107(7)</td>
</tr>
<tr>
<td>Hill and Robertson</td>
<td>0.0040(2)</td>
<td>0.0051(3)</td>
<td>0.0083(5)</td>
<td>0.0107(8)</td>
</tr>
<tr>
<td>Ohta and Kimura</td>
<td>0.0025(2)</td>
<td>0.0040(3)</td>
<td>0.0076(6)</td>
<td>0.0103(8)</td>
</tr>
<tr>
<td>$N = 16$</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Descent Measures</td>
<td>0.0026(2)</td>
<td>0.0033(3)</td>
<td>0.0065(8)</td>
<td>0.0105(15)</td>
</tr>
<tr>
<td>Hill and Robertson</td>
<td>0.0022(2)</td>
<td>0.0031(4)</td>
<td>0.0066(9)</td>
<td>0.0105(16)</td>
</tr>
<tr>
<td>Ohta and Kimura</td>
<td>0.0015(3)</td>
<td>0.0025(4)</td>
<td>0.0061(9)</td>
<td>0.0103(16)</td>
</tr>
</tbody>
</table>

and so requires a specification of $y_{(o)}$. With our initial conditions on the descent measures, from (16),

$$y_{(o)} = \frac{2N - 1}{2N} \begin{bmatrix} \frac{2N - 1}{2N} & \frac{2N - 1}{4N^2} & \frac{1}{2N^2} \\ 0 & \frac{(N - 1)^2}{N^2} & \frac{2(N - 1)}{N} \\ \frac{1}{2N} & \frac{2N - 1}{4N^2} & \frac{2N^2 - 2N + 1}{2N^2} \end{bmatrix} \begin{bmatrix} Y_1 \\ Y_2 \\ Y_3 \end{bmatrix}$$

$$= [(2N - 1)/2N] A Y,$$  \hspace{1cm} (20)

which defines matrix $A$. Writing $\mathcal{E} = \Psi_1 A$, then

$$\sigma_{\delta_{ij(x)}}^2 = [001] \mathcal{E} Y/[100] \mathcal{E} Y.$$  \hspace{1cm} (21)

Unless $\lambda = 1$, we cannot give a rational form of matrix $\mathcal{E}$ since it depends explicitly on the eigenvalues $r_2$ and $r_3$. When $\lambda = 1$ we can show that $\sigma_{\delta_{ij(x)}}^2 = 1$.

The matrix $[(2N - 1)/2N] A$ is given by $[(2N - 1)/2N] A[u_1(x), u_2(x), u_3(x)]$ and is equal to $\lambda \Omega_{BC} A^{-1}$ for $\lambda = 1$. We see then that $A$ is equivalent to $A$ of Serant and Villard (1972). The equality of the transformation matrix for $y_{(o)}$
from \( Y \) and the transition matrix for \( \lambda = 1 \) is a consequence of both being the result of sampling without recombination.

Numerical final values of \( \sigma_{D_{ij}}^2 \) for the equal chance case, \( N = 4, 8, 16 \) and \( \lambda = 0, 0.5, 0.9, 1.0 \) as calculated by the methods of descent measures, Ohta and Kimura (1969a), and Hill and Robertson (1968) are given in Table IV. The values given there for \( D_{ij} = 0 \) also follow from Serant and Villard (1972), although the approach of these authors gives \( \sigma_{D_{ij}}^2 \) final values which do not change with \( D_{ij} \).

\[
\begin{array}{cccc}
\lambda & 0.0 & 0.5 & 0.9 & 1.0 \\
N = 4 \\
\text{Descent Measures: } D_{ij} = 0.0 & 0.2125 & 0.2900 & 0.7101 & 1.0000 \\
\text{Descent Measures: } D_{ij} = 0.25 & 0.2136 & 0.2921 & 0.7131 & 1.0000 \\
\text{Hill and Robertson: all } D_{ij} & 0.1854 & 0.3011 & 0.7392 & 1.0000 \\
\text{Ohta and Kimura: all } D_{ij} & 0.1176 & 0.2271 & 0.6754 & 1.0000 \\
N = 8 \\
\text{Descent Measures: } D_{ij} = 0.0 & 0.1047 & 0.1472 & 0.4946 & 1.0000 \\
\text{Descent Measures: } D_{ij} = 0.25 & 0.1048 & 0.1475 & 0.4955 & 1.0000 \\
\text{Hill and Robertson: all } D_{ij} & 0.0875 & 0.1457 & 0.5130 & 1.0000 \\
\text{Ohta and Kimura: all } D_{ij} & 0.0600 & 0.1176 & 0.4749 & 1.0000 \\
N = 16 \\
\text{Descent Measures: } D_{ij} = 0.0 & 0.0521 & 0.0743 & 0.2874 & 1.0000 \\
\text{Descent Measures: } D_{ij} = 0.25 & 0.0521 & 0.0743 & 0.2876 & 1.0000 \\
\text{Hill and Robertson: all } D_{ij} & 0.0426 & 0.0717 & 0.2944 & 1.0000 \\
\text{Ohta and Kimura: all } D_{ij} & 0.0305 & 0.0600 & 0.2776 & 1.0000 \\
\end{array}
\]

We also present some numerical values for the case of two gametes per parent. For the descent measure approach we use the matrix \( \Omega_{ij} \), and its eigenvalues \( s_i \). For the approach of Ohta and Kimura (1969a), the inbreeding effective number \( N_e = 2N - 1 \) is used for populations of size \( N \). In Table V maximum values and generations of attainment of \( \sigma(D_{ij}^2) \) as calculated by the methods of descent measures and of Ohta and Kimura (1969a) are given. In Table VI final values of \( \sigma_{D_{ij}}^2 \), as calculated by both methods, are given. For both of these tables, \( N = 4, 8, 16 \) and \( \lambda = 0, 0.5, 0.9, 1.0 \).
TABLE V
Maximum Value of $\sigma(\hat{D}_{ij})$ and Generation of Attainment in the
Two Gametes Per Parent Case, with $p_i = q_i = 0.5$, $\theta_{ij} = 0.0$, as
Calculated by Two Methods

<table>
<thead>
<tr>
<th>$\lambda$</th>
<th>0.0</th>
<th>0.5</th>
<th>0.9</th>
<th>1.0</th>
</tr>
</thead>
<tbody>
<tr>
<td>$N = 4$</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Descent Measures</td>
<td>0.0076(1)</td>
<td>0.0080(1)</td>
<td>0.0100(3)</td>
<td>0.0115(5)</td>
</tr>
<tr>
<td>Ohta and Kimura</td>
<td>0.0028(2)</td>
<td>0.0043(3)</td>
<td>0.0078(5)</td>
<td>0.0103(7)</td>
</tr>
<tr>
<td>$N = 8$</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Descent Measures</td>
<td>0.0043(1)</td>
<td>0.0048(2)</td>
<td>0.0076(7)</td>
<td>0.0109(13)</td>
</tr>
<tr>
<td>Ohta and Kimura</td>
<td>0.0016(3)</td>
<td>0.0027(4)</td>
<td>0.0063(9)</td>
<td>0.0103(15)</td>
</tr>
<tr>
<td>$N = 16$</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Descent Measures</td>
<td>0.0023(2)</td>
<td>0.0027(4)</td>
<td>0.0053(12)</td>
<td>0.0106(29)</td>
</tr>
<tr>
<td>Ohta and Kimura</td>
<td>0.0009(3)</td>
<td>0.0015(6)</td>
<td>0.0045(14)</td>
<td>0.0103(31)</td>
</tr>
</tbody>
</table>

TABLE VI
Equilibrium Value of $\sigma^2_{D_{ij}}$ in the Two Gametes Per Parent Case, with
$p_i = q_i = 0.5$, as Calculated by Two Methods

<table>
<thead>
<tr>
<th>$\lambda$</th>
<th>0.0</th>
<th>0.5</th>
<th>0.9</th>
<th>1.0</th>
</tr>
</thead>
<tbody>
<tr>
<td>$N = 4$</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Descent Measures: $\theta_{ij} = 0.0$</td>
<td>0.1946</td>
<td>0.2448</td>
<td>0.6056</td>
<td>1.0000</td>
</tr>
<tr>
<td>Descent Measures: $\theta_{ij} = 0.25$</td>
<td>0.1942</td>
<td>0.2447</td>
<td>0.6061</td>
<td>1.0000</td>
</tr>
<tr>
<td>Ohta and Kimura: all $\theta_{ij}$</td>
<td>0.0684</td>
<td>0.1338</td>
<td>0.5156</td>
<td>1.0000</td>
</tr>
<tr>
<td>$N = 8$</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Descent Measures: $\theta_{ij} = 0.0$</td>
<td>0.0898</td>
<td>0.1142</td>
<td>0.3421</td>
<td>1.0000</td>
</tr>
<tr>
<td>Descent Measures: $\theta_{ij} = 0.25$</td>
<td>0.0898</td>
<td>0.1142</td>
<td>0.3425</td>
<td>1.0000</td>
</tr>
<tr>
<td>Ohta and Kimura: all $\theta_{ij}$</td>
<td>0.0325</td>
<td>0.0639</td>
<td>0.2937</td>
<td>1.0000</td>
</tr>
<tr>
<td>$N = 16$</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Descent Measures: $\theta_{ij} = 0.0$</td>
<td>0.0432</td>
<td>0.0552</td>
<td>0.1733</td>
<td>1.0000</td>
</tr>
<tr>
<td>Descent Measures: $\theta_{ij} = 0.25$</td>
<td>0.0432</td>
<td>0.0552</td>
<td>0.1733</td>
<td>1.0000</td>
</tr>
<tr>
<td>Ohta and Kimura: all $\theta_{ij}$</td>
<td>0.0159</td>
<td>0.0315</td>
<td>0.1503</td>
<td>1.0000</td>
</tr>
</tbody>
</table>
It is now clear that descent measures and indicator variables allow exact solutions to two-locus problems to be found in a straightforward manner. Results have been obtained for finite populations which have been previously incorrectly stated or based on approximations or simulations.

The method for determining descent measures in finite monoecious populations follows from general formulations (Weir and Cockerham, 1969; Cockerham and Weir, 1973) and the details have been given here in full for trigenic and quadrigenic measures. Digenic measures have already been considered (Cockerham and Weir, 1974). Once the transition equations relating successive values of various classes of measures have been established, a great deal of theory can be related in a systematic way. In particular, by introducing indicator variables to express gene frequencies we were able to relate various moments of gene functions to descent measures.

The first moment evaluated was the expected value of the linkage disequilibrium between a particular pair of genes. We refer to the paper immediately preceding this one (Cockerham and Weir, 1974) for a full discussion.

Three quadrigenic moments, including the expected value of the square of linkage disequilibrium, were found to satisfy three simple simultaneous transition equations. We now change notation a little and, omitting the time subscripts, write these moments as:

\[ y_{ij} = \begin{bmatrix} y_{1ij} \\ y_{2ij} \\ y_{3ij} \end{bmatrix} = \begin{bmatrix} \mathcal{E}[\hat{p}_i(1 - \hat{p}_i) \hat{q}_j(1 - \hat{q}_j)] \\ \mathcal{E}[(1 - 2\hat{p}_i)(1 - 2\hat{q}_j) \hat{D}_{ij}] \\ \mathcal{E}[\hat{D}_{ij}^2] \end{bmatrix}. \]

These moments explicitly involve only two genes, \( a_i \) and \( b_j \), and the inference is usually made that they apply only to the case of two alleles per locus. This assumption is not required in any part of our development however, and in fact we find three other sets of quadrigenic moments:

\[ y_{ij} = \begin{bmatrix} y_{1ij} \\ y_{2ij} \\ y_{3ij} \end{bmatrix} = \begin{bmatrix} \mathcal{E}[-\hat{p}_i\hat{q}_j(1 - \hat{p}_i) \hat{q}_j] \\ \mathcal{E}[-(1 - 2\hat{p}_i)(\hat{q}_j\hat{D}_{ij} + \hat{q}_i\hat{D}_{ji})] \\ \mathcal{E}[\hat{D}_{ij}\hat{D}_{ji}] \end{bmatrix}, \quad j \neq l, \]

\[ 653/6/3-6 \]
Corresponding definitions hold for initial population parameters $Y_{(ij)}$, $Y_{(il)}$, $Y_{(kl)}$, $Y_{(kl)}$. Each of the vectors $y_{(ij)}$, $y_{(il)}$, $y_{(kl)}$, $y_{(kl)}$ for all values of $i$, $j$, $k$, $l$ satisfies the recurrence relation (17), so that each is given by Eq. (19). In (19) and (21) the appropriate initial values must be used.

As a matter of interest we note that the fourth set of moments is the most basic, since the other three sets may be derived from this one by applying the heuristic rule found earlier (Cockerham and Weir, 1973). To change a function involving gene $a_k$ to one involving $a_i$, we substitute $-(1 - p_i)$ for $p_k$ and index $i$ for $k$. Similar rules apply to the other locus.

While $y_{(ij)}$ gave variances of linkage disequilibria, it can be seen that $y_{(il)}$ and $y_{(kl)}$ will give covariances of disequilibria with one gene in common, while $y_{(kl)}$ will give the sum of covariances for two disequilibria sharing no genes. These variances and covariances are constrained by the conditions $C_{ij} = 0$.

Quantities analogous to the squared standard linkage deviation can be defined for pairs of linkage disequilibria involving three or four genes. We give a general definition, for any values of $i$, $j$, $k$, $l$:

$$
\sigma_{D_{ij}, D_{kl}} = y_{(ij)} / y_{(kl)}.
$$

From Eq. (21) now we see that if the population has zero linkage disequilibrium initially, $\sigma_{ij} = 0$, then all of the final values of the standardized covariances will be equal:

$$
\sigma_{D_{ij}, D_{kl}} = \xi_{(i,j)}/\xi_{(k,l)},
$$

where $\xi_{ij}$ is the $i$, $j$th element of the matrix $\Xi$. Only in this special case will the final standard covariances be independent of initial gene frequencies.
The behavior over time of each of the sets of moments \( y^{(2)}_{	ext{ker}} \), as already mentioned, is governed by the eigenvalues of previously reported (Weir and Cockerham, 1969) matrices.

The same eigenvalues hold for the matrices of Watterson (1970), Serant and Villard (1972) and Littler (1973) although their matrices are different. In Table II we compared these values with those obtained from diffusion approximations by Ohta and Kimura (1969a) and with those for the different models of Hill and Robertson (1968) and Karlin and McGregor (1968). We note that Hill (1969) did work with the random union of zygotes and reported the same value of \( r_1 \) for \( \lambda = 0, N = 4 \) as given in Table II. The nature of the model of Karlin and McGregor has also been discussed by Ohta (1968) and that of Hill and Robertson by Galley and Curnow (1972).

All of these authors have pointed out that the variance of linkage disequilibrium tends to zero at a slower final geometric rate, \( r_1 \), than does its expected value \( \text{rate}[(1 + \lambda)/2] - (1/2N_0) \). The two rates are equal for \( \lambda = 1 \) and diverge further as linkage and population size decrease.

Although the expected value of the square of the linkage disequilibrium is eventually zero (unless sample gene frequencies are somehow held constant (Sved, 1968)), it does have a maximum value in an earlier generation. This maximum value increases with linkage and decreases as population size increases, as shown in Tables III and V. Values in Table III also follow from Serant and Villard (1972). The maximum is attained in a generation which is later as linkage and population size increase, although the whole effect may be swamped by a sufficiently large initial value of the linkage disequilibrium, in which case the second moment just decreases monotonically to zero. For the equal chance case, Table III also shows values calculated by the methods of Hill and Robertson, and Ohta and Kimura. In the former case there is quite good general agreement with descent measure values, and complete agreement of course for \( \lambda = 1 \). The difference in generation of attainment values follows from Hill and Robertson not allowing sampling to affect the 0th generation. The method of Ohta and Kimura does not give such good agreement. Note the equality of values in their case for common values of \( N_0c = N(1 - \lambda)/2 \), which is a consequence of their formulation. Both methods show increasing agreement with descent measure values with increasing population size and linkage intensity. For the case of two gametes per parent, the methods of descent measures and Ohta and Kimura are contrasted in Table V. In this case the diffusion approach is not as good as it was for equal chance, since Ohta and Kimura have modified only digenic sampling probabilities (via \( N_0 \)) rather than also considering trigenic and quadrigenic probabilities. For both sampling schemes, when \( \lambda = 1 \), their method gives a maximum value of 0.0103 at the \( N_0 \)th generation.

A related quantity, the ratio of final expected values of the square of linkage disequilibrium and product of gene frequencies, is shown in Tables IV and VI.
This quantity, $\sigma^2_{D_{ij}(a)}$, is seen to increase with linkage but decrease as population size increases. It also increases slightly with increasing initial linkage disequilibrium. Ohta and Kimura (1969a) obtained the approximate value $1/[2N_e(1 - \lambda)]$ for small $\lambda$. This approximation has some merit, although the one given by Sved (1971), $1/[1 + 2N_e(1 - \lambda)]$, seems to be better overall and improves with increasing linkage and population size. An analytical value of $\sigma^2_{D_{ij}(a)}$ was given in Eq. (27). We did not find great evidence for equality of $\sigma^2_{D_{ij}(a)}$ when $\lambda = 1$ and the one-locus inbreeding coefficient as suggested by Hill and Robertson (1968). Values of $\sigma^2_{D_{ij}(a)}$ obtained by the methods of Hill and Robertson, and Ohta and Kimura are also shown in Table IV for the equal chance case, and in Table VI for Ohta and Kimura only for the case of two gametes per parent. The amounts of agreement to descent measure values follow the same pattern as for $\delta(D_{ij})$ described above. Note the independence of $\sigma^2_{D_{ij}(a)}$ on initial disequilibrium for these two methods. For the method of Ohta and Kimura this independence is a consequence of the form of their general solutions for the three moments. For the method of Hill and Robertson it is further evidence of the insensitivity of $\sigma^2_{D_{ij}(a)}$ to initial conditions which these authors noted with reference to initial gene frequencies.

While quantities such as $\delta(D_{ij})$ and $\sigma^2_{D_{ij}(a)}$ have intrinsic interest, they have also found great use recently in the theory of associative overdominance. It can be shown that a neutral locus can have genotypic frequencies which indicate (apparent) overdominance at that locus when there are truly overdominant loci in the genome. Sved (1968) gave an expression showing that the magnitude of associative overdominance was proportional to the square of the linkage disequilibrium between the neutral and overdominant loci. Much work has since been done on this topic by Ohta and Kimura. For their model they showed (Ohta and Kimura, 1970) that the expected amount of associative overdominance was proportional to the value of $\sigma^2_{D_{ij}(a)}$ for the neutral and overdominant loci.

The discussion on $\delta(D_{ij})$ and $\sigma^2_{D_{ij}(a)}$ presented here is not directly relevant to this problem however since we have assumed neutrality at both loci throughout. The various transition equations for descent measures become invalid when selection at one or both loci is allowed. The only direct and exact application would be when selection was suddenly introduced at one locus after $t$ generations of neutrality. Our theory would then give the amount of associative overdominance at generation $t + 1$.

In summary we suggest that our application of descent measures to the problems involving two loci in finite populations provides a more straightforward and more powerful method than several of those previously reported. The initial machinery may appear a little cumbersome but, once established, it allows many generalizations. We have already shown that the multiallele case is explicitly covered. Different gametic distributions may be accommodated very easily as the treatment of monoecious mating with two gametes per parent
BEHAVIOR OF PAIRS OF LOCI IN FINITE MONOECIOUS POPULATIONS

shows. This extension, made via the gametic sampling probabilities, offers an alternative method to that of Trajstman (1972) and Watterson (1973). From earlier work (Weir and Cockerham, 1969) it is clear how dioecious or other group mating schemes could be handled.

APPENDIX A:
GENERAL TRANSITION EQUATIONS FOR THE QUADRIGENIC MEASURES
FOR MONOECIOUS MATING

From Cockerham and Weir (1973) the following trigametic expansions hold.

\[ \tilde{\gamma}_{BB,BB} = \left( \frac{1 + \lambda}{8} I + \frac{1 - \lambda}{8} V \right) \tilde{\delta}_c + \left( \frac{1 + \lambda}{8} \theta_1^{l} + \frac{1}{2} \theta_1^{n} + \frac{1 - \lambda}{8} \theta_2 \right) U, \]

\[ \tilde{\gamma}_{BB,B'B'} = \frac{1 + \lambda}{4} I \tilde{\delta}_c + \frac{1 - \lambda}{4} I \tilde{\Delta}_c, \]

\[ \tilde{\gamma}_{B'B',B'B} = \left( \frac{1 + \lambda}{4} I + \frac{1 - \lambda}{4} V \right) \tilde{\Phi}_c + \left( \frac{1 + \lambda}{4} \theta_1^{1} + \frac{1 - \lambda}{4} \theta_1^{n} \right) U, \]

\[ \tilde{\gamma}_{B'B',B'B'} = \frac{1 + \lambda}{2} \tilde{\Phi}_c + \frac{1 - \lambda}{2} I \tilde{\Delta}_c, \]

so that from (10)

\[ \tilde{\Phi}_{(t+1)} = \left[ \left( Q^3 + \frac{3}{6} Q^{21} \right) \frac{1 + \lambda}{8} I + Q^3 \left( \frac{1 - \lambda}{8} V \right) \right] \tilde{\delta}_{(t)} \]

\[ + \left[ \left( \frac{2 + \lambda}{6} Q^{21} + \frac{1 + \lambda}{2} Q^{111} \right) I + Q^{21} \left( \frac{1 - \lambda}{6} V \right) \right] \tilde{\Phi}_{(t)} \]

\[ + \left( Q^{21} \frac{1 - \lambda}{12} + Q^{111} \frac{1 - \lambda}{2} \right) \tilde{\Delta}_{(t)} \]

\[ + \left[ Q^3 \left( \frac{1 + \lambda}{8} \theta_1^{l} + \frac{1 - \lambda}{8} \theta_1^{n} \right) + \left( \frac{1 + \lambda}{6} Q^{21} \right) \right] \theta_1^{1(t)} \]

\[ + \left( \frac{1 - \lambda}{6} Q^{21} \Gamma_1^{1(t)} \right) U. \]

From Weir and Cockerham (1969),

\[ \gamma_{11B,BB} = \frac{1}{4} \left( 1 + \theta_{11c} \right) + \frac{1}{2} \theta_{1c}, \]

\[ \gamma_{11B,B'B'} = \left[ (1 + \lambda)/4 \right] \theta_{11c} + \frac{1}{2} \Gamma_{11c} + \left[ (1 - \lambda)/4 \right] \Delta_{11c}, \]

\[ \gamma_{11B,B'B'} = \frac{1}{2} \Gamma_{11c} + \frac{1}{2} \theta_{1c}, \]

\[ \gamma_{11B,B'B'} = \left[ (1 + \lambda)/2 \right] \Gamma_{11c} + \left[ (1 - \lambda)/2 \right] \Delta_{11c}, \]
and from (10),

$$
\Gamma_{11(t+1)} = \left( \frac{1}{2}Q^3 + \frac{1 + \lambda}{12}Q^{21} \right) \Theta_{11(t)} + \left( \frac{1}{2}Q^{21} + \frac{1 + \lambda}{2}Q^{111} \right)' \Gamma_{11(t)} + \left( \frac{1 - \lambda}{12}Q^{21} + \frac{1 - \lambda}{2}Q^{111} \right) A_{11(t)} + \left( \frac{1}{2}Q^3 + \frac{1}{2}Q^{21} \right) \Theta_{1(t)} + \frac{1}{2}Q^3.
$$

From Cockerham and Weir (1973) the following quadrigametic expansions hold.

$$
\begin{align*}
\tilde{\delta}_{BB, BB} &= \frac{1}{2}(I + V) \tilde{\Theta}_C + \frac{1}{2}(\Theta_1^1 + 4 \Theta_1^2 + 1 \Theta_C) U, \\
\tilde{\delta}_{BB, BB'} &= \frac{1}{4}(I + V) \tilde{f}_C + \frac{1}{4}(\Theta_1^1 + 1 \Gamma_1^2) U, \\
\tilde{\delta}_{BB, B'B'} &= \frac{1}{4}(I + V) \tilde{f}_C + \frac{1}{4}I \tilde{\Delta}_C, \\
\tilde{\delta}_{BB', BB} &= \frac{1}{4}(I + V) \tilde{f}_C + \frac{1}{4}I \tilde{\Delta}_C, \\
\tilde{\delta}_{BB', BB'} &= \frac{1}{4}(1 \Theta_C + 2 \Gamma_1^1) U, \\
\tilde{\delta}_{BB', B'B'} &= \frac{1}{4}V \tilde{f}_C + \frac{1}{4}I \tilde{\Delta}_C, \\
\tilde{\delta}_{BB', B'B'} &= \frac{1}{4}V \tilde{f}_C + \frac{1}{4}I \tilde{\Delta}_C,
\end{align*}
$$

and from (11),

$$
\tilde{\Delta}_{11(t+1)} = \left[ \left( \frac{1}{2}Q^4 + \frac{1}{2}Q^{22} \right) I + \left( \frac{1}{2}Q^4 + \frac{1}{2}Q^{22} \right) V \right] \tilde{\Theta}_{11(t)} + \left( \frac{1}{2}Q^{21} + \frac{1}{2}Q^{22} + \frac{1}{2}Q^{111} \right) (I + V) \tilde{f}_{11(t)} + \left( \frac{1}{2}Q^{22} + \frac{1}{2}Q^{211} + Q^{1111} \right) I \tilde{\Delta}_{11(t)} + \left( \frac{1}{2}Q^{21} + \frac{1}{2}Q^{22} + \frac{1}{2}Q^{111} \right) \Gamma_1^1 U.
$$

From Weir and Cockerham (1969),

$$
\begin{align*}
\delta_{11BB, BB} &= \frac{1}{2} \Theta_{11C} + \frac{1}{2} \Theta_1^1 + \frac{1}{2}, \\
\delta_{11BB, BB'} &= \frac{1}{2} \Gamma_{11C} + \frac{1}{2} \Theta_{11C}, \\
\delta_{11BB', BB} &= \frac{1}{2} \Gamma_{11C} + \frac{1}{2} \Theta_{11C}, \\
\delta_{11BB', B'B'} &= \frac{1}{2} \Theta_{11C} + \frac{1}{2} \Gamma_{11C} + \frac{1}{2} A_{11C}, \\
\delta_{11BB', B'B'} &= \frac{1}{2} \Theta_{11C} + \frac{1}{2} \Gamma_{11C} + \frac{1}{2} A_{11C}, \\
\delta_{11BB', B'B'} &= \frac{1}{2} \Theta_{11C} + \frac{1}{2} \Gamma_{11C} + \frac{1}{2} A_{11C}, \\
\delta_{11BB', B'B'} &= \frac{1}{2} \Theta_{11C} + \frac{1}{2} \Gamma_{11C} + \frac{1}{2} A_{11C},
\end{align*}
$$

and from (11),

$$
\begin{align*}
A_{11(t+1)} &= \left( \frac{1}{2}Q^4 + \frac{1}{2}Q^{22} \right) \Theta_{11(t)} + \left( \frac{1}{2}Q^{21} + \frac{1}{2}Q^{22} + \frac{1}{2}Q^{211} \right) \Gamma_{11(t)} + \left( \frac{1}{2}Q^{22} + \frac{1}{2}Q^{211} + Q^{1111} \right) A_{11(t)} + \left( \frac{1}{2}Q^4 + \frac{1}{2}Q^{22} \right) \Theta_{1(t)} + \left( \frac{1}{2}Q^4 + \frac{1}{2}Q^{22} \right).
\end{align*}
$$
APPENDIX B: QUADRIGENIC TRANSITION EQUATIONS FOR MONOECIOUS MATING

Equal Chance Gamete Formation

\[ \Omega_{EC} = \begin{bmatrix} \frac{(1 + \lambda)^2}{4N} - \frac{\lambda}{2N} & \frac{(N - 1)(1 - \lambda^2)}{2N} & \frac{(N - 1)(1 - \lambda)^2}{4N} \\ \frac{1 + \lambda}{4N} - \frac{\lambda}{4N^2} & \frac{(N - 1)[N + 1 + \lambda(N - 2)]}{2N^2} & \frac{(N - 1)(2N - 3)(1 - \lambda)}{4N^2} \\ \frac{2N - 1}{4N^3} & \frac{(N - 1)(2N - 1)}{N^3} & \frac{(N - 1)(2N - 1)(2N - 3)}{4N^3} \end{bmatrix}. \]

We write the elements of \( \Omega_{EC} \) as \( \Omega_{ij} \).

Digametic Equations

\[ \Theta_{11(t+1)} = \Omega_{11} \Theta_{11(t)} + \Omega_{12} \Gamma_{11(t)} + \Omega_{13} A_{11(t)} + \left[ \frac{(1 - \lambda^2)/2N} \right] \Theta_{1(t)} + \left[ \frac{(1 + \lambda^2)/4N} \right] \]

\[ \Theta_{11(t+1)} = \Omega_{11} \Theta_{11(t)} + \Omega_{12} \Gamma_{11(t)} + \Omega_{13} A_{11(t)} + L_1, \]

\[ \Theta_{11(t+1)} = \left[ \frac{(2N - 1)/N} \right] \left[ \frac{(1 - \lambda^2)/8N} \right] \Theta_{1(t)} + \left[ \frac{(1 - \lambda^2)/8N} \right] \Theta_{1(t)} + \Omega_{12} \Gamma_{1(t)} + \Omega_{13} A_{1(t)} + L_1, \]

where

\[ L_1 = \left[ \frac{(1 - \lambda^2)/8N} \right] \Theta_{1(t)} + \left[ \frac{(1 - \lambda^2)/2N} \right] \Theta_{1(t)} + \left[ \frac{(1 - \lambda^2)/8N} \right] \Theta_{1(t)}. \]

Trigametic Equations

\[ I_{11(t+1)} = \Omega_{21} \Theta_{11(t)} + \Omega_{22} \Gamma_{11(t)} + \Omega_{23} A_{11(t)} + \left[ \frac{(2N - 1)/2N^2} \right] \Theta_{1(t)} + \left[ \frac{1}{4N^2} \right] \]

\[ I_{11(t+1)} = \Omega_{21} \Theta_{11(t)} + \Omega_{22} \Gamma_{11(t)} + \Omega_{23} A_{11(t)} + M_1, \]

\[ I_{11(t+1)} = \left[ \frac{(2N - 1)(1 + \lambda)}{8N^2} \right] \Theta_{1(t)} + \left[ \frac{1 - \lambda}{8N^2} \right] \Theta_{1(t)} + \frac{(N - 1)[N(1 + \lambda) - \lambda]}{2N^2} I_{1(t)} \]

\[ + \frac{(N - 1)(1 - \lambda)}{2N^2} I_{1(t)} + \frac{(N - 1)[N(1 + \lambda) - \lambda]}{2N^2} I_{1(t)} + \Omega_{23} A_{1(t)} + M_1, \]

\[ I_{11(t+1)} = \left[ \frac{(2N - 1)(1 + \lambda)}{8N^2} \right] \Theta_{1(t)} + \left[ \frac{1 - \lambda}{8N^2} \right] \Theta_{1(t)} + \frac{(N - 1)[N(1 + \lambda) - \lambda]}{2N^2} I_{1(t)} \]

\[ + \frac{(N - 1)(1 - \lambda)}{2N^2} I_{1(t)} + \frac{(N - 1)[N(1 + \lambda) - \lambda]}{2N^2} I_{1(t)} + \Omega_{23} A_{1(t)} + M_1. \]
where

\[ M_1 = \frac{1}{N^2} \left( \frac{1 + \lambda}{8} \Theta_3^1(t) + \frac{1 - \lambda}{8} \Theta_1^1(t) \right) + \left[ \frac{(N - 1)(1 + \lambda)}{2N^2} + \frac{1}{2N^2} \right] \Theta_1^1(t) \]

\[ (N - 1)(1 - \lambda) \frac{1}{2N^2} \Theta_1^1(t). \]

**Quadrigamic Equations**

\[ A_{11(t+1)} = \Omega_{31} \Theta_{11}^1(t) + \Omega_{32} \Gamma_{11}^1(t) + \Omega_{33} A_{11}^1(t) + \frac{(2N - 1)/2N^2}{1 + 4N^2}, \]

\[ A_{11(t+1)} = \Omega_{31} \Theta_{11}^1(t) + \Omega_{32} \Gamma_{11}^1(t) + \Omega_{33} A_{11}^1(t) + N_1, \]

\[ A_{11(t+1)} = \frac{1}{2} \Omega_{31} (\Theta_{11}^1(t) + \Theta_{11}^1(t)) + \frac{1}{2} \Omega_{32} (\Gamma_{11}^1(t) + \Gamma_{11}^1(t)) + \Omega_{33} A_{11}^1(t) + N_1, \]

where

\[ N_1 = \frac{1}{8N^3} \Theta_1^1(t) + \frac{2N - 1}{8N^3} \Theta_1^1(t) + \frac{2N - 1}{2N^3} \Theta_1^1(t) + \frac{(N - 1)(2N - 1)}{2N^3} \Theta_1^1(t). \]

**Two Gametes Per Parent**

\[ \Omega_{TG} = \begin{bmatrix}
\frac{(1 + \lambda)^2}{4(2N - 1)} & \frac{(1 - \lambda^2)(N - 1)}{2N - 1} & \frac{(1 - \lambda)^2(N - 1)}{2(2N - 1)} \\
\frac{1 + \lambda}{4(2N - 1)} & \frac{\lambda(N - 2)}{2N - 1} & \frac{(1 - \lambda)(4N - 7)}{4(2N - 1)} \\
\frac{1}{2(2N - 1)(2N - 3)} & \frac{(2N - 1)(2N - 3)}{4N - 7} & \frac{16N^2 - 56N + 51}{4(2N - 1)(2N - 3)}
\end{bmatrix}. \]

We write the elements of \( \Omega_{TG} \) as \( \omega_{ij} \).

**Digamic Equations**

\[ \Theta_{11(t+1)} = \omega_{11} \Theta_{11}^1(t) + \omega_{12} \Gamma_{11}^1(t) + \omega_{13} A_{11}^1(t) \]

\[ + \frac{1}{2N - 1} \frac{1 - \lambda^2}{2} \Theta_{11}^1(t) + \frac{1}{2N - 1} \frac{1 + \lambda^2}{4}, \]

\[ \Theta_{11(t+1)} = \omega_{11} \Theta_{11}^1(t) + \omega_{12} \Gamma_{11}^1(t) + \omega_{13} A_{11}^1(t) + L_2, \]

\[ \Theta_{11(t+1)} = \frac{4N - 3}{2N - 1} \frac{(1 + \lambda)^2}{8} \Theta_{11}^1(t) + \frac{1}{2N - 1} \frac{(1 - \lambda)^2}{8} \Theta_{11}^1(t) \]

\[ + \omega_{12} \Gamma_{11}^1(t) + \omega_{13} A_{11}^1(t) + L_2, \]

\[ 1_{11}^1(t+1) = \frac{4N - 3}{2N - 1} \frac{(1 + \lambda)^2}{8} 1_{11}^1(t) + \frac{1}{2N - 1} \frac{(1 - \lambda)^2}{8} 1_{11}^1(t) \]

\[ + \omega_{12} 1_{11}^1(t) + \omega_{13} 1_{11}^1(t) + L_2, \]
where

\[ L_2 = \frac{1}{2N-1} \left( \frac{1 + \lambda}{8} + \frac{1 - \lambda^2}{2} + \frac{(1 - \lambda)^2}{8} \right). \]

**Trigametic Equations**

\[ \Gamma_{11(t+1)} = \omega_{21} \Theta_{11(t)} + \omega_{22} \Gamma_{11(t)} + \omega_{33} \Delta_{11(t)} + \left[ \frac{1}{(2N-1)} \right] \Theta_{2(t)} , \]

\[ \Gamma_{11(t+1)}^{II} = \omega_{21} \Theta_{11(t)}^{II} + \omega_{23} \Gamma_{11(t)}^{II} + \omega_{33} \Delta_{11(t)}^{II} + M_2 , \]

\[ \Gamma_{11(t+1)}^{III} = \omega_{21} \Theta_{11(t)}^{III} + \frac{2N-1 + \lambda(2N-3)}{2(2N-1)} \Gamma_{11(t)}^{III} + \frac{1 - \lambda}{2(2N-1)} \Gamma_{11(t)}^{IV} + \omega_{33} \Delta_{11(t)}^{III} + M_2 , \]

\[ 11\Gamma_{11(t+1)} = \omega_{21} 11\Theta_{11(t)} + \frac{2(N-1) + \lambda(2N-3)}{2(2N-1)} 11\Gamma_{11(t)} + \frac{1 - \lambda}{2(2N-1)} 11\Gamma_{11(t)}^{IV} + \omega_{33} 11\Delta_{11(t)} + M_2 , \]

where

\[ M_2 = \frac{1}{2N-1} \left( \frac{1 + \lambda}{2} + \frac{1 - \lambda}{2} - \frac{1}{4} \right). \]

**Quadrigametic Equations**

\[ \Delta_{11(t+1)} = \omega_{31} \Theta_{11(t)} + \omega_{32} \Gamma_{11(t)} + \omega_{33} \Delta_{11(t)} + \frac{4N-7}{2(2N-1)(2N-3)} \Theta_{2(t)} + \frac{1}{4(2N-1)(2N-3)} \Delta_{11(t)}^{IV} , \]

\[ \Delta_{11(t+1)}^{IV} = \omega_{31} \Theta_{11(t)}^{IV} + \omega_{32} \Gamma_{11(t)}^{IV} + \omega_{33} \Delta_{11(t)}^{IV} + N_2 , \]

\[ \Delta_{11(t+1)}^{V} = 11\Delta_{11(t+1)} = \omega_{31} \Theta_{11(t)} + 11\Theta_{11(t)} + \omega_{32}(\Gamma_{11(t)} + 11\Gamma_{11(t)}) + \omega_{33} \Delta_{11(t)} + N_2 , \]

where

\[ N_2 = \frac{1}{2N-1} \left( \frac{4N-7}{2} - \frac{1}{4} \right) \Theta_{2(t)} + \frac{1}{2N-2} \Delta_{11(t)}^{IV} , \]
APPENDIX C:
QUADRIGENIC MOMENTS AS FUNCTIONS OF DESCENT MEASURES

First Moment Function

\[ y_1(t) = \delta[\hat{p}_i(t)(1 - \hat{q}_i(t)) + \hat{q}_i(t)(1 - \hat{q}_i(t)) \] 

\[ = \frac{1}{4N^2} \delta \left[ \left( \frac{2N - 1}{2N} \right)^2 \sum_{m \neq n} x_{im}^2 y_{jm}^2 + \left( \frac{2N - 1}{2N} \right)^2 \sum_{m \neq n} x_{jn}^2 y_{jn}^2 \right. \]

\[ - \left. \frac{2N - 1}{4N^2} \left( \sum_{m \neq n} x_{im} y_{jm} x_{in} + \sum_{m \neq n} x_{im} y_{jm} y_{jn} \right) \right) \]

\[ + \frac{1}{2N^2} \sum_{m \neq n} x_{im} y_{jm} x_{in} y_{jn} + \frac{1}{N^2} \sum_{m \neq n} x_{im} y_{jm} x_{in} y_{jr} \]

\[ + \frac{1}{4N^2} \sum_{m \neq n} x_{im} y_{jm} x_{in} y_{jr} \]

\[ \left. + \frac{2N - 1}{2N} \left( \frac{2N - 1}{2N} \right)^2 \right] \]

\[ = \frac{2N - 1}{2N} \left[ \frac{2N - 1}{4N^2} P_{i\ell}^{ij}(t) + \left( \frac{2N - 1}{2N} \right)^2 P_{i\ell}^{ij}(t) - \frac{2N - 1}{2N^2} (P_{i\ell}^{ij}(t) + P_{i\ell}^{ij}(t)) \right. \]

\[ \left. - \frac{(N - 1)(2N - 1)}{2N^2} (P_{i\ell}^{ij}(t) + P_{i\ell}^{ij}(t)) \right) \]

\[ + \frac{1}{2N^2} P_{i\ell}^{ij}(t) + \frac{2N - 1}{N^2} P_{i\ell}^{ij}(t) + \frac{(N - 1)(2N - 3)}{2N^2} P_{i\ell}^{ij}(t) \].

Second Moment Function

\[ y_2(t) = \delta[(1 - 2\hat{p}_i(t))(1 - 2\hat{q}_i(t)) \hat{D}_{i\ell}(t)] \]

\[ = \frac{1}{2N^2} \delta \left[ \frac{2N - 1}{2} \left( \frac{N - 1}{N} \right)^2 \sum_{m \neq n} x_{im}^2 y_{jm}^2 - \frac{1}{2} \left( \frac{N - 1}{N} \right)^2 \sum_{m \neq n} x_{jn}^2 y_{jn}^2 \right. \]

\[ - \left. \left( \frac{N - 1}{N} \right)^2 \left( \sum_{m \neq n} x_{im}^2 y_{jm} y_{jn} + \sum_{m \neq n} x_{im} x_{in} y_{jm}^2 \right) \right) \]

\[ + \frac{1}{2N} \frac{N - 1}{N} \left( \sum_{m \neq n} x_{im}^2 y_{jm} y_{jn} + \sum_{m \neq n} x_{im} x_{in} y_{jm}^2 \right) \]

\[ + \frac{N - 1}{N^2} \sum_{m \neq n} x_{im} y_{jm} x_{in} y_{jn} + \frac{N - 2}{N^2} \sum_{m \neq n} x_{jm} x_{in} y_{jr} \]

\[ - \frac{1}{2N^2} \sum_{m \neq n} x_{im} x_{in} y_{jr} y_{js} \right] \].
\[
\frac{2N - 1}{2N} \left[ \left( \frac{N - 1}{N} \right)^2 P_{ij}(t) - \left( \frac{N - 1}{N} \right)^2 P_{ij}(t) - 2 \left( \frac{N - 1}{N} \right)^2 \right] \\
\times \left( P_{i1}(t) + P_{i2}(t) \right) + 2 \left( \frac{N - 1}{N} \right)^2 \left( P_{i1}(t) + P_{i2}(t) \right) + \frac{2(N - 1)}{N^2} P_{ij}(t) \\
+ \frac{4(N - 1)(N - 2)}{N^2} P_{i1}(t) - \frac{2(N - 1)(2N - 3)}{N^2} P_{i1}(t) \right].
\]

REFERENCES

GALLEY, S. J. AND CURNOW, R. N. 1972. The effects of finite population size and selection on the correlation between gene frequency changes at two different loci and on the amount of linkage disequilibrium, Theoret. and Appl. Genet. 42, 335-345.
KARLIN, S. AND MCGREGOR, J. 1968. Rates and probabilities of fixation for two locus random mating finite populations without selection, Genetics 58, 141-159.
OHTA, T. AND KIMURA, M. 1969b. Linkage disequilibrium at steady state determined by random genetic drift and recurrent mutation, Genetics 63, 229-238.
SVED, J. A. 1968. The stability of linked systems of loci with a small population size, Genetics 59, 543-563.