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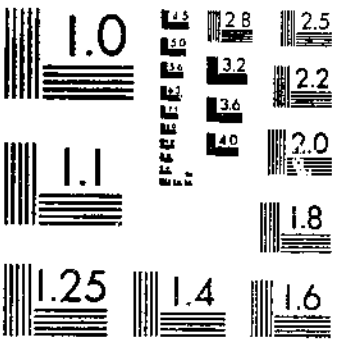

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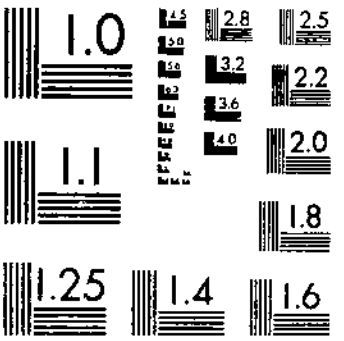

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Theoretical Segregation Ratios of Qualitatively Inherited Characters for Hexaploid Sweetpotato (*Ipomoea batatas* L.)

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CONTENTS

	Page
Theoretical F_2 ratios	1
Test-cross ratios	2
Population size	2
Conformity of data to a hypothesis	3
Example	4
Conclusions	5
Appendix	6

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Theoretical Segregation Ratios of Qualitatively Inherited Characters for Hexaploid Sweetpotato (*Ipomoea batatas* L.)

By ALFRED JONES, *research geneticist, Crops Research Division, Agricultural Research Service, U.S. Department of Agriculture; and Horticulture Department, Georgia Agricultural Experiment Stations*

Qualitative genetic data for sweetpotatoes is scarce, partially because it is a hexaploid with 90 somatic chromosomes and partially because of the difficulties of selfing due to sterility, incompatibility, and the failure of many types to bloom in temperate regions.

The accumulation of genetic data about many qualitative characters in sweetpotatoes can contribute to the understanding of the mode of inheritance and to the knowledge of its origin; and this information aids in the development of improved breeding procedures. Cytological information indicates that the sweetpotato contains three genomes and that two of these are probably more similar than the third.[1] [2] Chromosome pairing is generally as bivalents with very few quadrivalents; this greatly simplifies the expected genetic ratios by allowing the assumption that there will be no double reduction. Predominantly hexasomic ratios would indicate that all three genomes are alike; whereas, predominantly disomic ratios would indicate that the three genomes are distinct. Tetrasomic or tetradisomic ratios would support the hypothesis of two similar and one dissimilar genome.

Certain assumptions were necessary for construction of the tables. As mentioned previously, the assumption of no double reduction eliminates many complications. The consideration of only two classes of plant types (like the parent or different from it) allows comparison of various hypotheses and minimizes errors due to dividing populations into too many or too few classes. The parental type (F_1) is expressed first and then the nonparental (segregate) type. Parents are assumed to be F_1 of unknown parentage, because when sweetpotato breeders find a self-fertile plant that will produce enough offspring for a genetic study they often either do not know its parentage or the parents are not available. For this same reason, selfing and backcrossing to the F_1 are the test crosses used in the tables.

This bulletin brings together pertinent information needed for qualitative genetic studies of hexaploids, in particular the sweetpotato, and provides tables of theoretical segregation ratios that may make the breeder's task of interpreting genetic data much less laborious.

THEORETICAL F_2 RATIOS

Since the sweetpotato has three genomes all of which may be similar or different: disomic, tetrasomic, tetradisomic, and hexasomic

[1] JONES, A. CYTOLOGICAL OBSERVATIONS AND FERTILITY MEASUREMENTS OF SWEETPOTATO (IPOMOEA BATATAS (L.) LAM.). Amer. Soc. Hort. Sci. Proc. 86: 527–537. 1965.

[2] TING, Y. C., and KEHR, A. E. MEIOTIC STUDIES IN THE SWEETPOTATO (IPOMOEA BATATAS (L.) LAM.). Heredity 44: 207–211. 1953.

models must all be considered as possibilities. Many different genetic hypotheses can be considered, some of which have been used in constructing appendix table 1. Because there are three genomes a minimum of three factors for the disomic models must be considered.

In appendix table 1 dosage effects have been considered for the single-factor models, but not for other models because of the increasing complexity of models of more than one factor. Obviously, dosage effects could occur with the other models even though not considered in this table. Likewise, the table has not been extended beyond two-factor tetrasomic and hexasomic models. Up to three-factor disomic models have been included. As can be seen from the table, the complexity of possible genetic hypotheses increases rapidly as the number of factors increases. Even with these limitations, the table does provide a starting place and does include a considerable number of possibilities.

TEST-CROSS RATIOS

Appendix table 1 shows that often more than one genetic hypotheses fits a given F_2 ratio. Also, practical limitations of population size often make it necessary to consider those ratios a little larger or a little smaller than the ratio that corresponds best with the observed data. In order to show that a given hypothesis is better than other possible ones it is necessary to make test crosses. Many test crosses are possible, and the best crosses to use may vary according to the material available. For the purpose of this discussion and to develop appendix table 2, it was assumed that the parent plants were unknown or otherwise not available. Therefore, selfing of F_2's and backcrossing of F_2's to the F_1 were used in computing expected test-cross ratios. In this way a basis is available to compare the various hypotheses.

Appendix table 2 has been arranged with ratios in ascending frequency of F_1 types and gives the expected frequencies of the various F_2 genotypes and their expected test-cross ratios. No F_2 ratios beyond 399: 1 are included: testing higher ratios probably exceeds the limits of practicality for sweetpotatoes.

POPULATION SIZE

A question of importance is, "What size population is needed?" The general answer is: "As large as possible." With sweetpotatoes, 400 to 500 plants is a practical answer for a F_2 population. Actually, the answer depends on what ratios need to be discriminated between. The formulas for computing the size population needed to discriminate between two alternative ratios at the 0.05 probability level can be developed by simultaneously solving two equations (see pp. 148 to 157 of Kempthorne)[3] for two unknowns: the populations size (n) and a

[3] KEMPTHORNE, OSCAR. AN INTRODUCTION TO GENETIC STATISTICS. 345 pp. John Wiley & Sons, Inc., New York. 1957.

breaking point (r). The formula for "n", which was used to construct appendix table 3, is:

$$n = 2.7 \left(\frac{\sqrt{p_1 - p_1^2} + \sqrt{p_2 - p_2^2}}{p_2 - p_1} \right)^2$$

Values of "r" are not included in the table, but they may be computed by:

$$r = np_1 + 1.645 \sqrt{n(p_1 - p_1^2)}$$

In these formulas:
n = population size;
r = breaking point, above which the higher proportion is accepted; below which the lower proportion is accepted;
p_1 = lower proportion;
p_2 = higher proportion.

To find the population size necessary to distinguish between 3:1 and 15:1 ratios, the 3:1 could be used as the lower proportion and 15:1 as the higher proportion (3:1 = 0.750, 15:1 = 0.937) to obtain $n = 35$ approximately.

$$n = 2.7 \left(\frac{\sqrt{0.750 - 0.562} + \sqrt{0.937 - 0.878}}{0.937 - 0.750} \right)^2$$

$$= 2.7 \left(\frac{\sqrt{0.188} + \sqrt{0.059}}{0.187} \right)^2 = 2.7 \left(\frac{0.433 + 0.243}{0.187} \right)^2$$

$$= 2.7 \left(\frac{0.676}{0.187} \right)^2 = 2.7 (3.61)^2 = 2.7 (13.03)$$

$$= 35.18$$

The same answer would be obtained by looking at the proportion of segregate types and using 3:1 as the higher proportion and 15:1 as the lower proportion (3:1 = 0.250, 15:1 = 0.063). Appendix table 3 is meant as a guideline to give an indication of what can be learned with a given population size. It suggests the futility of trying to arrive at an answer with only F_2 data and can be useful in planning the necessary test crosses.

CONFORMITY OF DATA TO A HYPOTHESIS

The chi-square (X^2) goodness of fit test is the most widely used test of conformity of data to a hypothetical ratio. The X^2 test in terms

of "m" to "unity" with "a_1" and "a_2" the observed types as given by Kempthorne [4] is:

$$X^2 = \frac{(a_1 - ma_2)^2}{mn}$$

where n = the total number of plants,
a_1 = the type 1 (parental, or F_1, type) plants,
and a_2 = the type 2 (nonparental, or segregate, type) plants.
To test a 3:1:

$$X^2 = \frac{(a_1 - 3a_2)^2}{3n} \text{ with 1 degree of freedom.}$$

The value obtained would then be compared to a table of chi-squares (appendix table 4) for one degree of freedom. If the probability of a larger chi-square is $\geqq 0.05$, then it can be said that the observed ratio has an acceptable fit to the hypothesis.

The reader is referred to Kempthorne [4] for an adjustment when X^2 values come very close to the 0.05 probability level (*pp. 148 and 149*); for testing linkages (*p. 157*); for testing more than two classes (*p. 154*). Snedecor [5] (*chapter 9*) gives additional information on these procedures.

EXAMPLE

An example from work on sweetpotatoes published by Poole [6] in which 452 selfed progeny of a self-fertile plant segregated for red vs. green stems (G:g) will illustrate the procedure. The parent plant was red stemmed and 346 G:106g were obtained in the progeny, which he interpreted as a 3:1 ratio. Does his data fit a 3:1?

$$X^2 = \frac{[346 - (3 \times 106)]^2}{3 \times 452}$$

$$X^2 = \frac{(346 - 318)^2}{1{,}356} = \frac{(28)^2}{1{,}356} = \frac{784}{1{,}356} = 0.578$$

This falls between probability levels 0.50 and 0.30 in the X^2 table; therefore the observed ratio fits a 3:1 hypothesis. But the actual ratio is 3.26:1. According to appendix tables 1 and 2, the observed ratio probably fits other theoretical ratios equally well. In fact it fits the 3.26:1 three-factor disomic ratio perfectly. Certainly in a plant with three genomes, this is as likely as the 3:1 ratio postulated. Also ratios of 2.69:1, 2.70:1, 2.79:1, 2.98:1, 3.01:1, 3.11:1, and 3.17:1 all fit acceptably.

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[4] See footnote 3, p. 2.

[5] SNEDECOR, G. W. STATISTICAL METHODS. Ed. 4. Iowa State Col. Press, Ames. 1946.

[6] POOLE, C. F. SWEETPOTATO GENETIC STUDIES. Hawaii Agr. Expt. Sta. Tech. Bul. 27, 19 pp. 1955.

Increased population size would help to narrow the number of proposed ratios that fit the data and could be accomplished by repeating the test with a new group of seedlings. However, eventually test crosses would be necessary to determine which of the 39 genetic hypotheses within the above range of possible ratios is the proper one.

The expected test-cross ratios after selfing F_2 plants (appendix table 2) show how to find an answer. If all nonparental F_2 plants when selfed breed true (0:1) for the nonparental (segregate) type, then the number of possible genetic hypotheses is narrowed to 11. Conversely, if some nonparental F_2 plants continue to segregate for both types, there are 28 possibilities. If the parental type F_2 plants either breed true for the parental type (1:0) or segregate 3:1, then the number of possibilities is narrowed to about 7 (considering those segregations difficult to distinguish from 3:1). If the nonparental types breed true and the parental types are as above, then the possible genetic hypotheses narrow to the one-factor disomic. In like manner other hypotheses could be distinguished. In some cases backcross ratios may be needed in conjunction with selfed ratios; in others it may even be necessary to construct other test crosses.

CONCLUSIONS

Information relative to the qualitative characters in sweetpotatoes would be valuable to the understanding of its origin and contribute to the development of improved breeding procedures. Such information could be accumulated by sweetpotato breeders if they would follow systematic approaches in their studies of interesting plant characters noted in self-fertile plants and their progeny. Usually the inheritance of qualitative characters in sweetpotatoes can be determined if the solution is approached in a logical, systematic manner (describing the parent (F_1), giving the selfed (F_2) ratios as the basis for some hypothesis, and then testing the hypothesis with suitable crosses).

The tables presented are intended as a starting point only as many factors have not been included, notably: multiple class ratios; consideration of lethals; dosage effects beyond one-factor hypotheses; and many test-cross possibilities.

APPENDIX

TABLE 1.—*Theoretical (F_2) segregation ratios obtained from selfing various parental types assuming different genetic hypotheses*

[Expressed as parental (F_1) type: nonparental (segregate)]

Assumed parental (F_1) type	Number of factors	Type of inheritance	Necessary for expression of parental (F_1) type, with dosage of—				
			1	2	3	4	5
A a	1	Disomic	3:1				
A a^3	1	Tetrasomic	3:1				
A^2a^2	1	do	35:1	3:1			
A^3a	1	do	1:0	1:0	3:1		
A a^5	1	Hexasomic	3:1				
A^2a^4	1	do	24:1	2.57:1			
A^3a^3	1	do	399:1	20.05:1	2.39:1		
A^4a^2	1	do	1:0	1:0	24:1	2.57:1	
A^5a	1	do	1:0	1:0	1:0	1:0	3:1

Assumed parental (F_1) type	Number of factors	Type of inheritance	Necessary for expression of nonparental (segregate) type [1]				
			Rec. of A and B	Rec. of A or B	Dom. of A, rec. of B	Dom. of B, rec. of A	Dom. of A or B, rec. of the other
A a B b	2	Disomic	15:1	1.28:1	4.33:1	4.33:1	1.67:1
A a^3B b^3	2	Tetrasomic	15:1	1.28:1	4.33:1	4.33:1	1.67:1
A $a^3B^2b^2$	2	do	143:1	2.69:1	47:1	3.11:1	2.79:1
A a^3B^3b	2	do	1:0	3:1	1:0	3:1	3:1
A^2a^2B b^3	2	do	143:1	2.69:1	3.11:1	47:1	2.79:1
$A^2a^2B^2b^2$	2	do	1,295:1	17.25:1	36.02:1	36.02:1	17.5:1
$A^2a^2B^3b$	2	do	1:0	35:1	1:0	35:1	35:1
A^3a B b^3	2	do	1:0	3:1	3:1	1:0	3:1
A^3a B^2b^2	2	do	1:0	35:1	35:1	1:0	35:1
A^3a B^3b	2	do	1:0	1:0	1:0	1:0	1:0
A a^3B b	1–1	Tetradisomic	15:1	1.28:1	4.33:1	4.33:1	1.67:1
A^2a^2B b	1–1	do	143:1	2.69:1	3.11:1	47:1	2.79:1
A^3a B b	1–1	do	1:0	3:1	3:1	1:0	3:1

[1] Dom., dominant; rec., recessive.

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TABLE 1.—*Theoretical (F_2) segregation ratios obtained from selfing various parental types assuming different genetic hypotheses*—Continued

[Expressed as parental (F_1) type: nonparental (segregate)]

Assumed parental (F_1) type	Number of factors	Type of inheritance	Necessary for expression of nonparental (segregate) type [1]				
			Rec. of A and B	Rec. of A or B	Dom. of A, rec. of B	Dom. of B, rec. of A	Dom. of A or B, rec. of the other
A a^5B b^5	2	Hexasomic	15:1	1.28:1	4.33:1	4.33:1	1.67:1
A $a^5B^2b^4$	2	do	99:1	2.57:1	32.33:1	3.17:1	2.70:1
A $a^5B^3b^3$	2	do	1,600:1	2.97:1	532:1	3.01:1	2.98:1
A $a^5B^4b^2$	2	do	1:0	3:1	1:0	3:1	3:1
A a^5B^5b	2	do	1:0	3:1	1:0	3:1	3:1
A^2a^4B b^5	2	do	99:1	2.57:1	3.17:1	32.33:1	2.70:1
$A^2a^4B^2b^4$	2	do	624:1	11.75:1	25.04:1	25.04:1	12.02:1
$A^2a^4B^3b^3$	2	do	9,999:1	22.58:1	416:1	24:1	22.6:1
$A^2a^4B^4b^2$	2	do	1:0	24:1	1:0	24:1	24:1
$A^2a^4B^5b$	2	do	1:0	24:1	1:0	24:1	24:1
A^3a^3B b^5	2	do	1,600:1	2.97:1	3.01:1	532:1	2.98:1
$A^3a^3B^2b^4$	2	do	9,999:1	22.58:1	24:1	416:1	22.6:1
$A^3a^3B^3b^3$	2	do	159,999:1	199:1	400:1	400:1	199:1
$A^3a^3B^4b^2$	2	do	1:0	399:1	1:0	399:1	399:1
$A^3a^3B^5b$	2	do	1:0	399:1	1:0	399:1	399:1

$A^4a^2B\ b^5$	2	do	1:0	3:1	3:1	1:0	3:1
$A^4a^2B^2b^4$	2	do	1:0	24:1	24:1	1:0	24:1
$A^4a^2B^3b^3$	2	do	1:0	399:1	399:1	1:0	399:1
$A^4a^2B^4b^2$	2	do	1:0	1:0	1:0	1:0	1:0
$A^4a^2B^5b$	2	do	1:0	1:0	1:0	1:0	1:0
$A^5a\ B\ b^5$	2	do	1:0	3:1	3:1	1:0	3:1
$A^5a\ B^2b^4$	2	do	1:0	24:1	24:1	1:0	24:1
$A^5a\ B^3b^3$	2	do	1:0	399:1	399:1	1:0	399:1
$A^5a\ B^4b^2$	2	do	1:0	1:0	1:0	1:0	1:0
$A^5a\ B^5b$	2	do	1:0	1:0	1:0	1:0	1:0

Assumed parental (F_1) type	Number of factors	Type of inheritance	Necessary for expression of nonparental (segregate) type [1]							
			Rec. of all 3 factors	Rec. of at least 2 of the 3 factors	Rec. of at least 1 of the 3 factors	Dom. of A, rec. of B and C	Dom. of B and C, rec. of A	Dom. of A or B, rec. of C	Dom. of A, B, or C; rec. of the other 2	Dom. of A and B, B and C, or A and C; and rec. of the other
AaBbCc	3	Disomic...	63:1	5.4:1	1:1.37	20.33:1	6.11:1	3.26:1	6.11:1	1.37:1

[1] Dom., dominant; rec., recessive.

TABLE 2.—*Theoretical test-cross ratios for various possible genetic hypotheses of F_2 segregations in a hexaploid assuming no double reduction*

Observed F_2 ratio [1]	Hypothetical F_1 genotype	Genetic hypothesis [2 3]	F_2 phenotype [3]	F_2 genotype [2 4 5]	F_2 frequency	Test-cross ratios [1]	
						Self	Back-cross to F_1
1:1.37 (27:37)	A a B b C c	3 factor: disomic: rec. of at least 1 of the 3 loci for expression of seg. type.	F_1	A^2 B^2 C^2	1	1:0	1:0
			F_1	Homo. dom. at 2 loci, het. at 1 locus	6	3:1	3:1
			Seg.	Homo. dom. at 2 loci, homo. rec. at 1 locus.	3	0:1	1:1
			F_1	Homo. dom. at 1 locus, het. at 2 loci	12	1.28:1	1.28:1
			Seg.	Homo. dom. at 1 locus, homo. rec. at 2 loci.	3	0:1	1:3
			Seg.	Homo. dom. at 1 locus, homo. rec. at 1 locus, and het. at 1 locus.	12	0:1	1:1.67
			F_1	A a B b C c	8	1:1.37	1:1.37
			Seg.	Het. at 2 loci, homo. rec. at 1 locus	12	0:1	1:2.55
			Seg.	Het. at 1 locus, homo. rec. at 2 loci	6	0:1	1:4.33
			Seg.	a^2 b^2 c^2	1	0:1	1:7
1.28:1 (9:7)	A a B b	2 factor: disomic: rec. of A or B for expression of seg. type.	F_1	A^2 B^2	1	1:0	1:0
			F_1	A^2 B b	2	3:1	3:1
			Seg.	A^2 b^2	1	0:1	1:1
			F_1	A a B^2	2	3:1	3:1
			F_1	A a B b	4	1.28:1	1.28:1
			Seg.	A a b^2	2	0:1	1:1.67
			Seg.	a^2B^2	1	0:1	1:1
			Seg.	a^2B b	2	0:1	1:1.67
			Seg.	a^2 b^2	1	0:1	1:3
1.28:1 (9:7)	A a^2B b^3	2 factor: tetrasomic: rec. of A or B for expression of seg. type.	F_1	$A^2a^2B^2b^2$	1	17.2:1	5.26:1
			F_1	A^2a^2B b^3	2	2.69:1	2.20:1
			Seg.	A^2a^2 b^4	1	0:1	1:1.18
			F_1	A $a^2B^2b^2$	2	2.69:1	2.20:1

			F_1	A a^3B b^3	4	1.28:1	1.28:1
			Seg.	A a^3 b^4	2	0:1	1:1.67
			Seg.	$a^4B^2b^2$	1	0:1	1:1.18
			Seg.	a^4B b^3	2	0:1	1:1.67
			Seg.	a^4 b^4	1	0:1	1:3
1.28:1 (9:7)	A a^3B b	1–1 factor; tetradisomic; rec. of A or B for expression of seg. type.	F_1	$A^2a^2B^2$	1	35:1	11:1
			F_1	A^2a^2B b	2	2.69:1	2.20:1
			Seg.	A^2a^2 b^2	1	0:1	1:1.18
			F_1	A a^3B^2	2	3:1	3:1
			F_1	A a^3B b	4	1.28:1	1.28:1
			Seg.	A a^3 b^2	2	0:1	1:1.67
			Seg.	a^4B^2	1	0:1	1:1
			Seg.	a^4B b	2	0:1	1:1.67
			Seg.	a^4 b^2	1	0:1	1:3
1.28:1 (9:7)	A a^5B b^5	2 factor; hexasomic; rec. of A or B for expression of seg. type.	F_1	$A^2a^4B^2b^4$	1	11.7:1	4.26:1
			F_1	A^2a^4B b^5	2	2.57:1	2.07:1
			Seg.	A^2a^4 b^6	1	0:1	1:1.22
			F_1	A $a^5B^2b^4$	2	2.57:1	2.07:1
			F_1	A a^5B b^5	4	1.28:1	1.28:1
			Seg.	A a^5 b^6	2	0:1	1:1.67
			Seg.	$a^6B^2b^4$	1	0:1	1:1.22
			Seg.	a^6B b^5	2	0:1	1:1.67
			Seg.	a^6 b^6	1	0:1	1:3
1.37:1 (37:27)	A a B b C c	3 factor; disomic; dom. of A and B, B and C, or A and C and rec. of the other locus for expression of seg. type.	F_1	A^2 B^2 C^2	1	1:0	1:0
			F_1	Homo. dom. at 2 loci, het. at 1 locus	6	3:1	3:1
			Seg.	Homo. dom. at 2 loci, homo. rec. at 1 locus.	3	0:1	1:1
			F_1	Homo. dom. at 1 locus, het. at 2 loci	12	1.67:1	1.67:1
			F_1	Homo. dom. at 1 locus, homo. rec. at 2 loci.	3	1:0	1:1
			Seg.	Homo. dom. at 1 locus, homo. rec. at 1 locus, and het. at 1 locus.	12	1:3	1:1
			F_1	A a B b C c	8	1.37:1	1.37:1
			Seg.	Het. at 2 loci, homo. rec. at 1 locus	12	1.28:1	1.13:1
			F_1	Het. at 1 locus, homo. rec. at 2 loci	6	1:0	1.28:1
			F_1	a^2 b^2 c^2	1	1:0	1.67:1

See footnotes at end of table, p. 41.

TABLE 2.—*Theoretical test-cross ratios for various possible genetic hypotheses of F_2 segregations in a hexaploid assuming no double reduction*—Continued

Observed F_2 ratio [1]	Hypothetical F_1 genotype	Genetic hypothesis [2 3]	F_2 phenotype [3]	F_2 genotype [2 4 5]	F_2 frequency	Test-cross ratios [1]	
						Self	Backcross to F_1
1.67:1 (10:6)	A a B b	2 factor: disomic; dom. of A or B and rec. of the other locus for expression of seg. type.	F_1	A^2 B^2	1	1:0	1:0
			F_1	A^2 B b	2	3:1	3:1
			F_1	A a B^2	2	3:1	3:1
			F_1	A a B b	4	1.67:1	1.67:1
			Seg.	A^2 b^2	1	0:1	1:1
			Seg.	a^2B^2	1	0:1	1:1
			Seg.	A a b^2	2	1:3	1:1
			Seg.	a^2B b	2	1:3	1:1
			F_1	a^2 b^2	1	1:0	1:1
1.67:1 (10:6)	A a^3B b^3	2 factor: tetrasomic: dom. of A or B and rec. of the other locus for expression of seg. type.	F_1	$A^2a^2B^2b^2$	1	17.5:1	5.54:1
			F_1	A^2a^2B b^3	2	2.79:1	2.43:1
			F_1	A $a^3B^2b^2$	2	2.79:1	2.43:1
			F_1	A a^3B b^3	4	1.67:1	1.67:1
			Seg.	A^2a^2 b^4	1	1:35	1:1
			Seg.	$a^4B^2b^2$	1	1:35	1:1
			Seg.	A a^3 b^4	2	1:3	1:1
			Seg.	a^4B b^3	2	1:3	1:1
			F_1	a^4 b^4	1	1:0	1:1
1.67:1 (10:6)	A a^3B b	1–1 factor: tetradisomic: dom. of A or B and rec. of the other locus for expression of seg. type.	F_1	$A^2a^2B^2$	1	35:1	11:1
			F_1	A^2a^2B b	2	2.79:1	2.43:1
			F_1	A a^3B^2	2	3:1	3:1
			F_1	A a^3B b	4	1.67:1	1.67:1
			Seg.	A^2a^2 b^2	1	1:35	1:1
			Seg.	A a^3 b^2	2	1:3	1:1
			Seg.	a^4B^2	1	0:1	1:1

			Seg.	$a^4B\ b$	2	1:3	1:1
			F_1	$a^4\ b^2$	1	1:0	1:1
1.67:1 (10:6)	A $a^5B\ b^5$	2 factor: hexasomic; dom. of A or B and rec. of the other locus for expression of seg. type.	F_1	$A^2a^4B^2b^4$	1	12:1	4.55:1
			F_1	$A^2a^4B\ b^5$	2	2.70:1	2.33:1
			F_1	$A\ a^5B^2b^4$	2	2.70:1	2.33:1
			F_1	$A\ a^5B\ b^5$	4	1.67:1	1.67:1
			Seg.	$A^2a^4\ b^6$	1	1:24	1:1
			Seg.	$a^6B^2b^4$	1	1:24	1:1
			Seg.	$A\ a^5\ b^6$	2	1:3	1:1
			Seg.	$a^6B\ b^5$	2	1:3	1:1
			F_1	$a^6\ b^6$	1	1:0	1:1
2.39:1 (282:118)	A^3a^3	1 factor: hexasomic; triplex expression for F_1 type.	F_1	A^6	1	1:0	1:0
			F_1	A^5a	18	1:0	39:1
			F_1	A^4a^2	99	24:1	6.69:1
			F_1	A^3a^3	164	2.39:1	2.39:1
			Seg.	A^2a^4	99	1:2.57	1:1
			Seg.	$A\ a^5$	18	0:1	1:2.63
			Seg.	a^6	1	0:1	1:19
2.57:1 (18:7)	A^2a^4	1 factor: hexasomic; duplex expression for F_1 type.	F_1	A^4a^2	1	1:0	24:1
			F_1	A^3a^3	6	20:1	6.69:1
			F_1	A^2a^4	11	2.57:1	2.57:1
			Seg.	$A\ a^5$	6	1:3	1:1
			Seg.	a^6	1	0:1	1:4
2.57:1 (18:7)	A^4a^2	1 factor: hexasomic; quadruplex expression for F_1 type.	F_1	A^6	1	1:0	1:0
			F_1	A^5a	6	1:0	9:1
			F_1	A^4a^2	11	2.57:1	2.57:1
			Seg.	A^3a^3	6	1:2.39	1:1
			Seg.	A^2a^4	1	1:24	1:2.57
2.57:1 (72:28)	A $a^5B^2b^4$	2 factor; hexasomic; rec. of A or B for expression of seg. type.	F_1	$A^2a^4B^4b^2$	1	24:1	9:1
			F_1	$A^2a^4B^3b^3$	6	23:1	8.17:1
			F_1	$A^2a^4B^2b^4$	11	11.7:1	6.35:1
			F_1	$A^2a^4B\ b^5$	6	2.57:1	4.26:1

See footnotes at end of table, p. 41.

TABLE 2.—*Theoretical test-cross ratios for various possible genetic hypotheses of F_2 segregations in a hexaploid assuming no double reduction*—Continued

Observed F_2 ratio [1]	Hypothetical F_1 genotype	Genetic hypothesis [2 3]	F_2 phenotype [3]	F_2 genotype [2 4 5]	F_2 frequency	Test-cross ratios [1]	
						Self	Backcross to F_1
2.57:1 (72:28)—Con.	A $a^5B^2b^4$ —Con.	2 factor; hexasomic; rec. of A or B for expression of seg. type.—Con.	Seg.....	A^2a^4 b^6.....	1	0:1	2.57:1
			F_1.....	A $a^5B^4b^2$.....	2	3:1	3:1
			F_1.....	A $a^5B^3b^3$.....	12	2.97:1	2.88:1
			F_1.....	A $a^5B^2b^4$.....	22	2.57:1	2.57:1
			F_1.....	A a^5B b^5.....	12	1.28:1	2.07:1
			Seg.....	A a^5 b^6.....	2	0:1	1.50:1
			Seg.....	$a^6B^4b^2$.....	1	0:1	1:1
			Seg.....	$a^6B^3b^3$.....	6	0:1	1.02:1
			Seg.....	$a^6B^2b^4$.....	11	0:1	1:1.08
			Seg.....	a^6B b^5.....	6	0:1	1:1.22
			Seg.....	a^6b^6.....	1	0:1	1:1.50
2.69:1 (105:39)	A $a^3B^2b^2$	2 factor; tetrasomic; rec. of A or B for expression of seg. type.	F_1.....	$A^2a^2B^{3*}$.....	9	35:1	11:1
			F_1.....	$A^2a^2B^2b^2$.....	18	17.2:1	8.19:1
			F_1.....	A^2a^2B b^3.....	8	2.69:1	5.26:1
			Seg.....	A^2a^2 b^4.....	1	0:1	3.35:1
			F_1.....	A a^3B^{3*}.....	18	3:1	3:1
			F_1.....	A $a^3B^2b^2$.....	36	2.69:1	2.69:1
			F_1.....	A a^3B b^3.....	16	1.28:1	2.20:1
			Seg.....	A a^3 b^4.....	2	0:1	1.67:1
			Seg.....	a^4B^{3*}.....	9	0:1	1:1
			Seg.....	$a^4B^2b^2$.....	18	0:1	1:1.06
			Seg.....	a^4B b^3.....	8	0:1	1:1.18
			Seg.....	a^4 b^4.....	1	0:1	1:1.40
2.69:1 (105:39)	A^2a^2B b	1–1 factor; tetradisomic; rec. of A or B for expression of seg. type.	F_1.....	A^{3*} B^2.....	9	1:0	1:0
			F_1.....	A^{3*} B b.....	18	3:1	3:1
			Seg.....	A^{3*} b^2.....	9	0:1	1:1

			F_1				35:1
			F_1	$A^2a^1B^1b^1$	18	35:1	35:1
			F_1	A^2a^1B b	36	2.69:1	2.69:1
			Seg.	A^2a^2 b^2	18	0:1	1:1.06
			F_1	A $a^1B^1b^1$	8	3:1	11:1
			F_1	A a^1B b	16	1.28:1	2.20:1
			F_1	A a^1 b^2	8	0:1	1:1.18
			Seg.	a^1B^2	1	0:1	5:1
			Seg.	a^1B b	2	0:1	1.67:1
			Seg.	a^1 b^2	1	0:1	1:1.40
2.70:1 (73:27)	A $a^1B^1b^1$	2 factor; hexasomic; dom. of A or B and rec. of the other locus for expression of seg. type.	F_1	$A^2a^1B^1b^2$	1	24:1	9:1
			F_1	$A^2a^1B^1b^1$	6	23:1	8.26:1
			F_1	$A^2a^1B^2b^1$	11	12:1	6.57:1
			F_1	A^2a^1B b^1	6	2.70:1	4.55:1
			Seg.	A^2a^1 b^2	1	1:24	2.85:1
			F_1	A $a^1B^1b^2$	2	3:1	3:1
			F_1	A $a^1B^2b^1$	12	2.98:1	2.92:1
			F_1	A $a^1B^1b^1$	22	2.70:1	2.70:1
			F_1	A a^1B b^1	12	1.67:1	2.83:1
			Seg.	A a^1 b^2	2	1:3	1.86:1
			Seg.	a^1B b^2	1	0:1	1:1
			Seg.	$a^1B^1b^1$	6	1:399	1:1
			Seg.	$a^1B^2b^1$	11	1:24	1:1
			Seg.	a^1B b^1	6	1:3	1:1
			F_1	a^1 b^2	1	1:0	1:1
2.79:1 (106:38)	A $a^1B^1b^1$	2 factor; tetrasomic; dom. of A or B and rec. of the other locus for expression of seg. type.	F_1	$A^2a^1B^1b^1$	9	35:1	11:1
			F_1	$A^2a^1B^1b^2$	18	17.5:1	8.39:1
			F_1	A^2a^1B b^1	8	2.79:1	5.54:1
			Seg.	A^2a^2 b^1	1	1:35	3.50:1
			F_1	A $a^1B^1b^1$	18	3:1	3:1
			F_1	A $a^1B^1b^2$	36	2.79:1	2.79:1
			F_1	A a^1B b^1	16	1.67:1	2.33:1
			Seg.	A a^1 b^1	2	1:3	2:1
			Seg.	$a^1B^1b^1$	9	0:1	1:1
			Seg.	$a^1B^1b^2$	18	1:35	1:1
			Seg.	a^1B b^1	8	1:3	1:1
			F_1	a^1 b^1	1	1:0	1:1

See footnotes at end of table, p. 41.

226-441 O-67 - 3

TABLE 2.—*Theoretical test-cross ratios for various possible genetic hypotheses of F_2 segregations in a hexaploid assuming no double reduction*—Continued

Observed F_2 ratio [1]	Hypothetical F_1 genotype	Genetic hypothesis [2 3]	F_2 phenotype [3]	F_2 genotype [2 4 5]	F_2 frequency	Test-cross ratios [4]	
						Self	Back-cross to F_1
2.79:1 (106:38)	A^2a^2B b	1-1 factor: tetradisomic: dom. of A or B and rec. of the other locus for expression of seg. type.	F_1	A^{3*} B^2	9	1:0	1:0
			F_1	$A^2a^2B^2$	18	35:1	35:1
			F_1	A a^3B^2	8	3:1	11:1
			F_1	A^{3*} B 2_*	18	3:1	3:1
			F_1	A^2a^2B b_*	36	2.79:1	2.79:1
			F_1	A a^3B b_*	16	1.67:1	2.43:1
			Seg.	A^{3*} b^2	9	0:1	1:1
			Seg.	A^2a^2 b^2	18	1:35	1:1
			Seg.	A a^3 b^2	8	1:3	1:1
			Seg.	a^3B^{3*}	1	0:1	5:1
			Seg.	a^3B b_*	2	1:3	2:1
			F_1	a^4 b^2	1	1:0	1:1
2.97:1 (1197:403)	A $a^5B^5b^5$	2 factor: hexasomic: rec. of A or B for expression of seg. type.	F_1	$A^2a^5B^{5*}$	118	24:1	9:1
			F_1	$A^2a^5B^5b^5$	164	23:1	8.78:1
			F_1	$A^2a^5B^2b^5$	99	11.7:1	8.17:1
			F_1	A^2a^5B b^5	18	2.57:1	7.16:1
			Seg.	A^2a^5 b^6	1	0:1	5.90:1
			F_1	A a^5B^{5*}	236	3:1	3:1
			F_1	A $a^5B^5b^5$	328	2.97:1	2.97:1
			F_1	A $a^5B^2b^5$	198	2.57:1	2.88:1
			F_1	A a^5B b^5	36	1.28:1	2.72:1
			Seg.	A a^5 b^6	2	0:1	2.48:1
			Seg.	a^6B^{5*}	118	0:1	1:1
			Seg.	$a^6B^5b^5$	164	0:1	1:1.01
			Seg.	$a^6B^2b^5$	99	0:1	1:1.02

			Seg.	$a^6B\ b^5$	18	0:1	1:1.05
			Seg.	$a^6\ b^6$	1	0:1	1:1.10
2.98:1 (1198:402)	A $a^5B^3b^3$	2 factor; hexasomic; dom. of A or B and rec. of the other locus for expression of seg. type.	F_1	$A^2a^4B^4*$	118	24:1	9:1
			F_1	$A^2a^4B^3b^3$	164	23:1	8.80:1
			F_1	$A^2a^3B^2b^4$	99	12:1	8.26:1
			F_1	$A^2a^3B\ b^5$	18	2.70:1	7.33:1
			F_1	$A\ a^5B^4*$	236	3:1	3:1
			F_1	$A\ a^5B^3b^3$	328	2.98:1	2.98:1
			F_1	$A\ a^5B^2b^4$	198	2.70:1	2.92:1
			F_1	$A\ a^5B\ b^5$	36	1.67:1	2.81:1
			Seg.	$A^2a^4\ \ b^6$	1*	1:24	6.14:1
			Seg.	$A\ a^5\ \ b^6$	2	1:3	2.64:1
			Seg.	a^6B^4*	118	0:1	1:1
			Seg.	$a^6B^3b^3$	164	1:399	1:1
			Seg.	$a^6B^2b^4$	99	1:24	1:1
			seg.	$a^6B\ b^5$	18	1:3	1:1
			F_1	$a^6\ \ b^6$	1	1:0	1:1
3:1	A a	1 factor; disomic	F_1	A^2	1	1:0	1:0
			F_1	$A\ a$	2	3:1	3:1
			Seg.	a^2	1	0:1	1:1
3:1	A a^3	1 factor; tetrasomic	F_1	A^2a^2	1	35:1	11:1
			F_1	$A\ a^3$	2	3:1	3:1
			Seg.	a^4	1	0:1	1:1
3:1	A a^5	1 factor; hexasomic	F_1	A^2a^4	1	24:1	9:1
			F_1	$A\ a^5$	2	3:1	3:1
			Seg.	a^6	1	0:1	1:1
3:1 (27:9)	A^2a^2	1 factor; tetrasomic; duplex expression for F_1 type.	F_1	A^2	1	1:0	1:0
			F_1	A^2a	8	1:0	11:1
			F_1	A^2a^2	18	3:1	3:1
			Seg.	$A\ a^2$	8	1:3	1:1
			Seg.	a^4	1	0:1	1:5

See footnotes at end of table, p. 41.

TABLE 2.—*Theoretical test-cross ratios for various possible genetic hypotheses of F_2 segregations in a hexaploid assuming no double reduction*—Continued

Observed F_2 ratio [1]	Hypothetical F_1 genotype	Genetic hypothesis [2 3]	F_2 phenotype [3]	F_2 genotype [2 4 5]	F_2 frequency	Test-cross ratios [1]	
						Self	Backcross to F_1
3:1	A^3a	1 factor: tetrasomic: triplex expression for F_1 type.	F_1	A^4	1	1:0	1:0
			F_1	A^3a	2	3:1	3:1
			Seg.	A^2a^2	1	1:3	1:1
3:1	A^5a	1 factor: hexasomic: pentaplex expression for F_1 type.	F_1	A^6	1	1:0	1:0
			F_1	A^5a	2	3:1	3:1
			Seg.	A^4a^2	1	1:2.57	1:1
3:1 (12:4)	A^3a B b	1–1 factor: tetradisomic: rec. of A or B for expression of seg. type.	F_1	A^{3*} B^2	3	1:0	1:0
			F_1	A^{3*} B b	6	3:1	3:1
			F_1	$A^2a^2B^2$	1	35:1	1:0
			F_1	A^2a^2B b	2	2.69:1	3:1
			Seg.	A^{2*} b^2	4	0:1	1:1
3:1 (12:4)	A^3a B b	1–1 factor: tetradisomic: dom. of A and rec. of B for expression of seg. type.	F_1	A^{2*} B^2	4	1:0	1:0
			F_1	A^{3*} B b	6	3:1	3:1
			F_1	A^2a^2B b	2	3.11:1	3:1
			Seg.	A^{3*} b^2	3	0:1	1:1
			Seg.	A^2a^2 b^2	1	1:35	1:1
3:1 (12:4)	A^3a B b	1–1 factor: tetradisomic: dom. of A or B and rec. of the other locus for expression of seg. type.	F_1	A^{3*} B^2	3	1:0	1:0
			F_1	$A^2a^2B^2$	1	35:1	1:0
			F_1	A^{3*} B b	6	3:1	3:1
			F_1	A^2a^2B b	2	2.79:1	3:1
			Seg.	A^{3*} b^2	3	0:1	1:1
			Seg.	A^2a^2 b^2	1	1:35	1:1

3:1 (12:4)	A a^3B^3b	2 factor; tetrasomic; dom. of A or B and rec. of the other locus for expression of seg. type.	F_1	$A^2a^2B^{3*}$	3	35:1	11:1
			F_1	$A^2a^2B^2b^2$	1	17.5:1	11:1
			F_1	A a^3B^{3*}	6	3:1	3:1
			F_1	$A^2a^2B^2b^2$	2	2.79:1	3:1
			Seg.	a^3B^{3*}	3	0:1	1:1
			Seg.	$a^3B^2b^2$	1	1:35	1:1
3:1 (12:4)	A a^3B^3b	2 factor; tetrasomic; rec. of A or B for expression of seg. type.	F_1	$A^2a^2B^{3*}$	3	35:1	11:1
			F_1	$A^2a^2B^2b^2$	1	17.2:1	11:1
			F_1	A a^3B^{3*}	6	3:1	3:1
			F_1	A $a^3B^2b^2$	2	2.69:1	3:1
			Seg.	a^3B^{2*}	4	0:1	1:1
3:1 (12:4)	A a^3B^3b	2 factor; tetrasomic; dom. of B and rec. of A for expression of seg. type.	F_1	$A^2a^2B^{3*}$	3	35:1	11:1
			F_1	$A^2a^2B^2b^2$	1	36:1	11:1
			F_1	A a^3B^{3*}	6	3:1	3:1
			F_1	A $a^3B^2b^2$	2	3.11:1	3:1
			Seg.	a^3B^{3*}	3	0:1	1:1
			Seg.	$a^3B^2b^2$	1	1:35	1:1
3:1 (75:25)	A $a^5B^4b^2$	2 factor; hexasomic; rec. of A or B for expression of seg. type.	F_1	$A^2a^4B^{4*}$	18	24:1	9:1
			F_1	$A^2a^4B^3b^3$	3	22:1	9:1
			F_1	$A^2a^4B^2b^4$	1	11.7:1	9:1
			F_1	A a^5B^{4*}	36	3:1	3:1
			F_1	A $a^5B^3b^3$	12	2.97:1	3:1
			F_1	A $a^5B^2b^4$	2	2.57:1	3:1
			Seg.	a^5B^{2*}	25	0:1	1:1
3:1 (75:25)	A $a^5B^4b^2$	2 factor; hexasomic; dom. of B and rec. of A for expression of seg. type.	F_1	$A^2a^4B^{4*}$	18	24:1	9:1
			F_1	$A^2a^4B^3b^3$	6	24:1	9:1
			F_1	$A^2a^4B^2b^4$	1	25:1	9:1
			F_1	A a^5B^{4*}	36	3:1	3:1
			F_1	A $a^5B^3b^3$	12	3.01:1	3:1
			F_1	A $a^5B^2b^4$	2	3.17:1	3:1
			Seg.	a^6B^{4*}	18	0:1	1:1
			Seg.	$a^6B^3b^3$	6	1:399	1:1
			Seg.	$a^6B^2b^4$	1	1:24	1:1

See footnotes at end of table, p. 41.

TABLE 2.—*Theoretical test-cross ratios for various possible genetic hypotheses of F_2 segregations in a hexaploid assuming no double reduction*—Continued

Observed F_2 ratio [1]	Hypothetical F_1 genotype	Genetic hypothesis [2 3]	F_2 phenotype [3]	F_2 genotype [2 4 5]	F_2 frequency	Test-cross ratios [1]	
						Self	Back-cross to F_1
3:1 (75:25)	A $a^5B^4b^2$	2 factor; hexasomic; dom. of A or B and rec. of the other locus for expression of seg. type.	F_1	$A^2a^4B^{4*}$	18	24:1	9:1
			F_1	$A^2a^4B^3b^3$	6	23:1	9:1
			F_1	$A^2a^4B^2b^4$	1	12:1	9:1
			F_1	A a^5B^{4*}	36	3:1	3:1
			F_1	A $a^5B^3b^3$	12	2.98:1	3:1
			F_1	A $a^5B^2b^4$	2	2.70:1	3:1
			Seg.	a^6B^{4*}	18	0:1	1:1
			Seg.	$a^6B^3b^3$	6	1:399	1:1
			Seg.	$a^6B^2b^4$	1	1:24	1:1
3:1 (12:4)	A a^5B^5b	2 factor; hexasomic; rec. of A or B for expression of seg. type.	F_1	$A^2a^4B^{4*}$	4	24:1	9:1
			F_1	A a^5B^{4*}	8	3:1	3:1
			Seg.	a^6B^{4*}	4	0:1	1:1
3:1 (12:4)	A a^5B^5b	2 factor; hexasomic; dom. of B and rec. of A for expression of seg. type.	F_1	$A^2a^4B^{4*}$	4	24:1	9:1
			F_1	A a^5B^{4*}	8	3:1	3:1
			Seg.	a^6B^{4*}	4	0:1	1:1
3:1 (12:4)	A a^5B^5b	2 factor; hexasomic; dom. of A or B and rec. of the other locus for expression of seg. type.	F_1	$A^2a^4B^{4*}$	4	24:1	9:1
			F_1	A a^5B^{4*}	8	3:1	3:1
			Seg.	a^6B^{4*}	4	0:1	1:1
3.01:1 (1201:399)	A $a^5B^3b^3$	2 factor; hexasomic; dom. of B and rec. of A for expression of seg. type.	F_1	$A^2a^4B^{4*}$	118	24:1	9:1
			F_1	$A^2a^4B^3b^3$	164	24:1	9.02:1
			F_1	$A^2a^4B^2b^4$	99	25:1	9.10:1

			F_1	$A^2a^4B\ b^5$	18	32:1	9.25:1
			F_1	$A^2a^4\ \ b^6$	1	1:0	9.52:1
			F_1	$A\ a^5B^{4*}$	236	3:1	3:1
			F_1	$A\ a^5B^3b^3$	328	3.01:1	3.01:1
			F_1	$A\ a^5B^2b^4$	198	3.17:1	3.04:1
			F_1	$A\ a^5B\ b^5$	36	4.33:1	3.10:1
			F_1	$A\ a^5\ \ b^6$	2	1:0	3.21:1
			Seg.	a^6B^{4*}	118	0:1	1:1
			Seg.	$a^6B^3b^3$	164	1:399	1:1
			Seg.	$a^6B^2b^4$	99	1:24	1.02:1
			Seg.	$a^6B\ b^5$	18	1:3	1.05:1
			Seg.	a^6b^6	1	1:0	1.1:1
3.11:1 (109:35)	$A\ a^3B^2b^2$	2 factor; tetrasomic; dom. of B and rec. of A for expression of seg. type.	F_1	$A^2a^2B^{3*}$	9	35:1	11:1
			F_1	$A^2a^2B^2b^2$	18	36:1	11.3:1
			F_1	$A^2a^2B\ b^3$	8	47:1	12.1:1
			F_1	$A^2a^2\ \ b^4$	1	1:0	13.4:1
			F_1	$A\ a^3B^{3*}$	18	3:1	3:1
			F_1	$A\ a^3B^2b^2$	36	3.11:1	3.11:1
			F_1	$A\ a^3B\ b^3$	16	4.33:1	3.36:1
			F_1	$A\ a^3\ \ b^4$	2	1:0	3.80:1
			Seg.	a^4B^{3*}	9	0:1	1:1
			Seg.	$a^4B^2b^2$	18	1:35	1.05:1
			Seg.	$a^4B\ b^3$	8	1:3	1.18:1
			F_1	a^4b^4	1	1:0	1.40:1
3.11:1 (109:35)	$A^2a^2B\ b$	1–1 factor; tetradisomic; dom. of A and rec. of B for expression of seg. type.	F_1	$*\ \ B^3$	36	1:0	1:0
			F_1	$A^{3*}\ B\ b$	18	3:1	3:1
			F_1	$A^2a^2B\ b$	36	3.11:1	3.11:1
			F_1	$A\ a^3B\ b$	16	4.33:1	3.36:1
			F_1	$a^4B\ b$	2	1:0	3.80:1
			Seg.	$A^{3*}\ \ b^2$	9	0:1	1:1
			Seg.	$A^2a^2\ \ b^2$	18	1:35	1.05:1
			Seg.	$A\ a^3\ \ b^2$	8	1:3	1.18:1
			F_1	$a^4\ \ b^2$	1	1:0	1.40:1

See footnotes at end of table, p. 41.

TABLE 2.—*Theoretical test-cross ratios for various possible genetic hypotheses of F_2 segregations in a hexaploid assuming no double reduction*—Continued

Observed F_2 ratio [1]	Hypothetical F_1 genotype	Genetic hypothesis [2 3]	F_2 phenotype [3]	F_2 genotype [2 4 5]	F_2 frequency	Test-cross ratios [1]	
						Self	Back-cross to F_1
3.17:1 (76:24)	A $a^5B^2b^4$	2 factor: hexasomic: dom. of B and rec. of A for expression of seg. type.	F_1	$A^2a^4B^4b^2$	1	24:1	9:1
			F_1	$A^2a^4B^3b^3$	6	24:1	9.1:1
			F_1	$A^2a^4B^2b^4$	11	25:1	9.41:1
			F_1	$A^2a^4B\ b^5$	6	32:1	10.1:1
			F_1	$A^2a^4\ \ b^6$	1	1:0	11.5:1
			F_1	$A\ a^5B^4b^2$	2	3:1	3:1
			F_1	$A\ a^5B^3b^3$	12	3.01:1	3.04:1
			F_1	$A\ a^5B^2b^4$	22	3.17:1	3.17:1
			F_1	$A\ a^5B\ b^5$	12	4.33:1	3.44:1
			F_1	$A\ a^5\ \ b^6$	2	1:0	4:1
			Seg.	$a^6B^4b^2$	1	0:1	1:1
			Seg.	$a^6B^3b^3$	6	1:399	1.02:1
			Seg.	$a^6B^2b^4$	11	1:24	1.08:1
			Seg.	$a^6B\ b^5$	6	1:3	1.22:1
			F_1	$a^6\ \ b^6$	1	1:0	1.50:1
3.26:1 (49:15)	A a B b C c	3 factor: disomic: dom. of A or B and rec. of C for expression of seg. type.	F_1	$*\ \ *\ \ C^2$	16	1:0	1:0
			F_1	$A^2\ \ *\ \ C\ c$	8	3:1	3:1
			F_1	$*\ \ B^2\ \ C\ c$	6	3:1	3:1
			F_1	A a B b C c	8	3.26:1	3.26:1
			F_1	A a b^2C c	4	4.33:1	3.57:1
			F_1	a^2B b C c	4	4.33:1	3.57:1
			F_1	$a^2\ \ b^2C$ c	2	1:0	4.33:1
			F_1	$a^2\ \ b^2\ \ c^2$	1	1:0	1.67:1
			Seg.	$A^2\ \ *\ \ c^2$	4	0:1	1:1
			Seg.	$*\ \ B^2\ \ c^2$	3	0:1	1:1
			Seg.	A a B b c^2	4	1:15	1.13:1

			Seg.	A a b^2 c^2	2	1:3	1.28:1
			Seg.	a^2B b c^2	2	1:3	1.28:1
4.33:1 (13:3)	A a B b	2 factor; disomic; dom. of A and rec. of B for expression of seg. type.	F_1	* B^2	4	1:0	1:0
			F_1	A^2 B b	2	3:1	3:1
			Seg.	A^2 b^2	1	0:1	1:1
			F_1	A a B b	4	4.33:1	4.33:1
			Seg.	A a b^2	2	1:3	1.67:1
			F_1	a^2B b	2	1:0	7:1
			F_1	a^2 b^2	1	1:0	3:1
4.33:1 (13:3)	A a^2B b^2	2 factor; tetrasomic; dom. of A and rec. of B for expression of seg. type.	F_1	$A^2a^2B^2b^2$	1	36:1	12.1:1
			F_1	A^2a^2B b^2	2	3.11:1	3.36:1
			Seg.	A^2a^2 b^2	1	1:35	1.18:1
			F_1	A $a^2B^2b^2$	2	47:1	15:1
			F_1	A a^2B b^2	4	4.33:1	4.33:1
			Seg.	A a^2 b^2	2	1:3	1.67:1
			F_1	$a^2B^2b^2$	1	1:0	23:1
			F_1	a^2B b^2	2	1:0	?:1
			F_1	a^2 b^2	1	1:0	3:1
4.33:1 (13:3)	A a^2B b	1-1 factor; tetradisomic; dom. of A and rec. of B for expression of seg. type.	F_1	* B^2	4	1:0	1:0
			F_1	A^2a^2B b	2	3.11:1	3.36:1
			F_1	A a^2B b	4	4.33:1	4.33:1
			F_1	a^2B b	2	1:0	7:1
			Seg.	A^2a^2 b^2	1	1:35	1.18:1
			Seg.	A a^2 b^2	2	1:3	1.67:1
			F_1	a^2 b^2	1	1:0	3:1
4.33:1 (13:3)	A a^2B b	1-1 factor; tetradisomic; dom. of B and rec. of A for expssion of seg. type.	F_1	$A^2a^2B^2$	1	35:1	11:1
			F_1	A^2a^2B b	2	47:1	15:1
			F_1	A^2a^2 b^2	1	1:0	23:1
			F_1	A a^2B^2	2	3:1	3:1
			F_1	A a^2B b	4	4.33:1	4.33:1
			F_1	A a^2 b^2	2	1:0	7:1
			Seg.	a^2B^2	1	0:1	1:1
			Seg.	a^2B b	2	1:3	1.67:1
			F_1	a^2 b^2	1	1:0	3:1

See footnotes at end of table, p. 41.

TABLE 2.—*Theoretical test-cross ratios for various possible genetic hypotheses of F_2 segregations in a hexaploid assuming no double reduction*—Continued

Observed F_2 ratio [1]	Hypothetical F_1 genotype	Genetic hypothesis [2 3]	F_2 phenotype [3]	F_2 genotype [2 4 5]	F_2 frequency	Test-cross ratios [1]	
						Self	Backcross to F_1
4.33:1 (13:3)	A a^5B b^5	2 factor: hexasomic: dom. of A and rec. of B for expression of seg. type.	F_1	$A^2a^4B^2b^4$	1	25:1	10.1:1
			F_1	A^2a^4B b^5	2	3.17:1	3.44:1
			Seg.	A^2a^4 b^6	1	1:24	1.22:1
			F_1	A $a^5B^2b^4$	2	32:1	12.3:1
			F_1	A a^5B b^5	4	4.33:1	4.33:1
			Seg.	A a^5 b^6	2	1:3	1.67:1
			F_1	$a^6B^2b^4$	1	1:0	19:1
			F_1	a^6B b^5	2	1:0	7:1
			F_1	a^6 b^6	1	1:0	3:1
5.4:1 (54:10)	A a B b C c	3 factor: disomic: rec. of any 2 loci for expression of seg. type.	F_1	Homo. dom. at 2 loci	10	1:0	1:0
			F_1	Homo. dom. at 1 locus, het. at 2 loci	12	15:1	15:1
			F_1	Homo. dom. at 1 locus, homo. rec. at 1 locus, and het. at 1 locus.	12	3:1	7:1
			F_1	A a B b C c	8	5.4:1	5.4:1
			F_1	Het. at 2 loci, homo. rec. at 1 locus	12	1.28:1	3:1
			Seg.	Homo. dom. at 1 locus, homo. rec. at 2 loci.	3	0:1	3:1
			Seg.	Het. at 1 locus, homo. rec. at 2 loci	6	0:1	1.67:1
			Seg.	a^2 b^2 c^2	1	0:1	1:1
6.11:1 (55:9)	A a B b C c	3 factor: disomic: dom. of B and C and rec. of A for expression of seg. type.	F_1	A^2 * *	16	1:0	1:0
			F_1	A a B^2 C^2	2	3:1	3:1
			F_1	A a B^2 C c	4	4.33:1	4.33:1
			F_1	A a B b C^2	4	4.33:1	4.33:1
			F_1	A a B b C c	8	6.11:1	6.11:1
			F_1	A a B b c^2	4	1:0	9.67:1
			F_1	A a b^2C c	4	1:0	9.67:1
			F_1	A a B^2 c^2	2	1:0	7:1

			F_1	A a b^2C^2	2	1:0	7:1
			F_1	A a b^2 c^2	2	1:0	15:1
			F_1	a^2B^2 c^2	1	1:0	3:1
			F_1	a^2 b^2C^2	1	1:0	3:1
			F_1	a^2B b c^2	2	1:0	4.33:1
			F_1	a^2 b^2C c	2	1:0	4.33:1
			F_1	a^2 b^2 c^2	1	1:0	7:1
			Seg.	a^2B^2 C^2	1	0:1	1:1
			Seg.	a^2B^2 C c	2	1:3	1.67:1
			Seg.	a^2B b C^2	2	1:3	1.67:1
			Seg.	a^2B b C c	4	1:1.28	2.55:1
6.11:1 (59:9)	A a B b C c	3 factor: disomic: dom. of 1 locus and rec. of 2 loci for expression of seg. type.	F_1	Homo. dom. at 2 loci	10	1:0	1:0
			F_1	Homo. dom. at 1 locus, het. at 2 loci	12	15:1	15:1
			F_1	Homo. dom. at 1 locus, het. at 1 locus, and homo. rec. at 1 locus	12	3:1	7:1
			F_1	A a B b C c	8	6.11:1	6.11:1
			F_1	Het. at 2 loci, homo. rec. at 1 locus	12	1.66:1	3.57:1
			Seg.	Homo. dom. at 1 locus, homo. rec. at 2 loci.	3	0:1	3:1
			Seg.	Het. at 1 locus, homo. rec. at 2 loci	6	1:3	2.20:1
			F_1	a^2 b^2 c^2	1	1:0	1.67:1
11.75:1 (576:49)	$A^2a^4B^2b^4$	2 factor: hexasomic: rec. of A or B for expression of seg. type.	F_1	$A^4a^2B^4b^2$	1	1:0	1:0
			F_1	$A^4a^2B^3b^3$	6	399:1	99:1
			F_1	$A^4a^2B^2b^4$	11	24:1	24:1
			F_1	A^4a^2B b^5	6	3:1	9:1
			Seg.	A^4a^2 b^6	1	0:1	4:1
			F_1	$A^3a^3B^4b^2$	6	399:1	99:1
			F_1	$A^3a^3B^3b^3$	36	199:1	49:1
			F_1	$A^3a^3B^2b^4$	66	22:1	19.2:1
			F_1	A^3a^3B b^5	36	2.97:1	8.17:1
			Seg.	A^3a^3 b^6	6	0:1	3.81:1
			F_1	$A^2a^4B^4b^2$	11	24:1	24:1
			F_1	$A^2a^4B^3b^3$	66	22:1	19.2:1
			F_1	$A^2a^4B^2b^4$	121	11.7:1	11.7:1
			F_1	A^2a^4B b^5	66	2.57:1	6.35:1

See footnotes at end of table, p. 41.

TABLE 2.—*Theoretical test-cross ratios for various possible genetic hypotheses of F_2 segregations in a hexaploid assuming no double reduction*—Continued

Observed F_2 ratio [1]	Hypothetical F_1 genotype	Genetic hypothesis [2 3]	F_2 phenotype [3]	F_2 genotype [2 4 5]	F_2 frequency	Test-cross ratios [1]	
						Self	Backcross to F_1
11.75:1 (576:49) —Con.	$A^2a^4B^2b^4$ —Con.	2 factor; hexasomic; rec. of A or B for expression of seg. type.—Con.	Seg.....	A^2a^4 b^6.....	11	0:1	3.31:1
			F_1.....	A $a^5B^4b^2$.....	6	3:1	9:1
			F_1.....	A $a^5B^3b^3$.....	36	2.97:1	8.17:1
			F_1.....	A $a^5B^2b^4$.....	66	2.57:1	6.35:1
			F_1.....	A a^5B b^5.....	36	1.28:1	4.26:1
			Seg.....	A a^5 b^6.....	6	0:1	2.57:1
			Seg.....	$a^6B^4b^2$.....	1	0:1	4:1
			Seg.....	$a^6B^3b^3$.....	6	0:1	3.81:1
			Seg.....	$a^6B^2b^4$.....	11	0:1	3.31:1
			Seg.....	a^6B b^5.....	6	0:1	2.57:1
			Seg.....	a^6 b^6.....	1	0:1	1.78:1
12.02:1 (577:48)	$A^2a^4B^2b^4$	2 factor; hexasomic; dom. of A or B and rec. of the other for expression of seg. type.	F_1.....	$A^4a^2B^4b^2$.....	1	1:0	1:0
			F_1.....	$A^2a^2B^3b^3$.....	6	399:1	99:1
			F_1.....	$A^4a^2B^2b^4$.....	11	24:1	24:1
			F_1.....	$A^4a^2B^1b^5$.....	6	3:1	9:1
			Seg.....	A^4a^2 b^6.....	1	0:1	4:1
			F_1.....	$A^3a^3B^4b^2$.....	6	399:1	99:1
			F_1.....	$A^3a^3B^3b^3$.....	36	199:1	49:1
			F_1.....	$A^3a^3B^2b^4$.....	66	22:1	19.3:1
			F_1.....	A^3a^3B b^5.....	36	2.98:1	8.26:1
			Seg.....	A^3a^3 b^6.....	6	1:399	3.85:1
			F_1.....	$A^2a^4B^4b^2$.....	11	24:1	24:1
			F_1.....	$A^2a^4B^3b^3$.....	66	22:1	19.3:1
			F_1.....	$A^2a^4B^2b^4$.....	121	12:1	12:1
			F_1.....	A^2a^4B b^5.....	66	2.70:1	6.57:1
			Seg.....	A^2a^4 b^6.....	11	1:24	3.46:1

			F_1	A $a^5B^4b^2$	6	3:1	9:1
			F_1	A $a^5B^3b^3$	36	2.98:1	8.29:1
			F_1	A $a^5B^2b^4$	66	2.70:1	6.57:1
			F_1	A $a^5B\ b^5$	36	1.67:1	4.55:1
			Seg.	A $a^5\ \ b^6$	6	1:3	2.85:1
			Seg.	$a^6B^4b^2$	1	0:1	4:1
			Seg.	$a^6B^3b^3$	6	1:399	3.85:1
			Seg.	$a^6B^2b^4$	11	1:24	3.46:1
			Seg.	$a^6B\ b^5$	6	1:3	2.85:1
			F_1	$a^6\ \ b^6$	1	1:0	2.12:1
15:1	A a B b	2 factor: disomic: rec. of A and B for expression of seg. type.	F_1	$A^2\ \ *$	4	1:0	1:0
			F_1	$*\ \ B^2$	3	1:0	1:0
			F_1	A a B b	4	15:1	15:1
			F_1	A a $\ \ b^2$	2	3:1	7:1
			F_1	$a^2B\ b$	2	3:1	7:1
			Seg.	$a^2\ \ b^2$	1	0:1	3:1
15:1	A $a^3B\ b^3$	2 factor: tetrasomic: rec. of A and B for expression of seg. type.	F_1	$A^2a^2B^2b^2$	1	1295:1	143:1
			F_1	$A^2a^2B\ b^3$	2	143:1	47:1
			F_1	$A^2a^2\ \ b^4$	1	35:1	23:1
			F_1	A $a^3B^2b^2$	2	143:1	47:1
			F_1	A $a^3B\ b^3$	4	15:1	15:1
			F_1	A $a^3\ \ b^4$	2	3:1	7:1
			F_1	$a^4B^2b^2$	1	35:1	23:1
			F_1	$a^4B\ b^3$	2	3:1	7:1
			Seg.	$a^4\ \ b^4$	1	0:1	3:1
15:1	A $a^3B\ b$	1–1 factor: tetradisomic: rec. of A and B for expression of seg. type.	F_1	$*\ a^2B^2$	4	1:0	1:0
			F_1	$A^2a^2B\ b$	2	143:1	47:1
			F_1	$A^2a^2\ \ b^2$	1	35:1	23:1
			F_1	A $a^3B\ b$	4	15:1	15:1
			F_1	A $a^3\ \ b^2$	2	3:1	7:1
			F_1	$a^4B\ b$	2	3:1	7:1
			Seg.	$a^4\ \ b^2$	1	0:1	3:1

See footnotes at end of table, p. 41.

TABLE 2.—*Theoretical test-cross ratios for various possible genetic hypotheses of F_2 segregations in a hexaploid assuming no double reduction*—Continued

Observed F_2 ratio [1]	Hypothetical F_1 genotype	Genetic hypothesis [2,3]	F_2 phenotype [3]	F_2 genotype [2,4,5]	F_2 frequency	Test-cross ratios [1]	
						Self	Back-cross to F_1
15:1	A a^5B b^5	2 factor; hexasomic; rev. of A and B for expression of seg. type.	F_1	$A^2a^1B^2b^1$	1	624:1	99:1
			F_1	A^2a^1B b^5	2	99:1	39:1
			F_1	A^2a^4 b^6	1	24:1	19:1
			F_1	A $a^5B^2b^1$	2	99:1	39:1
			F_1	A a^3B b^5	4	15:1	15:1
			F_1	A a^5 b^6	2	3:1	7:1
			F_1	$a^6B^2b^1$	1	24:1	19:1
			F_1	a^6B b^5	2	3:1	7:1
			Seg.	a^6 b^6	1	0:1	3:1
17.25:1 (1225:71)	$A^2a^2B^2b^2$	2 factor; tetrasomic; rev. of A or B for expression of seg. type.	F_1	A^{3*} B^{3*}	81	1:0	1:0
			F_1	A^{3*} B^2b^2	162	35:1	35:1
			F_1	$A^2a^2B^{3*}$	162	35:1	35:1
			F_1	A^{3*} B b^3	72	3:1	11:1
			F_1	A a^2B^{3*}	72	3:1	11:1
			F_1	$A^2a^2B^2b^2$	324	17.2:1	17.2:1
			F_1	A^2a^2B b^3	144	2.69:1	8.19:1
			F_1	A $a^2B^2b^2$	144	2.69:1	8.19:1
			F_1	A a^2B b^3	64	1.28:1	5.26:1
			Seg.	A^3 * b^3	9	0:1	5:1
			Seg.	a^3B^{3*}	9	0:1	5:1
			Seg.	A^2a^2 b^4	18	0:1	4.27:1
			Seg.	$a^2B^2b^2$	18	0:1	4.27:1
			Seg.	A a^3 b^4	8	0:1	3.23:1
			Seg.	a^1B b^5	8	0:1	3.23:1
			Seg.	a^1 b^4	1	0:1	2.27:1

17.5:1 (1226:70)	$A^2a^2B^2b^2$	2 factor: tetrasomic: dom. of A or B and rec. of other locus for expression of seg. type.	F_1	A^{3*} B^{3*}	81	1:0	1:0
			F_1	A^{3*} B^2b^2	162	35:1	35:1
			F_1	$A^2a^2B^{3*}$	162	35:1	35:1
			F_1	A^{3*} B b^2	72	3:1	11:1
			F_1	A a^2B^{3*}	72	3:1	11:1
			F_1	$A^2a^2B^2b^2$	324	17.5:1	17.5:1
			F_1	A^2a^2B b^2	141	2.79:1	8.39:1
			F_1	A $a^2B^2b^2$	141	2.79:1	8.39:1
			F_1	A a^2B b^2	61	1.67:1	5.54:1
			Seg.	A^{3*} b^2	9	0:1	5:1
			Seg.	a^2B^{3*}	9	0:1	5:1
			Seg.	A^2a^2 b^2	18	1:35	1.4:1
			Seg.	$a^2B^2b^2$	18	1:35	1.4:1
			Seg.	A a^2 b^2	8	1:3	3.5:1
			Seg.	a^2B b^2	8	1:3	3.5:1
			F_1	a^2 b^2	1	1:0	2.6:1
20.05:1 (381:19)	A^3a^3	1 factor: hexasomic: duplex expression for F_1 type.	F_1	A^{5*}	19	1:0	1:0
			F_1	A^3a^3	99	1:0	99:1
			F_1	A^3a^3	161	20:1	20:1
			F_1	A^2a^3	99	2.57:1	6.7:1
			Seg.	A a^3	18	1:3	2.64:1
			Seg.	a^6	1	0:1	1:1
20.33:1 (61:3)	A a B b C c	3 factor: disomic: dom. of A and rec. of B and C for expression of seg. type.	F_1	Homo. dom. at B or C	28	1:0	1:0
			F_1	A^2 B b C c	4	15:1	15:1
			F_1	A^2 B b c^2	2	3:1	7:1
			F_1	A^2 b^2C c	2	3:1	7:1
			F_1	A a B b C c	8	20:1	20:1
			F_1	A a B b c^2	4	4.33:1	9.6:1
			F_1	A a b^2C c	4	4.33:1	9.6:1
			Seg.	A^2 b^2 c^2	1	0:1	3:1
			Seg.	A a b^2 c^2	2	1:3	4.33:1
			F_1	a^2B b C c	4	1:0	35:1
			F_1	a^2B b c^2	2	1:0	15:1
			F_1	a^2 b^2C c	2	1:0	15:1
			F_1	a^2 b^2 c^2	1	1:0	7:1

See footnotes at end of table, p. 41.

TABLE 2.—*Theoretical test-cross ratios for various possible genetic hypotheses of F_2 segregations in a hexaploid assuming no double reduction*—Continued

Observed F_2 ratio [1]	Hypothetical F_1 genotype	Genetic hypothesis [2 3]	F_2 phenotype [3]	F_2 genotype [2 4 5]	F_2 frequency	Test-cross ratios [1]	
						Self	Backcross to F_1
22.58:1 (9576:24)	$A^2a^4B^3b^3$	2 factor: hexasomic: rec. of A or B for expression of seg. type.	F_1	$A^4a^2B^4$*	118	1:0	1:0
			F_1	$A^4a^2B^3b^3$	164	399:1	399:1
			F_1	$A^4a^2B^2b^4$	99	24:1	99:1
			F_1	$A^4a^2B\ b^5$	18	3:1	39:1
			Seg.	$A^4a^2\ \ b^6$	1	0:1	19:1
			F_1	$A^3a^3B^4$*	708	399:1	99:1
			F_1	$A^3a^3B^3b^3$	984	199:1	79:1
			F_1	$A^3a^3B^2b^4$	594	22:1	49:1
			F_1	$A^3a^3B\ b^5$	108	2.97:1	28:1
			Seg.	$A^3a^3\ \ b^6$	6	0:1	15.8:1
			F_1	$A^2a^4B^4$*	1,298	24:1	24:1
			F_1	$A^2a^4B^3b^3$	1,804	22:1	22:1
			F_1	$A^2a^4B^2b^4$	1,089	11.7:1	19.2:1
			F_1	$A^2a^4B\ b^5$	198	2.57:1	14.6:1
			Seg.	$A^2a^4\ \ b^6$	11	0:1	10.4:1
			F_1	$A\ a^5B^4$*	708	3:1	9:1
			F_1	$A\ a^5B^3b^3$	984	2.97:1	8.78:1
			F_1	$A\ a^5B^2b^4$	594	2.57:1	8.17:1
			F_1	$A\ a^5B\ b^5$	108	1.28:1	7.16:1
			Seg.	$A\ a^5\ \ b^6$	6	0:1	5.9:1
			Seg.	a^6B^4*	118	0:1	4:1
			Seg.	$a^6B^3b^3$	164	0:1	3.95:1
			Seg.	$a^6B^2b^4$	99	0:1	3.81:1
			Seg.	$a^6B\ b^5$	18	0:1	3.54:1
			Seg.	$a^6\ \ b^6$	1	0:1	3.17:1

22.64:1 (9577:423)	$A^2a^4B^2b^3$	2 factor; hexasomic; dom. of A or B and rec. of the other locus for expression of seg. type.	F_1	$A^4a^2B^{4*}$	118	1:0	1:0
			F_1	$A^4a^2B^3b^3$	164	399:1	399:1
			F_1	$A^4a^2B^2b^4$	99	24:1	99:1
			F_1	$A^4a^2B\ b^5$	18	3:1	39:1
			Seg.	$A^4a^2\ \ b^6$	1	0:1	19:1
			F_1	$A^3a^3B^{4*}$	708	399:1	99:1
			F_1	$A^3a^3B^3b^3$	984	199:1	79:1
			F_1	$A^3a^3B^2b^4$	594	23:1	49:1
			F_1	$A^3a^3B\ b^5$	108	2.98:1	28:1
			Seg.	$A^3a^3\ \ b^6$	6	1:399	15.9:1
			F_1	$A^2a^4B^{4*}$	1,298	24:1	24:1
			F_1	$A^2a^4B^3b^3$	1,804	23:1	23:1
			F_1	$A^2a^4B^2b^4$	1,089	12:1	19.3:1
			F_1	$A^2a^4B\ b^5$	198	2.70:1	14.9:1
			Seg.	$A^2a^4\ \ b^6$	11	1:24	10.6:1
			F_1	$A\ a^5B^{4*}$	708	3:1	9:1
			F_1	$A\ a^5B^3b^3$	984	2.98:1	8.80:1
			F_1	$A\ a^5B^2b^4$	594	2.70:1	8.26:1
			F_1	$A\ a^5B\ b^5$	108	1.67:1	7.33:1
			Seg.	$A\ a^5\ \ b^6$	6	1:3	6.14:1
			Seg.	a^6B^{4*}	118	0:1	4:1
			Seg.	$a^6B^3b^3$	164	1:399	3.96:1
			Seg.	$a^6B^2b^4$	99	1:24	3.85:1
			Seg.	$a^6B\ b^5$	18	1:3	3.65:1
			F_1	$a^6\ \ b^6$	1	1:0	3.35:1
24:1	A^2a^4	1 factor; hexasomic; simplex expression for F_1 type.	F_1	A^4a^2	1	1:0	1:0
			F_1	A^3a^3	6	399:1	99:1
			F_1	A^2a^4	11	24:1	24:1
			F_1	$A\ a^5$	6	3:1	9:1
			Seg.	a^6	1	0:1	4:1
24:1	A^4a^2	1 factor; hexasomic; triplex expression for F_1 type.	F_1	A^6	1	1:0	1:0
			F_1	A^5a	6	1:0	1:0
			F_1	A^4a^2	11	24:1	24:1
			F_1	A^3a^3	6	2.39:1	6.69:1
			Seg.	A^2a^4	1	1:2.57	2.57:1

See footnotes at end of table, p. 41.

TABLE 2.—*Theoretical test-cross ratios for various possible genetic hypotheses of F_2 segregations in a hexaploid assuming no double reduction*—Continued

Observed F_2 ratio [1]	Hypothetical F_1 genotype	Genetic hypothesis [2 3]	F_2 phenotype [3]	F_2 genotype [3 4 5]	F_2 frequency	Test-cross ratios [1]	
						Self	Backcross to F_1
24:1 (600:25)	$A^2a^4B^4b^2$	2 factor: hexasomic: rec. of A or B for expression of seg. type.	F_1	$A^4a^2B^4*$	18	1:0	1:0
			F_1	$A^4a^2B^2b^2$	6	399:1	1:0
			F_1	$A^4a^2B^2b^4$	1	24:1	1:0
			F_1	$A^3a^3B^4*$	108	399:1	99:1
			F_1	$A^3a^3B^2b^3$	36	199:1	99:1
			F_1	$A^3a^3B^2b^1$	6	22:1	99:1
			F_1	$A^2a^4B^4*$	198	24:1	24:1
			F_1	$A^2a^4B^2b^3$	66	22:1	24:1
			F_1	$A^2a^4B^2b^1$	11	11.7:1	24:1
			F_1	$A\ a^5B^4*$	108	3:1	9:1
			F_1	$A\ a^5B^2b^3$	36	2.97:1	9:1
			F_1	$A\ a^5B^2b^1$	6	2.57:1	9:1
			Seg.	a^6B^2*	25	0:1	4:1
24:1 (600:25)	$A^2a^4B^4b^2$	2 factor: hexasomic: dom. of A or B and rec. of the other locus for expression of seg. type.	F_1	$A^4a^2B^4*$	18	1:0	1:0
			F_1	$A^4a^2B^2b^3$	6	399:1	1:0
			F_1	$A^4a^2B^2b^4$	1	24:1	1:0
			F_1	$A^3a^3B^4*$	108	399:1	99:1
			F_1	$A^3a^3B^2b^3$	36	199:1	99:1
			F_1	$A^3a^3B^2b^1$	6	23:1	99:1
			F_1	$A^2a^4B^4*$	198	24:1	24:1
			F_1	$A^2a^4B^2b^3$	66	23:1	24:1
			F_1	$A^2a^4B^2b^1$	11	12:1	24:1
			F_1	$A\ a^5B^4*$	108	3:1	9:1
			F_1	$A\ a^5B^2b^3$	36	2.98:1	9:1
			F_1	$A\ a^5B^2b^1$	6	2.70:1	9:1

			Seg.	a^6B^{4*}	16	0:1	4:1
			Seg.	$a^6B^3b^3$	6	1:399	4:1
			Seg.	$a^6B^2b^4$	1	1:24	4:1
					—		
24:1 (600:25)	$A^2a^4B^4b^2$	2 factor; *hexasomic*; dom. of B and rec. of A for expression of seg. type.	F_1	$A^4a^2B^{2*}$	25	1:0	1:0
			F_1	$A^3a^3B^{4*}$	108	399:1	99:1
			F_1	$A^3a^3B^3b^3$	36	400:1	99:1
			F_1	$A^3a^3B^2b^4$	6	416:1	99:1
			F_1	$A^2a^4B^{3*}$	264	24:1	24:1
			F_1	$A^2a^4B^2b^4$	11	25:1	24:1
			F_1	$A\ a^5B^{4*}$	108	3:1	9:1
			F_1	$A\ a^5B^3b^3$	36	3.01:1	9:1
			F_1	$A\ a^5B^2b^4$	6	3.17:1	9:1
			Seg.	a^6B^{4*}	18	0:1	4:1
			Seg.	$a^6B^3b^3$	6	1:399	4:1
			Seg.	$a^6B^2b^4$	1	1:24	4:1
24:1 (96:4)	$A^2a^4B^3b$	2 factor; hexasomic, rec. of A or B for *expression of seg. type*; dom. of A or B and rec. of the other locus for expression of seg. type; or dom. of B and rec. of A for *expression of seg.* type.	F_1	$A^4a^2B^{4*}$	4	1:0	1:0
			F_1	$A^3a^3B^{4*}$	24	399:1	99:1
			F_1	$A^2a^4B^{4*}$	44	24:1	24:1
			F_1	$A\ a^5B^{4*}$	24	3:1	9:1
			Seg.	a^6B^{4*}	4	0:1	4:1
24:1 (9601:399)	$A^2a^4B^3b^3$	2 factor; hexasomic; dom. of B and rec. of A for *expression of seg. type.*	F_1	A^4a^{2*}	400	1:0	1:0
			F_1	$A^3a^3B^{4*}$	708	399:1	99:1
			F_1	$A^3a^3B^3b^3$	984	400:1	99:1
			F_1	$A^3a^3B^2b^4$	594	416:1	100:1
			F_1	$A^3a^3B\ b^5$	108	532:1	101:1
			F_1	$A^3a^3\ \ b^6$	6	1:0	104:1
			F_1	$A^2a^4B^{3*}$	3,102	24:1	24:1
			F_1	$A^2a^4B^2b^4$	1,089	25:1	24:1
			F_1	$A^2a^4B\ b^5$	198	32:1	25:1
			F_1	$A^2a^4\ \ b^6$	11	1:0	25:1
			F_1	$A\ a^5B^{4*}$	708	3:1	9:1

See footnotes at end of table, p. 41.

TABLE 2.—*Theoretical test-cross ratios for various possible genetic hypotheses of F_2 segregations in a hexaploid assuming no double reduction*—Continued

Observed F_2 ratio [1]	Hypothetical F_1 genotype	Genetic hypothesis [2 3]	F_2 phenotype [3]	F_2 genotype [2 4 5]	F_2 frequency	Test-cross ratios [1]	
						Self	Backcross to F_1
24:1 (9601:399) —Con.	$A^2a^4B^3b^3$ —Con.	2 factor; hexasomic; dom. of B and rec. of A for expression of seg. type.—Con.	F_1	A $a^5B^3b^3$	984	3.01:1	9.02:1
			F_1	A $a^5B^2b^4$	594	3.17:1	9.10:1
			F_1	A a^5B b^5	108	4.33:1	9.26:1
			F_1	A a^5 b^6	6	1:0	9.53:1
			Seg.	a^6B^{4*}	118	0:1	4:1
			Seg.	$a^6B^3b^3$	164	1:399	4.01:1
			Seg.	$a^6B^2b^4$	99	1:24	4.05:1
			Seg.	a^6B b^5	18	1:3	4.13:1
			F_1	a^6 b^6	1	1:0	4.26:1
25.04:1 (601:24)	$A^2a^4B^2b^4$	2 factor; hexasomic; dom. of A and rec. of B for expression of seg. type	F_1	* B^4b^2	25	1:0	1:0
			F_1	$A^4a^2B^3b^3$	6	399:1	99:1
			F_1	$A^3a^3B^3b^3$	36	400:1	100:1
			F_1	$A^2a^4B^3b^3$	66	416:1	103:1
			F_1	A $a^5B^3b^3$	36	532:1	110:1
			F_1	$a^6B^3b^3$	6	1:0	124:1
			F_1	$A^4a^2B^2b^4$	11	24:1	24:1
			F_1	$A^3a^3B^2b^4$	66	24:1	24:1
			F_1	$A^2a^4B^2b^4$	121	25:1	25:1
			F_1	A $a^5B^2b^4$	66	32:1	27:1
			F_1	$a^6B^2b^4$	11	1:0	30:1
			F_1	A^4a^2B b^5	6	3:1	9:1
			F_1	A^3a^3B b^5	36	3.01:1	9.10:1
			F_1	A^2a^4B b^5	66	3.17:1	9.41:1
			F_1	A a^5B b^5	36	4.33:1	10.1:1
			F_1	a^6B b^5	6	1:0	11.5:1
			Seg.	A^4a^2 b^6	1	0:1	0:1

			Seg.	A^3a^3 b^6	6	1:399	4.05:1
			Seg.	A^2a^4 b^6	11	1:24	4.21:1
			Seg.	A a^5 b^6	6	1:3	4.55:1
			F_1	a^6 b^6	1	1:0	5.25:1
32.33:1 (97:3)	A $a^5B^2b^4$	do	F_1	* B^4b^2	4	1:0	1:0
			F_1	$A^2a^4B^3b^3$	6	416:1	110:1
			F_1	A $a^5B^3b^3$	12	532:1	132:1
			F_1	$a^6B^3b^3$	6	1:0	199:1
			F_1	$A^2a^4B^2b^4$	11	25:1	27:1
			F_1	A $a^5B^2b^4$	22	32:1	32:1
			F_1	$a^6B^2b^4$	11	1:0	49:1
			F_1	A^2a^4B b^5	6	3.17:1	10.1:1
			F_1	A a^5B b^5	12	4.33:1	12.3:1
			F_1	a^6B b^5	6	1:0	19:1
			Seg.	A^2a^4 b^6	1	1:24	4.55:1
			Seg.	A a^5 b^6	2	1:3	5.67:1
			F_1	a^6 b^6	1	1:0	9:1
35:1	A^2a^2	1 factor; tetrasomic; simplex expression for F_1 type.	F_1	A^{3*}	9	1:0	1:0
			F_1	A^2a^2	18	35:1	35:1
			F_1	A a^3	8	3:1	11:1
			Seg.	a^4	1	0:1	5:1
35:1 (140:4)	$A^2a^2B^4b$	2 factor; tetrasomic; dom. of A or B and rec. of the other locus for expression of seg. type.	F_1	A^{3*} B^{3*}	27	1:0	1:0
			F_1	A^{3*} B^2b^2	9	35:1	1:0
			F_1	$A^2a^2B^{3*}$	54	35:1	35:1
			F_1	$A^2a^2B^2b^2$	18	17:1	35:1
			F_1	A a^3B^{3*}	24	3:1	11:1
			F_1	A $a^3B^2b^2$	8	2.79:1	11:1
			Seg.	a^4B^{3*}	3	0:1	5:1
			Seg.	$a^4B^2b^2$	1	1:35	5:1
35:1 (140:4)	$A^2a^2B^3b$	2 factor; tetrasomic; rec. of A or B for expression of seg. type.	F_1	A^{3*} B^{3*}	27	1:0	1:0
			F_1	A^{3*} B^2b^2	9	35:1	1:0
			F_1	$A^2a^2B^{3*}$	54	35:1	35:1
			F_1	$A^2a^2B^2b^2$	18	17:1	35:1
			F_1	A a^3B^{3*}	24	3:1	11:1
			F_1	A $a^3B^2b^2$	8	2.69:1	11:1

See footnotes at end of table, p. 41.

TABLE 2.—*Theoretical test-cross ratios for various possible genetic hypotheses of F_2 segregations in a hexaploid assuming no double reduction*—Continued

Observed F_2 ratio [1]	Hypothetical F_1 genotype	Genetic hypothesis [2 3]	F_2 phenotype [3]	F_2 genotype [2 4 5]	F_2 frequency	Test-cross ratios [1]	
						Self	Backcross to F_1
35:1 (140:4) —Con.	$A^2a^2B^3b$ —Con.	2 factor: tetrasomic; rec. of A or B for expression of seg. type.—Con.	Seg.....	a^4B^{3*}.....	3	0:1	5:1
			Seg.....	$a^4B^2b^2$.....	1	0:1	5:1
35:1 (140:4)	$A^2a^2B^3b$	2 factor; tetrasomic; dom. of B and rec. of A for expression of seg. type.	F_1.....	A^{3*} B^{2*}.....	36	1:0	1:0
			F_1.....	$A^2a^2B^{3*}$.....	54	35:1	35:1
			F_1.....	$A^2a^2B^2b^2$.....	18	36:1	35:1
			F_1.....	$A\ a^3B^{3*}$.....	24	3:1	11:1
			F_1.....	$A\ a^3B^2b^2$.....	8	3.11:1	11:1
			Seg.....	a^4B^{3*}.....	3	0:1	5:1
			Seg.....	$a^4B^2b^2$.....	1	1:35	5:1
36.02:1 (1261:35)	$A^2a^2B^2b^2$	2 factor; tetrasomic; dom. of B and rec. of A for expression of seg. type.	F_1.....	A^{3*} *.....	324	1:0	1:0
			F_1.....	$A^2a^2B^{3*}$.....	162	35:1	35:1
			F_1.....	$A^2a^2B^2b^2$.....	324	36:1	36:1
			F_1.....	$A^2a^2B\ b^3$.....	144	47:1	38:1
			F_1.....	$A^2a^2\ \ b^4$.....	18	1:0	42:1
			F_1.....	$A\ a^3B^{3*}$.....	72	3:1	11:1
			F_1.....	$A\ a^3B^2b^2$.....	144	3.11:1	11.3:1
			F_1.....	$A\ a^3B\ b^3$.....	64	4.33:1	12.1:1
			F_1.....	$A\ a^3\ \ b^4$.....	8	1:0	13.4:1
			Seg.....	a^4B^{3*}.....	9	0:1	5:1
			Seg.....	$a^4B^2b^2$.....	18	1:35	5.17:1
			Seg.....	$a^4B\ b^3$.....	8	1:3	5.54:1
			F_1.....	$a^4\ \ b^4$.....	1	1:0	6.20:1
47:1 (141:3)	$A\ a^3B^2b^2$	2 factor; tetrasomic; dom. of A and rec. of B for expression of seg. type.	F_1.....	* B^{3*}.....	36	1:0	1:0
			F_1.....	$A^2a^2B^2b^2$.....	18	36:1	38:1
			F_1.....	$A\ a^3B^2b^2$.....	36	47:1	47:1

			F_1	$a^4B^2b^2$	18	1:0	71:1
			F_1	$A^2a^2B\ b^3$	8	3.11:1	12.1:1
			F_1	$A\ a^3B\ b^3$	16	4.33:1	15:1
			F_1	$a^4B\ b^3$	8	1:0	23:1
			Seg.	$A^2a^2\ \ b^4$	1	1:35	5.54:1
			Seg.	$A\ a^3\ \ b^4$	2	1:3	7:1
			F_1	$a^4\ \ b^4$	1	1:0	11:1
63:1	A a B b C c	3 factor; disomic; rec. of all 3 loci for expression of seg. type.	F_1	Homo. dom. at one or more loci	37	1:0	1:0
			F_1	A a B b C c	8	63:1	63:1
			F_1	Het. at 2 loci and homo. rec. at the other	12	15:1	31:1
			F_1	Het. at 1 locus and homo. rec. at 2	6	3:1	15:1
			Seg.	$a^2\ \ b^2\ \ c^2$	1	0:1	7:1
99:1	A $a^5B^2b^4$	2 factor; hexasomic; rec. of A and B for expression of seg. type.	F_1	$*\ \ B^4b^2$	4	1:0	1:0
			F_1	$A^2a^4B^2b^3$	6	1:0	999:1
			F_1	$A\ a^5B^2b^3$	12	1:0	399:1
			F_1	$a^6B^2b^3$	6	1:0	199:1
			F_1	$A^2a^4B^2b^4$	11	624:1	249:1
			F_1	$A\ a^5B^2b^4$	22	99:1	99:1
			F_1	$A^2a^4B\ b^5$	6	99:1	99:1
			F_1	$a^6B^2b^4$	11	24:1	49:1
			F_1	$A^2a^4\ \ b^6$	1	24:1	49:1
			F_1	$A\ a^5B\ b^5$	12	15:1	39:1
			F_1	$a^6B\ b^5$	6	3:1	19:1
			F_1	$A\ a^5\ \ b^6$	2	3:1	19:1
			Seg.	$a^6\ \ b^6$	1	0:1	9:1
143:1	$A^2a^2B\ b^3$	2 factor; tetrasomic; rec. of A and B for expression of seg. type.	F_1	$A^{3*}\ *$	36	1:0	1:0
			F_1	$A^2a^2B^2b^2$	18	1295:1	431:1
			F_1	$A^2a^2B\ b^3$	36	143:1	143:1
			F_1	$A\ a^3B^2b^2$	8	143:1	143:1
			F_1	$A^2a^2\ \ b^4$	18	35:1	71:1
			F_1	$a^4B^2b^2$	1	35:1	71:1
			F_1	$A\ a^3B\ b^3$	16	15:1	47:1
			F_1	$A\ a^3\ \ b^4$	8	3:1	23:1
			F_1	$a^4B\ b^3$	2	3:1	23:1
			Seg.	$a^4\ \ b^4$	1	0:1	11:1

See footnotes at end of table, p. 41.

TABLE 2.—*Theoretical test-cross ratios for various possible genetic hypotheses of F_2 segregations in a hexaploid assuming no double reduction*—Continued

Observed F_2 ratio [1]	Hypothetical F_1 genotype	Genetic hypothesis [2 3]	F_2 phenotype [3]	F_2 genotype [2 4 5]	F_2 frequency	Test-cross ratios [1]	
						Self	Back-cross to F_1
143:1	$A^2a^2B\ b$	1–1 factor; tetradisomic; rec. of A and B for expression of seg. type.	F_1	$A^{3*}\ *$	36	1:0	1:0
			F_1	$*\ \ B^2$	27	1:0	1:0
			F_1	$A^2a^2B\ b$	36	143:1	143:1
			F_1	$A^2a^2\ \ b^2$	18	35:1	71:1
			F_1	$A\ a^3B\ b$	16	15:1	47:1
			F_1	$A\ a^3\ \ b^2$	8	3:1	23:1
			F_1	$a^4B\ b$	2	3:1	23:1
			Seg.	$a^4\ \ b^2$	1	0:1	11:1
199:1 (159,202:798)	$A^3a^3B^3b^3$	2 factor; hexasomic; dom. of A or B and rec. of the other for expression of seg. type.	F_1	$A^{4*}\ B^{4*}$	13,924	1:0	1:0
			F_1	$A^{4*}\ B^3b^3$	19,352	399:1	399:1
			F_1	$A^3a^3B^{4*}$	19,352	399:1	399:1
			F_1	$A^3a^3B^3b^3$	26,896	199:1	199:1
			F_1	$A^{4*}\ B^2b^4$	11,682	24:1	99:1
			F_1	$A^2a^4B^{4*}$	11,682	24:1	99:1
			F_1	$A^3a^3B^2b^4$	16,236	23:1	79:1
			F_1	$A^2a^4B^3b^3$	16,236	23:1	79:1
			F_1	$A^2a^4B^2b^4$	9,801	12:1	49:1
			F_1	$A^{4*}\ B\ b^5$	2,124	3:1	39:1
			F_1	$A\ a^5B^{4*}$	2,124	3:1	39:1
			F_1	$A^3a^3B\ b^5$	2,952	2.98:1	35:1
			F_1	$A\ a^5B^3b^3$	2,952	2.98:1	35:1
			F_1	$A^2a^4B\ b^5$	1,782	2.70:1	28:1
			F_1	$A\ a^5B^2b^4$	1,782	2.70:1	28:1
			F_1	$A\ a^5B\ b^5$	324	1.67:1	19.5:1
			Seg.	$A^{4*}\ \ b^6$	118	0:1	19:1

			Seg.	a^6B^{4*}	118	0:1	19:1
			Seg.	A^3a^3 b^6	164	1:399	18.1:1
			Seg.	$a^6B^3b^3$	164	1:399	18.1:1
			Seg.	A^2a^4 b^6	99	1:24	15.9:1
			Seg.	$a^6B^2b^4$	99	1:24	15.9:1
			Seg.	A a^5 b^6	18	1:3	12.8:1
			Seg.	a^6B b^5	18	1:3	12.8:1
			F_1	a^6 b^6	1	1:0	9.52:1
199:1 (159,201:799)	$A^3a^3B^3b^3$	2 factor; hexasomic; rec. of A or B for expression of seg. type.	F_1	A^{4*} B^{4*}	13,924	1:0	1:0
			F_1	A^{4*} B^3b^3	19,352	399:1	399:1
			F_1	$A^3a^3B^{4*}$	19,352	399:1	399:1
			F_1	$A^3a^3B^3b^3$	26,896	199:1	199:1
			F_1	A^{4*} B^2b^4	11,682	24:1	99:1
			F_1	$A^2a^4B^{4*}$	11,682	24:1	99:1
			F_1	$A^3a^3B^2b^4$	16,236	22:1	79:1
			F_1	$A^2a^4B^3b^3$	16,236	22:1	79:1
			F_1	$A^2a^4B^2b^4$	9,801	11.7:1	49:1
			F_1	A^{4*} B b^5	2,124	3:1	39:1
			F_1	A a^5B^{4*}	2,124	3:1	39:1
			F_1	A^3a^3B b^5	2,952	2.97:1	35:1
			F_1	A $a^5B^3b^3$	2,952	2.97:1	35:1
			F_1	A^2a^4B b^5	1,782	2.57:1	28:1
			F_1	A $a^5B^2b^4$	1,782	2.57:1	28:1
			F_1	A a^5B b^5	324	1.28:1	19:1
			Seg.	A^{4*} b^6	118	0:1	19:1
			Seg.	a^6B^{4*}	118	0:1	19:1
			Seg.	A^3a^3 b^6	164	0:1	18:1
			Seg.	$a^6B^3b^3$	164	0:1	18:1
			Seg.	A^2a^4 b^6	99	0:1	15.8:1
			Seg.	$a^6B^2b^4$	99	0:1	15.8:1
			Seg.	A a^5 b^6	18	0:1	12.5:1
			Seg.	a^6B b^5	18	0:1	12.5:1
			Seg.	a^6 b^6	1	0:1	9.25:1

See footnotes at end of table, p. 41.

TABLE 2.—*Theoretical test-cross ratios for various possible genetic hypotheses of F_2 segregations in a hexaploid assuming no double reduction*—Continued

Observed F_2 ratio [1]	Hypothetical F_1 genotype	Genetic hypothesis [2 3]	F_2 phenotype [3]	F_2 genotype [2 4 5]	F_2 frequency	Test-cross ratios [1]	
						Self	Back-cross to F_1
399:1	A^3a^3	1 factor; hexasomic; simplex expression.	F_1	A^{4*}	118	1:0	1:0
			F_1	A^3a^3	164	399:1	399:1
			F_1	A^2a^4	99	24:1	99:1
			F_1	$A\ a^5$	18	3:1	39:1
			Seg.	a^6	1	0:1	19:1
399:1 (1596:4)	$A^3a^3B^5b$	2 factor; hexasomic; rec. of A or B for expression of seg. type; dom. of B and rec. of A for expression of seg. type; or dom. of A or B and rec. of the other locus for expression of seg. type.	F_1	$A^{4*}\ B^{4*}$	472	1:0	1:0
			F_1	$A^3a^3B^{4*}$	656	399:1	399:1
			F_1	$A^2a^4B^{4*}$	396	24:1	99:1
			F_1	$A\ a^5B^{4*}$	72	3:1	39:1
			Seg.	a^6B^{4*}	4	0:1	19:1
399:1 (9975:25)	$A^3a^3B^4b^2$	2 factor; hexasomic; rec. of A or B for expression of seg. type.	F_1	$A^{4*}\ B^{4*}$	2,124	1:0	1:0
			F_1	$A^{4*}\ B^3b^3$	708	399:1	1:0
			F_1	$A^3a^3B^{4*}$	2,952	399:1	399:1
			F_1	$A^3a^3B^3b^3$	984	199:1	399:1
			F_1	$A^{4*}\ B^2b^4$	118	24:1	1:0
			F_1	$A^2a^4B^{4*}$	1,782	24:1	99:1
			F_1	$A^2a^4B^3b^3$	594	23:1	99:1
			F_1	$A^3a^3B^2b^4$	164	23:1	399:1
			F_1	$A^2a^4B^2b^4$	99	11.7:1	99:1
			F_1	$A\ a^5B^{4*}$	324	3:1	39:1

			F_1.....	A $a^5B^2b^3$.....	108	2.97:1	39:1
			F_1.....	A $a^5B^2b^4$.....	18	2.57:1	39:1
			Seg.....	a^6B^2*.....	25	0:1	19:1
399:1 (9975:25)	$A^3a^3B^4b^2$	2 factor; hexasomic; dom. of A or B and rec. of the other locus for expression of seg. type.	F_1.....	A^4** B^4*.....	2,124	1:0	1:0
			F_1.....	A^4** B^3b^3.....	708	399:1	1:0
			F_1.....	$A^3a^3B^4$*.....	2,952	399:1	399:1
			F_1.....	$A^3a^3B^3b^3$.....	984	199:1	399:1
			F_1.....	A^4** B^2b^4.....	118	24:1	1:0
			F_1.....	$A^2a^4B^4$*.....	1,782	24:1	99:1
			F_1.....	$A^2a^4B^3b^3$.....	594	23:1	99:1
			F_1.....	$A^3a^3B^2b^4$.....	164	23:1	399:1
			F_1.....	$A^2a^4B^2b^4$.....	99	12:1	99:1
			F_1.....	A a^5B^4*.....	324	3:1	39:1
			F_1.....	A $a^5B^3b^3$.....	108	2.98:1	39:1
			F_1.....	A $a^5B^2b^4$.....	18	2.70:1	39:1
			Seg.....	a^6B^4*.....	18	0:1	19:1
			Seg.....	$a^6B^3b^3$.....	6	1:399	19:1
			Seg.....	$a^6B^2b^4$.....	1	1:24	19:1
399:1 (9975:25)	$A^3a^3B^4b^2$	2 factor; hexasomic; dom. of B and rec. of A for expression of seg. type.	F_1.....	A^4** B^2*.....	2,950	1:0	1:0
			F_1.....	$A^3a^3B^4$*.....	2,952	399:1	399:1
			F_1.....	$A^3a^3B^3b^3$.....	984	400:1	399:1
			F_1.....	$A^3a^3B^2b^4$.....	164	416:1	399:1
			F_1.....	$A^2a^4B^3$*.....	2,376	24:1	99:1
			F_1.....	$A^2a^4B^2b^4$.....	99	25:1	99:1
			F_1.....	A a^5B^4*.....	324	3:1	39:1
			F_1.....	A $a^5B^3b^3$.....	108	3.01:1	39:1
			F_1.....	A $a^5B^2b^4$.....	18	3.17:1	39:1
			Seg.....	a^6B^4*.....	18	0:1	19:1
			Seg.....	$a^6B^3b^3$.....	6	1:399	19:1
			Seg.....	$a^6B^2b^4$.....	1	1:24	19:1

[1] All ratios expressed as parental (F_1) type vs. nonparental (segregate) type.
[2] Rec., recessive; dom., dominant.
[3] F_1, parental type; seg., segregate, or nonparental, type.
[4] *, indicates the allele may be dominant or recessive because the test cross would not distinguish between types. In these cases, the F_2 frequency column reflects a sum of two or more genotypes.
[5] Homo., homozygous; het., heterozygous.

TABLE 3.—*Approximate population size (n) needed to distinguish between 2 genetic ratios*[1]

Larger proportion (p_2)	Smaller proportion (p_1)																														
	1:1	1.28:1	1.37:1	1.67:1	2.39:1	2.57:1	2.69:1	2.79:1	3:1	3.26:1	4.33:1	5.4:1	6.1:1	12:1	15:1	17.5:1	20:1	22.6:1	24:1	25:1	32.3:1	35:1	47:1	63:1	99:1	143:1	199:1					
1:1	–																														
1.28:1	675	–																													
1.37:1	438	11,488	–																												
1.67:1	167	674	1,168	–																											
2.39:1	59	121	162	373	–																										
2.57:1	50	97	119	261	9,817	–																									
2.69:1	46	87	104	216	3,801	26,607	–																								
2.79:1	43	79	94	188	2,259	8,350	43,186	–																							
3:1	38	67	78	145	1,053	2,334	4,712	10,514	–																						
3.26:1	33	55	65	112	561	971	1,485	2,239	7,728	–																					
4.33:1	22	34	39	59	169	225	273	323	478	845	–																				
5.4:1	17	25	28	41	94	116	133	150	194	275	1,499	–																			
6.1:1	15	22	24	34	74	89	100	111	139	160	572	5,164	–																		
12:1	9	12	13	17	30	34	36	39	44	52	95	172	249	–																	
15:1	8	10	12	15	25	28	30	32	35	41	70	115	155	3,576	–																
17.5:1	7	10	10	13	22	25	26	27	31	35	57	90	117	1,239	7,239	–															
20:1	7	9	10	13	20	22	24	25	28	32	51	77	99	740	2,495	14,507	–														
22.6:1	7	9	9	12	18	20	22	23	25	29	45	66	83	481	1,202	3,411	12,874	–													
24:1	7	8	9	11	18	20	21	22	25	28	43	63	78	422	983	2,453	7,084	106,129	–												
25:1	6	8	9	11	17	19	20	21	24	27	41	60	74	370	815	1,836	4,431	25,905	101,251	–											
32.3:1	6	7	8	10	15	17	18	19	21	23	34	49	59	234	424	737	1,231	2,582	3,629	5,524	–										
35:1	6	7	8	10	15	16	17	18	20	22	33	46	56	209	376	610	968	1,840	2,442	3,426	75,978	–									
47:1	5	7	7	9	13	14	15	16	17	19	28	38	45	145	229	339	473	725	861	1,047	3,289	5,239	–								
63:1	5	6	6	8	12	13	14	14	16	17	25	33	39	112	166	231	304	424	484	559	1,206	1,579	7,804	–							
99:1	4	5	6	7	11	12	12	13	14	16	21	27	32	81	113	148	184	237	262	291	492	583	1,110	3,789	–						
143:1	4	5	6	7	10	11	11	12	12	14	19	25	28	68	92	117	142	177	194	212	329	377	707	1,447	10,000	–					
199:1	4	5	5	6	9	10	10	11	12	13	18	23	26	60	79	99	119	145	157	170	252	283	484	858	3,129	15,967	–				
399:1	4	5	5	6	9	9	10	10	11	12	16	20	23	51	67	82	96	116	125	134	189	209	328	518	1,312	3,208	10,632				

[1] Computed according to formulas of Kempthorne in "An Introduction to Genetic Statistics," with a probability level of 0.05. The breaking point (r), above which the larger proportion (p_2) would be accepted and below which the smaller proportion (p_1) would be accepted, can be computed by use of: $r = np_1 + 1.645\sqrt{n(p_1 - p_1^2)}$.

TABLE 4.—*Values of chi-square*[1]

D.f.	Probability of a larger value of chi-square												
	0.99	0.98	0.95	0.90	0.80	0.70	0.50	0.30	0.20	0.10	0.05	0.02	0.01
1	0.000	0.001	0.004	0.016	0.064	0.148	0.455	1.074	1.642	2.706	3.841	5.412	6.635
2	.020	.040	.103	.211	.446	.713	1.386	2.408	3.219	4.605	5.991	7.824	9.210
3	.115	.185	.352	.584	1.005	1.424	2.366	3.665	4.642	6.251	7.815	9.837	11.341
4	.297	.429	.711	1.064	1.649	2.195	3.357	4.878	5.989	7.779	9.488	11.668	13.277
5	.554	.752	1.145	1.610	2.343	3.000	4.351	6.064	7.289	9.236	11.070	13.388	15.086
6	.872	1.134	1.635	2.204	3.070	3.828	5.348	7.231	8.558	10.645	12.592	15.033	16.812
7	1.239	1.564	2.167	2.833	3.822	4.671	6.346	8.383	9.803	12.017	14.067	16.622	18.475
8	1.646	2.032	2.733	3.490	4.594	5.527	7.344	9.524	11.030	13.362	15.507	18.168	20.090
9	2.088	2.532	3.325	4.168	5.380	6.393	8.343	10.656	12.242	14.684	16.919	19.679	21.666
10	2.558	3.059	3.940	4.865	6.179	7.267	9.342	11.781	13.442	15.987	18.307	21.161	23.209
11	3.053	3.609	4.575	5.578	6.989	8.148	10.341	12.899	14.631	17.275	19.675	22.618	24.725
12	3.571	4.178	5.226	6.304	7.807	9.034	11.340	14.011	15.812	18.549	21.026	24.054	26.217
13	4.107	4.765	5.892	7.042	8.634	9.926	12.340	15.119	16.985	19.812	22.362	25.472	27.688
14	4.660	5.368	6.571	7.790	9.467	10.821	13.339	16.222	18.151	21.064	23.685	26.873	29.141
15	5.229	5.985	7.261	8.547	10.307	11.721	14.339	17.322	19.311	22.307	24.996	28.259	30.578
16	5.812	6.614	7.962	9.312	11.152	12.624	15.338	18.418	20.465	23.542	26.296	29.633	32.000
17	6.408	7.255	8.672	10.085	12.002	13.531	16.338	19.511	21.615	24.769	27.587	30.995	33.409
18	7.015	7.906	9.390	10.865	12.857	14.440	17.338	20.601	22.760	25.989	28.869	32.346	34.805
19	7.633	8.567	10.117	11.651	13.716	15.352	18.338	21.689	23.900	27.204	30.144	33.687	36.191
20	8.260	9.237	10.851	12.443	14.578	16.266	19.337	22.775	25.038	28.412	31.410	35.020	37.566
21	8.897	9.915	11.591	13.240	15.445	17.182	20.337	23.858	26.171	29.615	32.671	36.343	38.932
22	9.542	10.600	12.338	14.041	16.314	18.101	21.337	24.939	27.301	30.813	33.924	37.659	40.289
23	10.196	11.293	13.091	14.848	17.187	19.021	22.337	26.018	28.429	32.007	35.172	38.968	41.638
24	10.856	11.992	13.848	15.659	18.062	19.943	23.337	27.096	29.553	33.196	36.415	40.270	42.980
25	11.524	12.697	14.611	16.473	18.940	20.867	24.337	28.172	30.675	34.382	37.652	41.566	44.314
26	12.198	13.409	15.379	17.292	19.820	21.792	25.336	29.246	31.795	35.563	38.885	42.856	45.642
27	12.879	14.125	16.151	18.114	20.703	22.719	26.336	30.319	32.912	36.741	40.113	44.140	46.963
28	13.565	14.847	16.928	18.939	21.588	23.647	27.336	31.391	34.027	37.916	41.337	45.419	48.278
29	14.256	15.574	17.708	19.768	22.475	24.577	28.336	32.461	35.139	39.087	42.557	46.693	49.588
30	14.953	16.306	18.493	20.599	23.364	25.508	29.336	33.530	36.250	40.256	43.773	47.962	50.892

[1] Taken from table III of "Statistical Tables for Bilogical, Agricultural and Medical Research," published by Oliver & Boyd Ltd., Edinburgh. Used by permission of the authors (Fisher, R. A., and Yates, F.) and publishers.

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