EFFECTS OF LINKAGE ON PARENTAL-COMBINATION AND RECOMBINATION FREQUENCIES IN F_2

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DESPITE mendelian inheritance, recombinations in the F_2 generation of characteristics of P individuals are not always readily obtained nor can a particular recombination necessarily be produced at all. Among circumstances inhibitory of recombination may be mentioned the following: (1) Structural disharmonies between the two chromosome sets of an F_1 hybrid, (2) Physiological incompatibilities, (3) Pleiotropy, (4) The multifactorial bases of some character differences which can greatly reduce the frequency of parental extremes in the F_2; and (5) Genetic linkage.

The various mechanisms mentioned above have somewhat different implications with respect to evolutionary and breeding problems and it is therefore desirable to be able to discriminate between them. Structural disharmonies, which are more apt to be encountered in inter-specific rather than intraspecific crosses, may be reflected by observable cytological behavior at meiosis. Physiological incompatibility, pleiotropy, and linkage however are quite likely to be confounded and the difficulties in distinguishing between them enhanced by multifactorial inheritance. ANDERSON (1939a, b, 1948) who has discussed these problems at considerable length, fully recognizes the variety of causes that can restrict recombination in F_2 and later generations. He is inclined, however, to lay particular stress on the importance of linkage, on account of its universality, in preventing the amalgamation of related and interfertile species that come into contact with one another, and in explaining a relative lack of non-parental combinations of characters in inbred lines of maize derived from morphologically distinct strains. It is the aim of the present paper to re-examine the theoretical effects of linkage on the frequencies of parental combinations and recombinations of characters in the individuals of F_2 populations by a method permitting a clear distinction between them and those effects expected from multifactorial inheritance.

STATEMENT OF THE PROBLEM

Two graded characters, A and B, will be considered. Each character is measured in arbitrary units such that one P individual has both an A-value and a B-value of $+1/2$ and the other P individual has an A-value and B- value of $-1/2$, as illustrated in figure 1. The parents thus differ by unity for each character and the means of the parental values are zero.

The *recombination value* of an F_2 individual is defined as its A-value minus its B-value. In terms of figure 1, this is proportional to the perpendicular distance from the point representing a given F_2 individual to the dotted line connecting the points representing the two P individuals. Thus the recombina-

tion value of either P individual is zero as is also that of any F_2 for which the measures of the two characters are the same. The positions in figure 1 of all such individuals lie along the diagonal +P to −P. In the absence of transgressive inheritance the recombination value can vary between limits of +1 and −1; the extreme recombination individuals are like one P with respect to character A and like the other with respect to character B. The expected variance, under specified conditions, of the recombination value is a reasonable measure of the tendency of F_2 individuals to possess A and B characteristics like opposite P individuals. This measure will be referred to as the *recombination variance.*

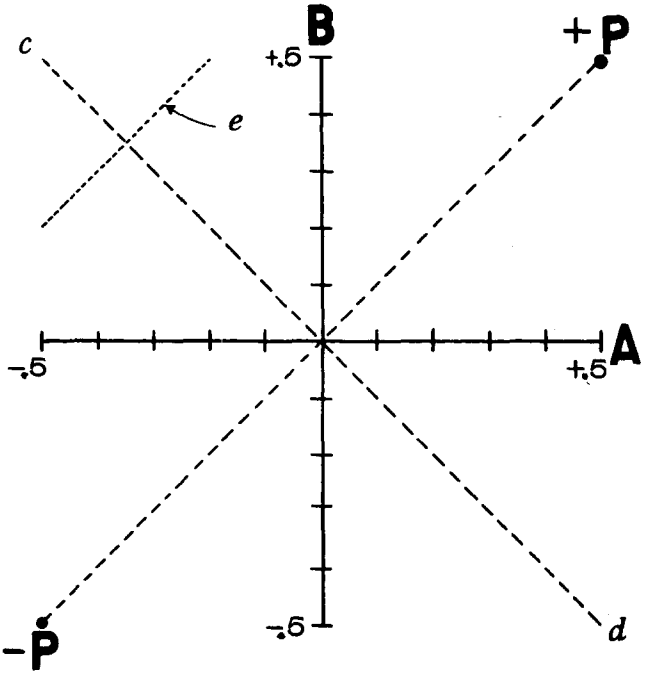

FIGURE 1.—Graphical Representation of Individuals Characterized by Different Grades of Characters A and B. The *recombination value* of any individual, equal to its A-coordinate minus its B-coordinate, is proportional to its distance from the dashed line connecting the two P's. The *parental-combination value* of any individual, equal to the sum of its coordinates, is proportional to its distance from the line *c-d*. Line *e* represents the positions in the figure of individuals having a *recombination value* of −0.7.

Another property of an F_2 individual, its *parental-combination value*, is defined as its A-value *plus* its B-value. In terms of figure 1, this is proportional to the distance of a point representing a given F_2 individual from dotted line *c-d*. The expected variance, under specified conditions, of the parental-combination value is a reasonable measure of the tendency of F_2 individuals to be similar to one or the other P individual with respect to *both* characters simultaneously. This measure will be referred to as the *parental-combination variance.*

The following postulates are made for purposes of computation:

1. The character variation is due entirely to genetic differences.

2. The allelic differences responsible for the variation of character A are at different loci (called *a*-type loci) from those responsible for the variation of character B (at *b*-type loci).

3. The effects of allelic substitutions are additive.

4. One P individual is homozygous for all plus alleles at *a*-type and *b*-type loci, the other is homozygous for the minus alleles.

The following postulates apply to those cases involving linkage:

5. Each locus has an equal and independent probability of lying on any particular chromosome.

6. Linkage, within each chromosome, is complete.

The effects of relaxation of some of these postulates will be considered in the discussion.

Symbols used

1. a_i—any particular *a*-type locus, called the *i*th locus.
2. α_i—the effect on character of A of making a single substitution of a plus allele in place of a minus allele at any *a*-type locus.
3. A_c—the summation of α_i for all the *a*-type loci on a given chromosome—hence also the effect on character A of making a single substitution of a particular chromosome derived from the plus P in place of its homolog from the minus P.
4. b_i—same as a_i for character B.
5. β_i—same as α_i for character B.
6. B_c—same as A_c for character B.
7. m—number of chromosome pairs.
8. n_a—the number of *a*-type loci—that is, the number of loci for which the P individuals have alleles with differential effects on character A.
9. n_b—the same as n_a for character B.

RECOMBINATION VARIANCE AND PARENTAL-COMBINATION VARIANCE WITH INDEPENDENT ASSORTMENT

As a standard for comparing cases involving linkage we take the case in which linkage is completely absent and the individual pairs of alleles assort independently. Consider first the variance due to a particular pair of alleles at, say, the a_i locus. Half the F_2 individuals will be heterozygous, and half will be homozygous for either the plus or minus allele. The homozygous individuals, as far as this locus is concerned, will differ from the mean by either $+\alpha_i$ or $-\alpha_i$ so that the variance contribution of this locus is:

$$\frac{(+\alpha_i)^2 + 2(0)^2 + (-\alpha_i)^2}{4} = \frac{\alpha_i^2}{2}.$$

Since the mean value contributed by each locus is zero and the assortment is independent, the recombination and the parental combination variances are

the same and are equal to the sum of the contributions of all the alleles. This may be expressed as follows:

$$E\frac{1}{2}\left[\sum_{i=1}^{n_a}\alpha_i^2+\sum_{i=1}^{n_b}\beta_i^2\right] \tag{1}$$

where E means *expectation of.*

Consider also the special case in which all allelic differences at *a*-type loci have equal effects on character A, and all allelic differences at *b*-type loci similarly have equal effects on character B. In this case every α has the value $1/2n_a$ and every β has the value $1/2n_b$. For this case then expression (1) has the following form:

$$\frac{n_a}{2}\left(\frac{1}{2n_a}\right)^2+\frac{n_b}{2}\left(\frac{1}{2n_b}\right)^2=\frac{1}{8}\left[\frac{1}{n_a}+\frac{1}{n_b}\right]. \tag{2}$$

RECOMBINATION VARIANCE WITH COMPLETE LINKAGE

With complete linkage, the m pairs of chromosomes assort independently. The contribution of any particular chromosome pair to F_2 recombination variance depends on the difference between the sum of the α's ($=A_c$) and the sum of the β's ($=B_c$) for all *a*-type and *b*-type loci respectively on this pair of chromosomes. In the F_2 half the individuals are heterozygous for the two homologs which therefore contribute nothing to recombination value and the other half are homozygous for one or the other which therefore contribute either (A_c-B_c) or $-(A_c-B_c)$ to the recombination value. The variance contribution of this pair of chromosomes is therefore $(1/2)(A_c-B_c)^2$. To evaluate this expression we note that the mean values of A_c and B_c, for all possible distributions of loci on the m pairs of chromosomes, are each equal to $1/2m$. Therefore subtracting from both A_c and B_c their mean values does not alter the value of the binomial in the expression above, which becomes:

$$\tfrac{1}{2}[(A_c-\bar{A}_c)-(B_c-\bar{B}_c)]^2.$$

The deviations of A_c from its mean, for all possible assignments of the *a*-type and *b*-type loci to the various chromosomes, are independent of the deviations of B_c from its mean. Therefore in expanding the square of the binomial the cross products vanish on the average, and the mean value or expectation of this expression may be written as follows:

$$\tfrac{1}{2}E(A_c-\bar{A}_c)^2+\tfrac{1}{2}E(B_c-\bar{B}_c)^2. \tag{3}$$

In $(1/m)$ proportion of the distributions of loci on chromosomes, some particular locus a_1 will be present on a particular pair of chromosomes and will contribute $(\alpha_i-\alpha_i/m)$ to the value of $(A_c-\bar{A}_c)$, in $(m-1)/m$ proportion of the distributions, locus a_1 will be absent and will therefore contribute $(-\alpha_i/m)$ to the value of $(A_c-\bar{A}_c)$. The mean contribution is of course zero, and since the probability of each *a*-type locus lying on a particular chromosome pair is equal to and indepencent of the probabilities of the others, each locus can be con-

sidered to make its separate contribution to the value of $E(A_c-\bar{A}_c)^2$, the total value for all distributions of a-type loci being the summation of the independent contributions. The mean contribution of locus a_1 is:

$$\frac{1}{m}\left(\alpha_i-\frac{\alpha_i}{m}\right)^2+\frac{m-1}{m}\left(\frac{\alpha_i}{m}\right)^2=\frac{m-1}{m^2}(\alpha_i)^2$$

and the summation for all a-type loci is:

$$\left(\frac{m-1}{m^2}\right)\sum_1^{n_a}\alpha_i^2.$$

A corresponding expression gives the mean contribution of all n_b loci to $E(B_c-\bar{B}_c)^2$, and expression (3) may, then, be written:

$$\frac{(m-1)}{2m^2}\left[\sum_1^{n_a}\alpha_i^2+\sum_1^{n_b}\beta_i^2\right].$$

Considering the population of all possible pairs of chromosomes in the F_2 for all possible distributions of loci on the chromosomes, a *random* selection of m pairs of chromosomes would have a variance of m times this value, or:

$$\frac{(m-1)}{2m}\left[\sum_1^{n_a}\alpha_i^2+\sum_1^{b}\beta_i^2\right]. \tag{4}$$

Since the mean A-value and B-value of all F_2 individuals from a given F_1 parent are both zero, the above expression also gives the mean recombination variance of the m pairs of chromosomes corresponding to F_2 individuals.

Consider also, as before, the special case in which all allelic differences at a-type loci have equal effects on character A, and all allelic differences at b-type loci similarly have equal effects on character B. In this case every α has the value $1/2n_a$ and every β the value $1/2n_b$, and expression (4) becomes:

$$\frac{(m-1)}{8m}\left[\frac{1}{n_a}+\frac{1}{n_b}\right]. \tag{5}*$$

Comparing expressions (1) and (2) with (3) and (4) we see that, under the conditions postulated, and regardless of the number of loci involved and the equality or inequality of their differential effects, complete linkage has reduced the expectation of recombination variance over that expected in independent assortment by the proportion $1/m$ where m is the number of chromosomes. With ten pairs of chromosomes and linkage complete the reduction is thus only 10 percent.

The proportion $1/m$ is easily checked for simple special cases. For example if $n_a=n_b=1$, the probability of the a- and b-type loci being on the same chromosome pair is $1/m$; if they are on the same pair of chromosomes, and linkage is

* Expression (5) may also be obtained directly from (3) since $E(A_c-\bar{A}_c)^2$ for a particular pair of chromosomes is the variance of a binomial (=pqn) multiplied by the variance contribution of a single item. Here $p=1/m$, $q=1-p$, $n=n_a$, and the contribution of a single item is $(1/2n_a)^2$.

complete, the recombination variance is zero, if they are on different chromosomes, the recombination variance is that for independent assortment. The mean variance is thus reduced by the proportion $1/m$ of the value it would have in the entire absence of linkage. As another example we may take $n_a=2$ and $n_b=1$ in which case the probability of all loci being on separate chromosomes is $(m-1/m)(m-2/m)$, of the a-type loci being on separate chromosomes and the b-type locus on one of the same chromosomes is $(2/m)(m-1/m)$, of the a-type loci being on the same chromosome and the b-type locus on a different one is $(1/m)(m-1/m)$, and of all loci being on the same chromosome is $(1/m)(1/m)$. If we assign a contribution to variance of an independently assorting a-type locus of $(1)^2$, that of an independently assorting b-type locus must be $(2)^2$ and the variances for the four cases described are 6, 2, 8, and 0 respectively. Weighting these values in proportion to their probabilities yields a mean of $(m-1/m)$ (6) as compared to the value (6) under independent assortment. Similar checks have been made for more complicated cases.

It may appear surprising that linkage would not, under the conditions postulated, reduce the recombination variance to a greater extent than the foregoing analysis indicates. The explanation is that with multifactorial inheritance linkage actually increases the F_2 variance of the individual characters, and this increase in variance of the separate characters over that afforded by independent assortment nearly compensates for the tendency of linkage to prevent the separation of alleles lying in the same linkage group. This variance increase due to linkage will be demonstrated in the next section.

EFFECT OF LINKAGE ON THE F_2 VARIANCE OF A SINGLE CHARACTER WHERE ALL PLUS ALLELES COME FROM ONE P

With independent assortment, as shown in a previous section, each a-type locus makes an independent contribution toward the variance of character A in the F_2 equal to $\alpha_i^2/2$. The total contributions of all a-type loci may then be written as expression (1) without the term for b-type loci, and substituting n for n_a, as follows:

$$\sum_{1}^{n} \frac{\alpha_i^2}{2}. \tag{6}$$

For the special case where all allelic substitutions have equal effects we can similarly use the corresponding part of expression (2) without the term for b-type loci, again substituting n for n_a:

$$\frac{1}{8n}. \tag{7}$$

With complete linkage within chromosomes, however, each chromosome pair makes its independent contribution and the total F_2 variance for any given F_1 individual may be written:

$$\sum_{1}^{m} \frac{A_c^2}{2} \tag{8}$$

where A_c is the summation of the α's corresponding to all the a-type loci in a given chromosome. This expression is clearly greater than expression (6) providing at least one chromosome pair possesses more than one a-type locus.

In order to gain some idea of comparative magnitudes we consider again the case where all allelic substitutions have equal effects. The expected distribution of the number of a-type loci on individual chromosome pairs is given by the expansion of $(q+p)^n$ where p, the probability of a given locus lying on a particular chromosome, is $1/m$, q is $[1-1/m]$, and the successive terms are the probabilities of a chromosome pair possessing 0, 1, 2, . . . etc. a-type loci. If we multiply each term of this expansion by the square of the corresponding number of loci, then multiply each of the products by $[1/8n^2]$ which is the contribution that a single independently assorting locus would make, and finally sum all the terms thus obtained, the result is the expected contribution to F_2 variance of a single pair of chromosomes. These operations are indicated below:

$$\frac{1}{8n^2}\left[q^n(0) + nq^{n-1}p(1)^2 + \frac{n(n-1)q^{n-2}p^2(2)^2}{2!} + \frac{n(n-1)(n-2)q^{n-3}p^3(3)^2}{3!} + \cdots\right]$$

$$= \frac{p}{8n}\left[q^{n-1} + (n-1)q^{n-2}p(2) + \frac{(n-1)(n-2)q^{n-3}p^2(3)}{2!} + \cdots\right]$$

$$= \frac{p}{8n}\left[q^{n-1} + (n-1)q^{n-2}p + \frac{(n-1)(n-2)q^{n-3}p^2}{2!} + \cdots\right.$$

$$\left. + \frac{p}{8n}\left[q^{n-1}(0) + (n-1)q^{n-2}p(1) + \frac{(n-1)(n-2)q^{n-3}p^2(2)}{2!} + \cdots\right.\right.$$

$$= \frac{p}{8n}[1 + p(n-1)] = \frac{1}{8nm}\left[\frac{m+n-1}{m}\right].$$

We may multiply this expression by m in order to obtain the F_2 variance for m pairs of chromosomes, the same considerations applying here as were discussed in the section on recombination variance with complete linkage. The F_2 variance is therefore:

$$\frac{1}{8n}\left[\frac{m+n-1}{m}\right]. \tag{9}$$

Comparing expressions (9) and (7) we see that, under the conditions postulated, linkage increases the F_2 variance of a single character by the factor $[(m+n-1)/m]$. This factor is always greater than unity (unless $n=1$) but approaches unity when the number of chromosome pairs, m, is large compared to the number of loci, n; in this case most loci will be on separate chromosomes and will therefore assort independently of all other loci. It should be noted,

furthermore, that expression (9) is always greater than $1/8m$ except when $m=1$ and approaches this value when n, the number of loci, is very large compared to m, the number of chromosomes. The F_2 variance under complete linkage is thus somewhat greater than $1/8m$ or $1/8n$, being characteristic of either the number of chromosome pairs or the number of gene pairs, whichever is the smaller and yields, therefore, the higher variance.

PARENTAL-COMBINATION VARIANCE

Following the method of the last section it is easy to determine the parental-combination variance for the special case where $n_a=n_b$ and all allelic differences have equal effects. In this case the parental-combination variance contributed by a given chromosome pair depends only on the total number of loci it contains irrespective of the proportions of these that are a-type and b-type. There are therefore $2n$ loci distributed at random on m chromosomes, but the values of α_i and of β_i are all $1/2n$ as before. The variance contributed by a single chromosome is, therefore, equal to:

$$\frac{1}{8n^2}\left[q^{2n}(0) + (2n)q^{2n-1}p(1)^2 + \frac{2n(2n-1)q^{2n-1}p^2(2)^2}{2!} \cdots\right.$$

and proceeding as before this may be shown to yield:

$$\frac{2p}{8n}\left[1 + p(2n-1)\right] = \frac{1}{4nm}\left[\frac{m+2n-1}{m}\right].$$

Multiplying by m in order to obtain the variance of m pairs of chromosomes, we have:

$$\frac{1}{4n}\left[\frac{m+2n-1}{m}\right]. \tag{10}$$

To obtain the variance in the comparable case with independent assortment we substitute n for n_a and n_b in expression (2) which then becomes:

$$\frac{1}{4n}. \tag{11}$$

A comparison of expressions (10) and (11) shows that linkage increases the parental-combination variance under the conditions mentioned by the factor $(m+2n-1)/m$. This factor is close to unity where m, the number of chromosomes, is large compared to $2n$, the number of a-type and b-type loci combined; in this case there is an approach to independent assortment. Where $2n$ is large compared to m the parental type variance may be greatly increased over that expected in independent assortment. For example, if the number of chromosome pairs is 10 and the numbers of a-type and b-type loci are each 20, the parental-combination variance will average 4.9 times the value under independent assortment.

CORRELATION IN THE F_2

With independent assortment, characters A and B would not be correlated under the postulates given. With linkage, however, correlation is to be expected and this correlation can be expressed in terms of the ratio of the parental and recombination variances. It is not difficult to show that the correlation coefficient, in the case of a normal surface with equal variances along the two axes, is given by the following expression where k is the ratio of the two diameters of the ellipses composed of contours of uniform density: $r=(1-k^2)/(1+k^2)$. Substituting for k^2 the ratio of parental combination variance (formula 9) to recombination variance (formula 5 setting $n_a=n_b=n$) the following expression is obtained: $r=n/(m+n-1)$. This expression gives the precise ratio of mean covariance to the root-product of the mean variances for all distributions of loci under the postulates listed, even where the number of loci is small. The correlation coefficient itself is slightly biased since the ratio of two unbiased estimates is itself not necessarily unbiased.

The mean correlation for all distributions of loci is unity only where there is one chromosome pair with complete linkage. Where there are several chromosomes with complete linkage and the number of loci for each character equals the number of chromosomes, the correlation is slightly greater than 0.5. Where loci for each character are several times as numerous as complete linkage groups, the correlation becomes high with unity as a limit.

DISCUSSION

It has been shown that complete linkage, under the conditions postulated, decreases the F_2 *recombination variance* by only the proportion $1/m$ on the average where m is the number of chromosome pairs; the *parental combination* variance, on the other hand, may be considerably *increased* over that expected with independent assortment, the factor of increase being $(m+2n-1)/m$ for the case in which the numbers of a-type and b-type loci are each equal to n and all allelic substitutions have numerically equal effects. Table 1 gives the *standard deviations* expected under independent assortment and under linkage for ten pairs of chromosomes and different values of n, the unit of measurement being the P difference. From the table it can be seen that, under independent assortment, as the number of factor pairs per character increases from one to 1000, the F_2 standard deviation decreases by the square root of this ratio, or by a factor of over 30. Under linkage, with ten chromosome pairs, the F_2 recombination standard deviation is always nine-tenths of this value and hence is also reduced by a factor of over 30, but the parental-combination standard deviation by contrast is only reduced by a factor of a little more than one-half. The parental-combination variance does not decrease very much after the number of factor pairs per character becomes equal to the number of chromosome pairs.

The cases for 10 and 100 factor pair differences per character are illustrated in figure 2, the circles indicating the two standard deviation limits for inde-

TABLE 1

F_2 standard deviations for ten pairs of chromosomes (for other conditions see text).

NO. OF *a*-TYPE AND OF *b*-TYPE LOCI (*n*)	STANDARD DEVIATIONS			CORELATION BETWEEN A AND B
	INDEPENDENT ASSORTMENT	LINKAGE		
		RECOMBINATION	PARENTAL-COMBINATION	
1	.5	.474	.524	.1
3	.289	.273	.343	.25
10	.158	.150	.269	.53
30	.091	.087	.240	.77
100	.050	.047	.229	.92
300	.029	.027	.225	.97
1000	.016	.015	.224	.99

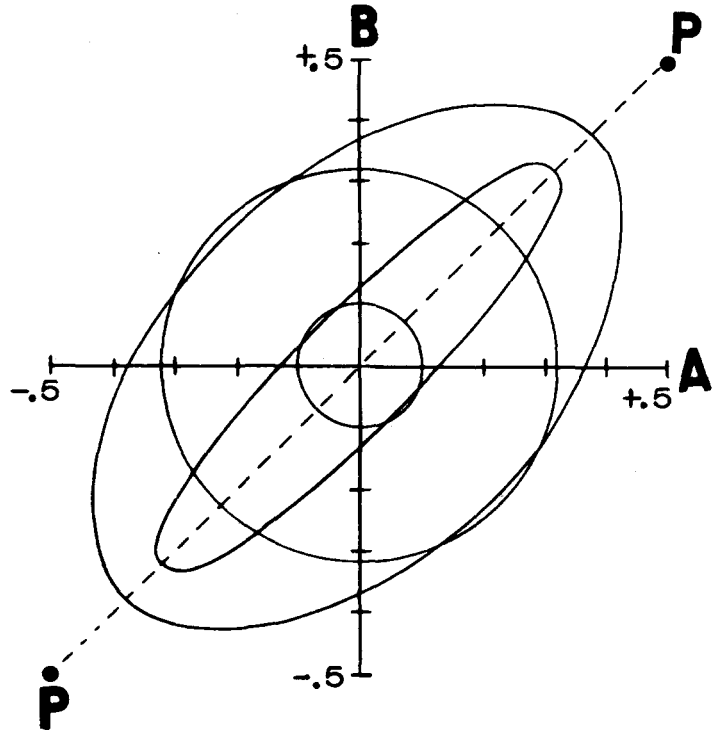

FIGURE 2.—F_2 Populations With and Without Linkage. The small circle and the small ellipse represents the two standard deviation limits, for independent assortment and linkage respectively, for one hundred *a*-type and one hundred *b*-type loci. The large circle and large ellipse represent the same for ten *a*-type and ten *b*-type loci. Based on ten equal chromosome pairs with complete linkage within chromosomes.

pendent assortment and the ellipses the same for complete linkage. As this figure shows, the narrowness of the distributions with many loci under linkage is mainly due to its *extension* in the direction of parental-combination types rather than its *contraction* in the direction of recombination types. The major restriction of F_2 recombination variance with multifactorial inheritance is thus a consequence of the large number of loci among which the total genetic differences are apportioned.

Where there are many loci and few linkage groups, extreme F_2 recombination individuals, that is those very similar to different P individuals with respect to different characters, are impossible. The elimination of such individuals from the F_2 distributions might be expected to decrease recombination variance to a greater extent than the foregoing analysis indicates. Even under independent assortment, however, where many factor pairs are segregating the probability of obtaining the extreme recombination type individuals is vanishingly small. If there are ten pairs of *a*-type genes and ten pairs of *b*-type genes, the probability of an F_2 individual possessing all twenty *a*-type alleles from either P parent and all twenty *b*-type alleles from the other, under independent assortment, is $(1/2)^{39}$ or less than one in five-hundred-thousand-million. The probability of an F_2 individual possessing four-fifths or more of the *a*-type alleles from either parent and, at the same time, four-fifths or more of the *b*-type alleles from the other, in this case, is about one in fourteen thousand. Within the range of reasonably probable combinations, and under the conditions postulated, linkage reduces only slightly the degree to which characteristics of opposite parents are likely to be combined except where the number of chromosome pairs is quite small.

The postulates underlying the foregoing analysis are never completely realized in practice. Linkage is ordinarily far from complete, and crossing-over is expected to modify the results in the direction corresponding to a larger number of chromosome pairs and of independent assortment. With incomplete linkage, then, the reduction in recombination variance should be even less than the proportion $1/m$ and the factor of increase of parental-combination variance less than $(m+2n-1)/m$. As a reasonable first order allowance for incompleteness of linkage, m could be set equal to the number of chromosome pairs plus the mean number of chiasmata in all the chromosomes, or equal to the number of chromosome pairs plus the total number of map units divided by 50. In maize the value of m, on this basis, would be at least 24; therefore it would require about 24 equally effective gene pair differences affecting each character to bring the expected correlation due to linkage as high as 0.5. Another likely departure from the idealized model is the possession by the plus parent of some minus alleles and by the minus parent of the corresponding plus alleles for each character. The modification of expected F_2 variance due to this situation is toward that of independent assortment; in the extreme case, where the plus alleles at all the loci have equal and independent probabilities of coming from either P individual, the expected F_2 variances are exactly those expected

in independent assortment. In such a case, however, the character differences of P individuals would furnish no criterion of the sum of the genetic differentials and in intermediate cases the F_2 variances would be proportionately large in terms of P differences for any particular values of m and n.

The deviations from the postulated model just discussed would tend to reduce the effects of linkage on F_2 variances. Other circumstances could, however, accentuate its effects. With unequal genic content of different chromosomes, more loci would tend to lie on fewer chromosomes, and the variance would be modified in the direction characteristic of fewer chromosomes. In case parental differences are due chiefly to one or a few chromosomal segments introduced by introgressive hybridization, the results could be that expected for one or a very few chromosome pairs. Where the number of allelic differences is small, chance distribution may sometimes lead to results quite different from the mean expectation. F_1 heterozygosity for reciprocal translocations or other chromosomal disharmonies can result in effective linkage between loci of different chromosomes through modified meiotic distributions and inviability of some gametic and zygotic combinations. Conceivably other causes might lead to closer linkage between differentials for different characters than would be expected by chance.

Other sources of F_2 variance are always superimposed on those due to segregation of linked and unlinked genes. Pleiotropy if present acts like complete linkage of gene differentials affecting two or more characters and can increase either parental or recombination variance. The former is, however, somewhat more likely either for the reason that whatever selection may have been responsible for the divergence of the P types would utilize those pleiotropic differences, if available, affecting both characters in the direction of selection, or that a preponderance of a given type of pleiotropy among gene differentials for the characters concerned could restrict genetic plasticity and hence also the P types likely to exist. Non-genetic influences almost inevitably increase variances and the increases in the F_2 parental-combination and F_2 recombination variances due to these causes may be very different, because environmental variables, like pleiotropic genes, can have simultaneous effects on two or more characters.

SUMMARY

The apportionment of total genetic differences between parents among a large number of loci severely restricts genetic recombination variance in F_2 populations; only a slight additional reduction is, on the average and in the absence of special circumstances, attributable to linkage. Linkage, however, can be expected to *increase* the variation of F_2 character combinations *in the direction of the parental types* and this increase can be very great where the number of factor pair differences is large compared to the number of chromosome pairs. Formulae are derived for estimating the effects of linkage on F_2 recombination variance and parental-combination variance and correlation in terms of number of chromosome pairs and number of loci involved.

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