

LINKAGE STUDIES WITH BIOCHEMICAL MUTANTS OF NEUROSPORA CRASSA†*

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IN 1946 a tentative chromosome map of *Neurospora crassa* was published (BEADLE) showing members, among the biochemical mutants obtained at the Stanford laboratory, of the five linkage groups then known. The data have not been published since they were considered not sufficiently extensive, in most cases, to establish relative positions of the various genes within the linkage groups. Since that time, however, a number of requests from other laboratories have indicated that these data may be useful to other workers. They are presented here, along with more recent data.

EXPERIMENTAL RESULTS

The crosses are listed in five tables with the types of segregation obtained tabulated for each cross. Types of segregation are numbered at the head of the table and the number of each type observed is tabulated under the appropriate type-number. The various arrangements of spore pairs possible for each type of segregation are not considered. Tables 1, 2 and 3 contain crosses showing segregation of sex and one mutant, sex and two mutants, and two mutants respectively. Table 4 gives the numbers of first and second division segregations from crosses in which segregation of only one mutant was observed. Table 5 shows results from crosses between two mutants, usually with the same growth requirement, which could not be, or were not, distinguished from one another. Centromere distances cannot, of course, be obtained from these data, but cases of linkage or possible allelism are demonstrated. The crosses are listed numerically by the isolation numbers of the mutants. When two mutants are involved the smaller number is placed first and the cross listed under that number. The following abbreviations for requirements and descriptions have been used:

<i>ad</i>	adenineless	<i>phen</i>	phenylalanineless
<i>ad-p</i>	purple adenineless	<i>prol</i>	prolineless
<i>arg</i>	arginineless	<i>pyr</i>	pyrimidineless
<i>chol</i>	cholineless	<i>pyro</i>	pyridoxinless
<i>hist</i>	histidineless	<i>pyro-p</i>	pyridoxinless-pH sensitive
<i>inos</i>	inositolless	<i>ribo</i>	riboflavinless
<i>isol-val</i>	isoleucine-valineless	<i>ser</i>	serineless

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TABLE 1

Crosses showing segregation of sex and one mutant

TYPES OF SEGREGATION									
	<i>Xa</i> × <i>+A</i>			OR			<i>XA</i> × <i>+a</i>		
1	<i>Xa</i>	<i>Xa</i>	<i>+A</i>	<i>+A</i>			<i>XA</i>	<i>XA</i>	<i>+a</i>
2	<i>XA</i>	<i>XA</i>	<i>+a</i>	<i>+a</i>			<i>Xa</i>	<i>Xa</i>	<i>+A</i>
3	<i>Xa</i>	<i>+a</i>	<i>XA</i>	<i>+A</i>			<i>Xa</i>	<i>+a</i>	<i>XA</i>
4	<i>Xa</i>	<i>XA</i>	<i>+a</i>	<i>+A</i>			<i>Xa</i>	<i>XA</i>	<i>+a</i>
5	<i>Xa</i>	<i>+A</i>	<i>Xa</i>	<i>+A</i>			<i>XA</i>	<i>+a</i>	<i>XA</i>
6	<i>Xa</i>	<i>+A</i>	<i>XA</i>	<i>+a</i>			<i>Xa</i>	<i>+A</i>	<i>XA</i>
7	<i>XA</i>	<i>+a</i>	<i>XA</i>	<i>+a</i>			<i>Xa</i>	<i>+A</i>	<i>+A</i>

	STRAINS	TYPES OF SEGREGATION							TOTAL	NO. ISO- LATED
		1	2	3	4	5	6	7		
263	<i>A pyr</i>	×	Abbott 12	<i>a</i> Wild	11	7	2	3	23	24
*299	<i>a pyro-p</i>	×	nonconidial	<i>A</i> vis	5	6	2	7	1	21
*1090	<i>a thi</i>	×	nonconidial	<i>A</i> "			6	3	4	13
1298	<i>a pyr</i>	×	1	<i>A</i> Wild	7	7	5		19	20
9185	<i>A thi</i>	×	Abbott 12	<i>a</i> "	7	1	9	1	1	20
9460	<i>a vis</i>	×	1	<i>A</i> "	8				8	10
15300	<i>A</i> "	×	25	<i>a</i> "	24	3	23	3	1	54
15300	<i>a</i> "	×	33458	<i>A</i> vis	12	2	4	2		20
20705	<i>a ad</i>	×	Abbott 4	<i>A</i> Wild	6	3	13	2	24	24
27663	<i>a</i> "	×	Abbott 4	<i>A</i> "	3	9	4		1	18
28610	<i>a</i> "	×	Abbott 4	<i>A</i> "	8	13	3		24	24
28815	<i>a</i> "	×	Abbott 4	<i>A</i> "	4	1	10	1	2	18
32213	<i>A un-t</i>	×	Em 5297	<i>a</i> "	5		9		1	20
34508	<i>A vis</i>	×	25	<i>a</i> "	7	11	17	1		36
34542	<i>A chol</i>	×	25	<i>a</i> "	4	5	20	1	1	34
34547	<i>A nitr</i>	×	Chilton	<i>a</i> "	18		19	1	1	40
34547	<i>a</i> "	×	Em 5256	<i>A</i> "	16		7	1	1	30
35402	<i>a suc</i>	×	Abbott 4	<i>A</i> "	17			1		18
35405	<i>a pyro</i>	×	1	<i>A</i> "	8	4	5	1		20
35810	<i>a isol-val</i>	×	Abbott 4	<i>A</i> "	5	10	3		18	20
37401	<i>a inos</i>	×	Abbott 4	<i>A</i> "	8	14	20		1	45
37602	<i>a suc</i>	×	Em 5256	<i>A</i> "	12	1	1	5		20
38502	<i>A pyr</i>	×	Em 5297	<i>a</i> "	3	4	9	1	1	20
39106	<i>A pyro-p</i>	×	Chilton	<i>a</i> "	3	4		3		10
39303	<i>a nic</i>	×	Abbott 4	<i>A</i> "	19			1		20
39311	<i>a suc</i>	×	Abbott 4	<i>A</i> "	16			2		20
39401	<i>a nic-tryp</i>	×	Abbott 4	<i>A</i> "	7	7	4	1		20
39404	<i>a suc</i>	×	Em 5256	<i>A</i> "	15		1	3	1	20
40008	<i>A tryp</i>	×	Abbott 12	<i>a</i> "	4	6	4			14
43002	<i>A nic</i>	×	25	<i>a</i> "	19					20
44008	<i>a tryp</i>	×	1	<i>A</i> "	8	6	3	1		20
44101	<i>a pyr</i>	×	Abbott 4	<i>A</i> "	5	6	1	6		18
44204	<i>a pyro-p</i>	×	1	<i>A</i> "	5	4		2		11
44206	<i>A ad-t</i>	×	25	<i>a</i> "	10	9		1		20

TABLE 1—(continued)

	STRAINS	<i>X</i>	<i>X</i>	+	TYPES OF SEGREGATION							TOTAL	NO. ISO- LATED
					1	2	3	4	5	6	7		
44302	<i>A pyr</i>	×	25	<i>a</i>	"	7	5	2	4			18	20
44409	<i>a un-t</i>	×	Abbott 4	<i>A</i>	"	14		4	1		1	20	20
44411	<i>a ad</i>	×	1		<i>A Wild</i>	1	2	12		3	1	19	20
44504	<i>A pyr</i>	×	Abbott 12	<i>a</i>	"	8	6	2	5	1		22	24
44601	<i>A un</i>	×	25	<i>a</i>	"	8	10		3			21	24
44602	<i>A pyro-p</i>	×	Chilton	<i>a</i>	"	4	7	4	1			16	20
45004	<i>A ad</i>	×	Abbott 12	<i>a</i>	"	2	5	7	5	1		20	20
45208	<i>a un-t</i>	×	Abbott 4	<i>A</i>	"	1		6		1	1	9	10
45304	<i>A tryp</i>	×	25	<i>a</i>	"	11	16	4		1	1	33	40
45502	<i>A pyr</i>	×	Abbott 12	<i>a</i>	"	10	7		5			22	22
45612	<i>A un</i>	×	Abbott 12	<i>a</i>	"	4	10		4	1		19	20
46006	<i>a un-t</i>	×	Abbott 4	<i>A</i>	"	15			3			18	20
46403	<i>a un</i>	×	1	<i>A</i>	"	11		1		2	1	15	20
46407	<i>A prol</i>	×	25	<i>a</i>	"	6		6	2	1		15	20
46705	<i>A ad</i>	×	Abbott 12	<i>a</i>	"	4	2	7	2	1		16	20
46904	<i>A pyro-p</i>	×	Chilton	<i>a</i>	"	3	4	1	2			10	10
47305	<i>A un-t</i>	×	25	<i>a</i>	"	3	4	6	1	2	1	18	20
47807	<i>a suc</i>	×	1	<i>A</i>	"	16			1	2	1	20	20
47904	<i>a chol</i>	×	Abbott 4	<i>A</i>	"	3	1	6		1	1	13	20
51505	<i>A prol</i>	×	Abbott 12	<i>a</i>	"	2	5	9				16	20
51602	<i>a ribo-t</i>	×	Abbott 4	<i>A</i>	"	5	14		1			20	20
55701	<i>a un-t</i>	×	1	<i>A</i>	"	36				2		38	40
56501	<i>a thi</i>	×	1	<i>A</i>	"	6		7	1	1		15	20
63904	<i>a pyr</i>	×	Abbott 4	<i>A</i>	"	2	5	7	4	1	2	21	24
66204	<i>A un-t</i>	×	25	<i>a</i>	"	8	8					16	20
66210	<i>A chol</i>	×	Chilton	<i>a</i>	"	1	1	9	2		2	15	20
66702	<i>a suc</i>	×	1	<i>A</i>	"	6			1			7	8
67602	<i>a pyr</i>	×	Abbott 4	<i>A</i>	"	6	6	1	4			17	20
67701	<i>a pyr</i>	×	1	<i>A</i>	"	5	7	1	2		1	16	20
68305	<i>a pyr</i>	×	Abbott 4	<i>A</i>	"	2	10	7	5			24	24
70004	<i>A ad-t</i>	×	25	<i>a</i>	"	3	4	4	1			12	20
71104	<i>a ad</i>	×	1	<i>A</i>	"	16			3	1		20	20
75001	<i>A tryp</i>	×	25	<i>a</i>	"	9	4	5	1			19	20
83106	<i>a un-t</i>	×	Abbott 4	<i>A</i>	"	4	8	5	1			18	20
85902	<i>A thi</i>	×	Em 5297	<i>a</i>	"	11	8		18			37	40

1392 1548

* *Neurospora sutophilis*.

<i>leu</i>	leucineless	<i>sfo</i>	sulfonamide-requiring
<i>lys</i>	lysineless	<i>suc</i>	succinicless
<i>meth</i>	methionineless	<i>thi</i>	thiaminless
<i>nic</i>	nicotinicless	<i>thr</i>	threonineless
<i>nic-tryp</i>	nicotinic or tryptophanless	<i>tryp</i>	tryptophanless
<i>nitr</i>	unable to use nitrate	<i>un</i>	unknown requirement
<i>pab</i>	para aminobenzoicless	<i>val</i>	valineless
<i>pan</i>	pantothenicless		

TABLE 2

CROSSES SHOWING SEGREGATION OF SEX AND TWO MUTANTS

TYPES OF SEGREGATION				
	X+a	X	+yA	
1	X+a	X+a	+yA	+yA
2	X+A	X+A	+ya	+ya
3	X+a	X+A	+ya	+yA
4	X ya	X ya	++A	++A
5	X yA	X yA	++a	++a
6	X ya	X yA	++a	++A
7	X+a	X ya	++A	+yA
8	X+A	X yA	++a	+ya
9	X+a	X yA	++a	+yA
10	X+A	X ya	++A	+ya
11	X+a	X yA	++A	+ya
12	X+A	X ya	++a	+yA
13	X+a	++a	X yA	+yA
14	X+A	++A	X ya	+ya
15	X+a	++A	X ya	+yA
16	X+A	++a	X yA	+ya
17	X+a	++A	X yA	+ya
18	X+A	++a	X ya	+yA
19	X+a	+ya	X+A	+yA
20	X+a	+yA	X+a	+yA
21	X+A	+ya	X+A	+ya
22	X+a	+yA	X+A	+ya
23	X+a	+ya	X yA	++A
24	X+A	+yA	X ya	++a
25	X+a	+yA	X ya	++A
26	X+A	+ya	X yA	++a
27	X+a	+yA	X yA	++a
28	X+A	+ya	X ya	++A
29	X ya	++a	X yA	++A
30	X ya	++A	X ya	++A
31	X yA	++a	X yA	++a
32	X ya	++A	X yA	++a

(This table continues on facing page)

The appearance of -t after a symbol indicates that the mutant is temperature sensitive. All morphological mutants as well as the albinos are listed as "v s," abbreviating visible.

In tables 1, 2, 3 and 4 ascospores are included if at least one member of each of three spore pairs germinated and could be tested. In table 5 only ascospores from which at least one member of each spore pair germinated are included. It should be pointed out that if failure of spores to mature or to germinate is associated with particular genotypes or types of segregation then selection of complete ascospores for dissection, and after germination, for classification, will lead to errors which are not easily avoided. Crosses which gave few complete ascospores, as well as those from which germination was poor, were rather frequently encountered in the course of this work, particularly when two mutants having the same growth requirement were involved.

In table 6 an attempt is made to summarize the information pertinent to linkage by listing the mutants in the appropriate linkage group, when this is known. Centromere distance was calculated from all crosses (except those in

TABLE 2—(continued)

STRAINS			TYPES OF SEGREGATION										TO-TAL	NUM-BER		
	X +	X + y												ISO-LATED		
517	<i>A fat</i>	× 4637	<i>a vis</i>	1-9	2-1	5-12	13-1							23	27	
1633	<i>A pab</i>	× 4637	<i>a "</i>	1-2	2-1	5-4	7-2	13-9	14-1	16-1				20	20	
1752	<i>A fat</i>	× 4637	<i>a "</i>	1-3	2-1	13-5	14-3	24-1						13	17	
3254	<i>a ad</i>	× 4637	<i>A "</i>	1-5	3-1	4-1	5-10	7-1						18	20	
3416	<i>a nic</i>	× 4637	<i>A "</i>	1-18	2-2	13-1	18-1	19-1						23	31	
3717	<i>A vis</i>	× 55701	<i>a un-t</i>	1-13	9-3									16	16	
4540	<i>A nic</i>	× 4637	<i>a vis</i>	1-15	3-1	4-1	7-1							18	33	
4637	<i>a vis</i>	× 5531	<i>A pan</i>	1-1	2-1	4-4	7-9	8-1	12-1	13-1	14-1			19	20	
4637	<i>A "</i>	× 9185	<i>a thi</i>	1-1	3-1	4-2	7-2							6	6	
4637	<i>a "</i>	× 10575	<i>A tryp</i>	2-2	4-4	5-1	7-6	8-1	12-1	29-1				16	18	
4637	<i>a "</i>	× 14789	<i>A nitr</i>	1-2	4-2	7-8	11-1	14-1	19-1	23-1				16	20	
4637	<i>a "</i>	× 16117	<i>A isol-val</i>	1-5	2-1	3-2	4-6	7-2	8-1	12-1	13-1	14-1				
				24-1										21	22	
4637	<i>A "</i>	× 21863	<i>a prol</i>	1-11	2-3	3-7	4-14	6-2	7-2	13-3	14-2	29-1	45	45		
4637	<i>A "</i>	× 33026	<i>a val</i>	1-7	3-1	4-4	6-1	7-1	13-3	14-2	29-1			20	20	
4637	<i>A "</i>	× 34486	<i>a chol</i>	1-5	4-4	6-1	7-8	9-1	16-1					20	20	
9460	<i>a "</i>	× 49001	<i>A pyr</i>	1-6	4-7	7-2	13-1	14-1						17	20	
15300	<i>A "</i>	× 38701	<i>A ad-p</i>	1-11	3-2	5-1	13-19	15-1	16-1	18-1	23-2			38	46	
28815	<i>A lys</i>	× 34508	<i>a vis</i>	1-6	2-1	3-2	19-8	20-2	24-1					20	23	
34508	<i>a vis</i>	× 37301	<i>A pyr</i>	1-2	3-1	7-3	14-4							10	10	
34508	<i>a "</i>	× 38620	<i>A phen</i>	1-5	4-5	6-1	7-1	13-3	14-1	19-2	20-1	21-1				
				24-1	29-1									22	24	
34547	<i>a nitr</i>	× 34547-10	<i>A tryp</i>	1-2	6-1	7-2	8-1	9-1	12-1	13-7	14-8	16-1			33	40
				17-1	18-1	22-1	23-1	24-2	25-2	29-1						
55701	<i>a un-t</i>	× 68902	<i>A pyr</i>	1-2	4-9	7-8	15-2	25-1						22	24	

456 521

Note: The number of the segregation type precedes the number of ascii of that type. Segregation type 1 represents ascii in which sex and both mutant genes segregated in the first division and there was no recombination. Type 2 represents those in which the three genes segregated in the first division but in which *y* and sex and *X* and sex recombined, etc., etc.

table 5) involving a given gene and no corrections were made. All of the genes which appear on the tentative map published earlier (BEADLE 1946) are listed here although in some cases linkage was shown by other workers at the Stanford laboratory, namely BELL, BUSS, DOERMANN, F. HUNGATE, REGNERY and SRB. Their data are not included here, but, when possible, references are given. When relative positions of genes are not indicated by the data presented here the order given is based simply on centromere distance. When numbers of mutants are indented under the number of another mutant with the same requirement this indicates that attempts to demonstrate non-allelism have, so far, been unsuccessful. A small "l" following the description of a mutant means that the mutant has been lost.

In only one case, that of the sex linkage group, do these data give evidence that any of the genes listed are on opposite sides of the centromere. In the sex group there is evidence, although in many cases it is based on rather limited data, that the genes are located in the arm in which they are listed. No crosses have been made between any of the mutants which appear in the same arm as sex. In the other arm, 3416 and 34547 are shown to be farther from the centromere than 4637. The data of M. HUNGATE (1945) indicate that 15300 is ge-

TABLE 3
Crosses showing segregation of two mutants.

TYPES OF SEGREGATION									
	X+	X	+y				Xy	X	++
1	X+	X+	+y	+y			Xy	Xy	++
2	Xy	Xy	++	++			X+	X+	+y
3	X+	Xy	++	+y			X+	Xy	+y
4	X+	++	Xy	+y			X+	++	+y
5	X+	+y	X+	+y			Xy	++	Xy
6	X+	+y	++	Xy			X+	+y	++
7	Xy	++	Xy	++			X+	+y	X+

STRAINS	TYPES OF SEGREGATION							TOTAL	NUMBER ISOLATED
	X+	X	+y	or	1	2	3		
Xy	X	++							
263	a pyr	X 4545	A lys	2	7	1		10	10
263	A "	X 44204	a pyro-p	24		6		30	40
263	a "	X 37815	A pyr-t	79	7	1	11	98	120
263	a "	X 67602	A pyr	52	9		5	66	70
1298	a "	X 4545	A lys		5			3	8
1633	a pab	X fluffy	A vis	1	2	6	4	1	2
1633	A "	X 45304	a tryp	2		1	6		1
3254	A ad	X 21863	a prol	7	4				11
3254	a "	X 16117	A isol-val	8	9	1	2		20
3254	a "	X 37401	A inos	7	4	8			19
3254	a "	X 38602	A phen	7		4		1	12
3254, 38701	A ad, ad-p	X Abbott 12	a Wild	8	11				19
3254	a ad	X 44206	A ad-t	4	12	4			20
3254, 44206	a ad, ad-t	X 1	A Wild	11	8	1			20
3254	a ad	X 45502	A pyr	10					10
3254	a "	X 51602	A ribo-t	17					20
3254	a "	X 66204	A un-t	14		5			19
3254	a "	X 70004	A ad-t	5	6	9			20
3254, 70004	a ad, ad-t	X 1	A Wild	6	8				14
3717	A vis	X 67602	a pyr	6	5	4	2	1	20
4545	A lys	X 37301	a "	2		1	4	2	9
4545, 37301	A lys, pyr	X Em. 8815-3	a Wild	2		4		1	9
4545	A lys	X 37815	a pyr-t		2	7	1		10
4545	a "	X 38502	A pyr		3	2	2	3	10
4545	a "	X 67602	A pyr	4		4			8
4637, 9185	a vis, thi	X 1	A Wild	6	6	3	2	2	20
5531	A pan	X 10575	a tryp	6	3	2	8		20
5531	A "	X 33933	a lys	5	9	1	10	3	38
5531	A "	X 34542	a chol	13		1	9		24
5531	A pan	X 37301	a pyr	7		4	4	1	18
5531	A "	X 37803	a pyro	15	1	1	17	13	49
5531	A "	X 37903	a chol	5				14	20
5531	A "	X 44101	a pyr	15			12	1	28
5531	a "	X 44104	a thr	9	5		5		19
5531	A "	X 45502	a pyr	27			2		30
5531	A "	X 47904	a chol	3	1	4	4	1	19
5801	a vis	X 21863	A prol	9		1			10
9185, 15300	A thi, vis	X Chilton	a Wild	2	5		2	3	12
9185	A thi	X 37803	a pyro	5	3	1	7		16
9460	a vis	X 47102	A pyr	4	10	1			15
9460	a "	X 63902	A "	3	8	6		1	20
9666	A meth	X 51602	A ribo-t	5	10		5		20
10575	A tryp	X 34508	a vis		3	13	3	2	23
15069	a lys	X 37301	A pyr	2	7	4		1	14

TABLE 3—(continued)

	STRAINS		TYPES OF SEGREGATION							TOTAL	NUMBER ISOLATED	
	X +	X +y	or	1	2	3	4	5	6	7		
	Xy	X ++										
15300	A vis	× 34508	a vis	19			13				32	36
15300	a "	× 34542	A chol	3	4	9	11	2	3	3	35	36
16117	a isol-val	× 33757	A leu	12	5		4	1			22	22
16117	A "	× 37401	a inos	9		7		4			20	20
16117	A "	× 39401	a nic-tryp	4	2	16		2	2		26	40
16117	a "	× 44206	A ad-t	7	11		2				20	20
16117	a "	× 45502	A pyr		7		1				8	20
16117	a "	× 47904	A chol	2	1	11	2		1		17	20
16117	A "	× 63904	a pyr	12	5	1	3			1	22	30
16117	a "	× 66204	A un-t	7	7	1	3		1		19	20
16117	A "	× 68305	a pyr	7	5	2	4		2		20	30
16117	A "	× As 7980-5	a vis	3	6	4	5		2		20	20
17084	a thi	× 37803	A pyro	4	9	3					16	20
17084	a "	× 44602	A "	8	2	7					17	20
20705	A ad	× 38709	a ad-p	3	4		1				8	10
20705, 38709	a ad, ad-p	× Abbott 4	A Wild	3	1		13				17	20
21863	a prol	× 34508	A vis	7	12	18	1	2	1		41	47
21863	a "	× 44206	A ad-t	20							20	20
21863	a "	× 47904	A chol	4		8		2	4		18	20
21863	A "	× 51602	a ribo-t	7	9		1	1			18	20
27663	A ad	× 38709	a ad-p	4	3		2				9	10
27663, 38709	a ad, ad-p	× Abbott 4	A Wild	3	2		15				20	20
27663	A od	× 44206	a ad-t	11				3			14	20
27663	a "	× 44206	A "	55				3			58	60
27663	a "	× 70004	A "	28				5			33	40
28610, 35203	a ad, ad-p	× Abbott 4	A Wild	7	3		7	2			19	20
28610	A "	× 44206	a ad-t	8	2	2	6				18	20
28610, 44206	A ad, ad-t	× 25	a Wild	9	6	2	3				20	20
28815	a lys	× 34508	A vis	5		2		4			11	22
33757	A leu	× 33933	a lys	8	3		4				15	45
33757	A "	× 37401	a inos	4	3	5	2				14	14
33757	a "	× 66204	A un-t	5	4	2	5				16	20
33933, 37301	A lys, pyr	× Em. 88153	a Wild	6	2		1				9	10
33933	A lys	× 44101	a pyr	8	7						15	20
34508	a vis	× 34542	A chol	3	5	3	9	1	4	3	28	34
34508	a "	× 34547	A nitr	5		1		4			10	10
34508	a "	× 35301	A ad	2	3	5	4	2	1		17	20
34508	A "	× 37401	a inos	1	1	4	8	1	3	2		20
34508, 83201	A vis, inos	× Em. 5297	a Wild	4	2	23	36	19	22	16	122	179
35203, 35301	a ad-p, ad	× Abbott 4	A "	11	3	2					16	20
35203, 44206	a ad-p, ad-t	× 1	A "	4	11	1					16	20
35203	a ad-p	× 44411	A ad		7	13				1	21	40
35203	a "	× 70004	A ad-t	5	5	6	1				17	40
35405	A pyro	× 37803	a pyro	42				5			47	50
35405	A "	× 39106	a pyro-p	18				2			20	20
35405	A "	× 39706	a "	17				3			20	20
35405	A "	× 44204	a "	14		1		5			20	20
35405	a "	× 44602	A "	15				2			17	20
35405	A "	× 44602	a "	17				3			20	20
35405	A "	× 46904	a "	20							20	20
36104	A meth	× 51602	a ribo-t	2	6		10		1	1		20
37301	A pyr	× 37401	a inos	1	1	6	6	2	2	2		20
37301	a "	× 37803	A pyro	31		1	7				39	40
37301	A "	× 37815	a pyr-t	18				18			36	40
37301	a "	× 37815	A "	33				7			40	40
37301	a "	× 38602	A phen	2	4	2	4	1			13	16
37301	A "	× 55701	a un-t	3	4	1	1				9	10
37301	a "	× 67602	A pyr	20				9			29	40
37401	a inos	× fluffy	A vis	1	2	5	7	1	2	2		20
37401	A inos	× 83201	a inos-t	10				10			20	20

TABLE 3—(continued)

	STRAINS	X+ X +y Xy X ++	or	TYPES OF SEGREGATION							TOTAL	NUMBER ISOLATED
				1	2	3	4	5	6	7		
37803	<i>a</i> <i>pyro</i>	X As-7980-5	<i>A</i> <i>vis</i>	4	2	3	6				15	20
37803	<i>A</i> "	X 39401	<i>a</i> <i>nic-tryp</i>	7	9	11	5				32	40
37803	<i>A</i> "	X 50005	<i>a</i> <i>thi</i>	6		7	3	4			20	20
37803	<i>a</i> "	X 51602	<i>A</i> <i>ribo-t</i>	4	5						9	20
37815, 38502	<i>A</i> <i>pyr-t</i> , <i>pyr</i>	X Em 8815-3	<i>a</i> <i>Wild</i>	4	1	5					10	10
37815	<i>A</i> <i>pyr-t</i>	X 44101	<i>a</i> <i>pyr</i>	15				2			17	20
37815	<i>a</i> "	X 67602	<i>A</i> "	26				5			31	41
37903	<i>a</i> <i>chol</i>	X 45502	<i>A</i> "	12			1	1	1		15	20
38502	<i>A</i> <i>pyr</i>	X 55701	<i>a</i> <i>un-t</i>	2	1	3	2		1		9	10
38502	<i>A</i> "	X 65001	<i>a</i> <i>nic-tryp</i>			3	6			1	10	10
39401	<i>a</i> <i>nic-tryp</i>	X 44101	<i>A</i> <i>pyr</i>	4	3		6				13	30
39401	<i>a</i> "	X 44206	<i>A</i> <i>ad-t</i>	2	2		9				13	18
39401	<i>a</i> "	X 51602	<i>A</i> <i>ribo-t</i>	6	5		3			1	15	15
44101	<i>A</i> <i>pyr</i>	X 44204	<i>a</i> <i>pyro-p</i>	14				5			19	20
44101	<i>a</i> "	X 66204	<i>A</i> <i>un-t</i>	1	5				2		8	20
44206, 44411	<i>A</i> <i>ad-t</i> , <i>ad</i>	X 25	<i>a</i> <i>Wild</i>	2		8	1	1			12	20
44206	<i>A</i> <i>ad-t</i>	X 45502	<i>a</i> <i>pyr</i>	4	7		9				20	20
44206	<i>A</i> "	X 70004	<i>a</i> <i>ad-t</i>	8		1		7			16	20
44206, 70004	<i>a</i> <i>ad-t</i> , <i>ad-t</i>	X 1	<i>A</i> <i>Wild</i>	21	1	2	4				28	40
44206	<i>A</i> <i>ad-t</i>	X 71104	<i>a</i> <i>ad</i>	9	9	1					19	20
44206, 71104	<i>A</i> <i>ad-t</i> , <i>ad</i>	X Abbott 12	<i>a</i> <i>Wild</i>	4	6	3	3				16	20
44411	<i>A</i> <i>ad</i>	X 70004	<i>a</i> <i>ad-t</i>	3		4	4	3		2	16	20
44411, 70004	<i>a</i> <i>ad</i> , <i>ad-t</i>	X 1	<i>A</i> <i>Wild</i>		1	6	8	1		1	17	20
47904	<i>a</i> <i>chol</i>	X 66204	<i>A</i> <i>un-t</i>	6		1	1				8	10
											2655	3164

netically different from 4637 and 34508, but the relative positions of these two loci are not known. DOERMANN'S (1946) work has shown 4545 to be more distant than 15300, while the work of BUSS (1945), DEROMEDI (whose data appear here) and SRB (1947) shows 35809, 38701 and 27947 to be nearer the centromere than 15300. As can be seen from table 5, 18558 shows linkage to 17084 and 56501, but there are no crosses from which its centromere distance can be calculated. In Group B 3254 is nearer the centromere than 66204 and 38602. There are no crosses which show other relative locations. In Group C BELL, F. HUNGATE and REGNERY have shown 5801, 33757, 10575 and 9185 to be located in the order given, while F. HUNGATE has shown that 605 is located between 5801 and 21863. The data given here show 5801 nearer than 21863, and 44206 nearer than 70004. In Group D the order is established by the data with three exceptions. The relative positions of 263 and the pyridoxin-less genes are not shown, nor is the position of 38502 relative to 5531, 9666 and 34486. BUSS (1944) has shown 9666 to be more distant than 37301 but its position relative to 34486 is not known. In Group E the data here show the order of 16117 and 37401 while BUSS (1944) has shown the position of 36104 relative to these two genes. Linkage of 33933 to 37401 was shown by CALHOUN (1945) in a cross from which spores were isolated at random. On the map previously published (BEADLE 1946) 33933 was placed on the opposite side of the centromere on the basis of the distance, obtained from this cross, between

the two genes, and the centromere distance of 37401. Genes for which no linkage has been observed are listed also, since some idea of their location relative to the centromere can be obtained from these data.

It will be seen that 45502 shows linkage to Group B as well as to Group D. This is explained by the fact, reported by McCLEINTOCK (1945) that this strain carries a translocation. McCLEINTOCK (1945) reported a translocation in strain 4637 also, and SINGLETON (1948) has studied these two, among others, both

TABLE 4
CROSSES SHOWING SEGREGATION OF ONE MUTANT.

MUTANT	WILD, OR OTHER STRAIN	SEGREGATION		TOTAL	NUMBER ISOLATED
		1ST DIVISION	2ND DIVISION		
C 84 <i>A hist</i>	× Em 8815-3 <i>a</i> Wild	7	3	10	10
1633 <i>A pab</i>	× Abbott 12 <i>a</i> "	8	27	35	41
3254 <i>a ad</i>	× Abbott 4 <i>A</i> "	18		18	20
3254 <i>A</i> "	× Chilton <i>a</i> "	26		26	30
4637 <i>a vis</i>	× Abbott 4 <i>A</i> "	43	1	44	50
5531 <i>A pan</i>	× peach <i>a vis</i>	9	8	17	20
5801 <i>A vis</i>	× Abbott 12 <i>a</i> wild	29	1	30	31
9185 <i>A thi</i>	× Em 5297 <i>a</i> Wild	104	28	132	180
9185 <i>A</i> "	× Abbott 12 <i>a</i> "	20	21	41	75
17084 <i>a</i> "	× Em 5256 <i>A</i> "	16	1	17	20
21863 <i>a prol</i>	× tuft <i>A vis</i>	17	3	20	24
34556 <i>A pan</i>	× Abbott 12 <i>a</i> Wild	9	6	15	20
37401 <i>A inos</i>	× peach <i>a vis</i>	12	8	20	20
37803 <i>A pyro</i>	× Abbott 12 <i>a</i> Wild	15	4	19	20
37815 <i>a pyr-t</i>	× Em 5256 <i>A</i> "	9	4	13	20
37903 <i>a chol</i>	× Abbott 4 <i>A</i> "	25	5	30	40
38502 <i>a pyr</i>	× 1 <i>A</i> "	11	25	36	40
39706 <i>A pyro-p</i>	× Chilton <i>a</i> "	6	1	7	20
39709 <i>A isol-val</i>	× Abbott 12 <i>a</i> "	9	3	12	20
44104 <i>A thr</i>	× Abbott 12 <i>a</i> "	8	8	16	18
44206 <i>a ad-t</i>	× peach <i>A vis</i>	35	4	39	40
44206 <i>A</i> "	× Abbott 12 <i>a</i> Wild	10		10	10
45208 <i>a un-t</i>	× Abbott 4 <i>A</i> "	6	3	9	20
46807 <i>A isol-val</i>	× Abbott 12 <i>a</i> "	11	3	14	20
47101 <i>a isol-val</i>	× 1 <i>A</i> "	18	2	20	20
48504 <i>A ad</i>	× 25 <i>a</i> "	12	8	20	20
55701 <i>a un-t</i>	× 1 <i>A</i> "	119	12	131	180
66702 <i>a suc</i>	× 1 <i>A</i> "	11		11	12
71103 <i>A un</i>	× Em 5297 <i>a</i> "	11	7	18	20
				830	1061

genetically and cytologically. The genetic behavior of 17084 and 27663 suggests the presence of chromosomal aberrations. The former behaves as an allele of 56501 but the two centromere distances differ widely. Also, both

TABLE 5

Crosses involving two mutants not distinguished from each other

Types of ascospores						NUMBER ISO- LATED			
	1	m	m	m	m				
	2	m	m	m	+				
	3	m	m	+	+				
263	<i>a pyr</i>	×	1298	<i>A pyr</i>	40	1	41	50	
263, 1298	<i>A pyr, pyr</i>	×	Abbott 12	<i>a Wild</i>	6	25	31	40	
263	<i>a pyr</i>	×	37301	<i>A pyr</i>	32	5	37	40	
263, 37301	<i>A pyr, pyr</i>	×	Abbott 12	<i>a Wild</i>	8	25	33	40	
263, 37815	<i>a pyr, pyr-t</i>	×	Abbott 4	<i>A "</i>	2	16	18	40	
263	<i>a pyr</i>	×	38502	<i>A pyr</i>	6	11	17	20	
263, 38502	<i>a pyr, pyr</i>	×	Abbott 4	<i>A Wild</i>	1	7	5	30	
263	<i>a pyr</i>	×	44101	<i>A pyr</i>	16		16	20	
263	<i>a "</i>	×	44302	<i>A "</i>	33	2	35	40	
263, 44302	<i>A pyr, pyr</i>	×	25	<i>a Wild</i>		15	15	20	
263	<i>a " "</i>	×	45502	<i>A pyr</i>	13		13	20	
263, 67602	<i>A " "</i>	×	Abbott 12	<i>a Wild</i>	2	26	28	40	
263	<i>A pyr</i>	×	67701	<i>a pyr</i>	50		50	60	
263	<i>a "</i>	×	67701	<i>A "</i>	31	1	32	40	
1298	<i>a "</i>	×	38502	<i>A "</i>	7	18	1	26	30
3254	<i>a ad</i>	×	20705	<i>A ad</i>	3	5	9	17	20
3254	<i>a ad</i>	×	27663	<i>A "</i>	5	3	7	15	20
3254	<i>a "</i>	×	28610	<i>A "</i>	2	8	5	15	20
3254	<i>a "</i>	×	35301	<i>A "</i>	5	11		16	20
3254	<i>a "</i>	×	44206	<i>A ad-t</i>	8	1	4	13	20
3254	<i>A "</i>	×	44411	<i>a ad</i>	4	5	1	10	20
3254	<i>a "</i>	×	44411	<i>A "</i>	4	14	1	19	20
3254	<i>A "</i>	×	44415	<i>a ad-t</i>	6	3	8	17	20
3254	<i>A "</i>	×	71104	<i>a ad</i>	11	1	8	20	20
3416	<i>A nic</i>	×	39303	<i>a nic</i>	4	7	2	13	40
4540	<i>a "</i>	×	39113	<i>A "</i>	1	3	1	5	20
9185	<i>A thi</i>	×	17084	<i>a thi</i>	7	3	3	13	20
9185	<i>a "</i>	×	18558	<i>A "</i>	6	7	5	18	22
9185	<i>A "</i>	×	50005	<i>a "</i>	5	18	6	29	40
9185	<i>A "</i>	×	56501	<i>a "</i>	3	18	3	24	40
9185	<i>A "</i>	×	85902	<i>a "</i>	13	3	1	17	20
14789	<i>A nitr.</i>	×	34547	<i>a nitr.</i>	3	11	6	20	20
14789, 34547	<i>a "</i>	×	Em 5256	<i>A Wild</i>	10	19		29	40
16117	<i>A isol-val</i>	×	35810	<i>A isol-val</i>	20			20	20
16117	<i>A " "</i>	×	39709	<i>a " "</i>	37	1		38	40
16117	<i>a " "</i>	×	39709	<i>A " "</i>	9		1	10	20
16117	<i>a " "</i>	×	46807	<i>A " "</i>	10	1		11	20
17084	<i>a thi</i>	×	18558	<i>A thi</i>	17			17	20

TABLE 5—(continued)

	STRAINS		TYPES OF ASCI			TOTAL	NUMBER ISO- LATED	
			1	2	3			
17084	<i>A</i> "	× 50005	<i>a</i> "	6	20	3	29	30
17084	<i>A</i> "	× 56501	<i>a</i> "	17			17	20
18558	<i>A</i> "	× 50005	<i>a</i> "	5	10	5	20	20
18558	<i>A</i> "	× 56501	<i>a</i> "	1	9		10	20
20705	<i>A ad</i>	× 28610	<i>a ad</i>	3	5	7	15	20
20705	<i>a ad-</i>	× 35301	<i>A ad</i>	1	3	1	5	20
20705	<i>a</i> "	× 44411	<i>A</i> "	6	12	3	21	40
20705	<i>A</i> "	× 46705	<i>a</i> "	3	5	7	15	20
21863	<i>a prol</i>	× 46407	<i>A prol</i>	6	3	6	15	20
21863, 46407	<i>A prol, prol</i>	× Abbott 12	<i>a Wild</i>	1	5		6	20
27663	<i>A ad</i>	× 28610	<i>a ad</i>	2	3	3	8	20
27663	<i>a</i> "	× 35301	<i>A</i> "		4		4	10
27663	<i>A</i> "	× 44411	<i>a</i> "	4	7	2	13	20
27663	<i>A</i> "	× 71104	<i>a</i> "	4	6	5	15	20
27663, 71104	<i>A ad, ad</i>	× Abbott 12	<i>a Wild</i>	2	13		15	20
28610	<i>A ad</i>	× 44411	<i>a ad</i>	4	8	2	14	20
28610	<i>A</i> "	× 71104	<i>a</i> "	4	1	7	12	20
34486	<i>A chol</i>	× 34542	<i>a chol</i>	18			18	24
34486	<i>a</i> "	× 47904	<i>A</i> "	3	11	1	15	30
34486	<i>a</i> "	× 66210	<i>A</i> "	3	4	4	11	20
34542	<i>A</i> "	× 37903	<i>a</i> "	18			18	20
34542	<i>A</i> "	× 47904	<i>a</i> "	3	15	2	20	20
35301	<i>a ad</i>	× 44411	<i>A ad</i>	3	7	3	13	20
35405	<i>A pyro</i>	× 44204	<i>a pyro-p</i>	25			25	40
37301	<i>A pyr</i>	× 38502	<i>a pyr</i>	7	11		18	40
37401	<i>A inos</i>	× 83201	<i>a inos-t</i>	19			19	20
37815	<i>a pyr-t</i>	× 38502	<i>A pyr</i>	12	5	1	18	20
37815, 38502	<i>A pyr-t, pyr</i>	× Chilton	<i>a Wild</i>	1	8	1	10	10
37815	<i>a pyr-t</i>	× 67602	<i>A pyr</i>	73			73	100
38502	<i>a pyr</i>	× 67602	<i>A pyr</i>	15	7		22	40
38502, 67602	<i>a pyr, pyr</i>	× 1	<i>A Wild</i>		4	2	6	10
39113	<i>A nic</i>	× 39401	<i>a nic-tryp</i>			5	5	9
39303	<i>a</i> "	× 39401	<i>A</i> "	1	5	15	21	40
39401	<i>a nic-tryp</i>	× 43002	<i>A nic</i>	10	14	13	37	50
44101	<i>a pyr</i>	× 67602	<i>A pyr</i>	9			9	20
44206	<i>A ad-t</i>	× 66204	<i>a un-t</i>	7	4	6	17	20
44409	<i>A un-t</i>	× 45208	<i>a</i> "	4	15	1	20	20
44409	<i>a</i> "	× 46006	<i>A</i> "	20			20	20
44411	<i>A ad</i>	× 71104	<i>a ad</i>	4	10	4	18	20
46407	<i>a prol</i>	× 51505	<i>A prol</i>	15			15	20
47904	<i>a chol</i>	× 66210	<i>A chol</i>	7			7	20
50005	<i>a thi</i>	× 56501	<i>A thi</i>	7	13	8	28	30
55701, 66204	<i>a un-t, un-t</i>	× 1	<i>A Wild</i>	7	4	4	15	20
66204	<i>A un-t</i>	× 83106	<i>a un-t</i>	10	7	2	19	20
70004	<i>A ad-t</i>	× 71104	<i>a ad</i>	4	3	2	8	20

TABLE 6
Linkage group and centromere distance.

GROUP	MUTANT	NUMBER OF CROSSES	NUMBER OF ASCI	CENTRO-MERE DISTANCE	LINKAGE FIRST DEMONSTRATED BY
A	sex	88	1811	5.80	
	39311 <i>suc</i>	1	18	5.6	
	55701 <i>un-t</i>	5	216	4.9	
	71104 <i>ad</i>	3	55	4.5	
	15069 <i>lys</i>	1	14	3.6	DOERMANN (1946)
	4540 <i>nic</i>	1	18	0	
	39303 "	1	20	0	
	43002 "	1	19	0	
Centromere					
	35203 <i>ad-p</i>	5	89	2.1	
	38701 "	2	57	1.8	
	38709 "	4	54	0	
	9460 <i>vis</i> (1)	4	55	2.6	
	35402 <i>suc</i>	1	18	0	
	37602 "	1	19	2.8	
	39404 "	1	19	2.5	
	47807 "	1	19	7.5	
	66702 "	1	19	0	
	3717 <i>vis</i>	2	36	6.9	
	44409 <i>un-t</i>	1	20	10	
	46006 "	1	18	0	
	46403 <i>un</i>	1	19	16	
	17084 <i>thi</i>	3	50	1.0	
	56501 "	1	15	27	
	15300 <i>vis</i>	6	191	24.6	
	4637 "	16	342	4.97	
	34508 "	13	392	29.84	
	3416 <i>nic</i>	1	23	6.5	
	39113 "				
	34547 <i>nitr</i>	4	108	27.7	
	4545 <i>lys</i>	6	64	37.5	DOERMANN (1946)
	28815 "	2	31	24.2	
	18558 <i>thi</i>				
	27947 <i>arg</i>				SRB (1947)
	35809 <i>meth</i>				BUSS (1944)
B	3254 <i>ad</i>	15	266	0.56	
	45502 <i>pyr</i>	6	104	0.96	
	51602 <i>ribo-t</i>	7	111	1.7	
	66204 <i>un-t</i>	6	86	6.97	
	38602 <i>phen</i> (1)	3	47	4.8	
C	85902 <i>thi</i>	1	37	0	
	5801 <i>vis</i>	2	40	1.2	REGNERY (1947)
	21863 <i>prol</i>	8	183	5.19	
	44206 <i>ad-t</i>	19	399	5.64	
	44415 "				

TABLE 6—(continued)

GROUP	MUTANT	NUMBER OF CROSSES	NUMBER OF ASCI	CENTRO- MERE DISTANCE	LINKAGE FIRST DEMONSTRATED BY
	33757 <i>leu</i>	4	67	8.95	REGNERY (1947)
	10575 <i>tryp</i>	3	59	15.2	F. HUNGATE (1946)
	9185 <i>thi</i>	6	227	16.3	BELL (unpublished) & F. HUNGATE (1946)
	20705 <i>ad</i>	3	49	27.6	
	27663 "	6	152	11.2	
	70004 <i>ad-t</i>	9	173	18.2	
	605 <i>ser</i>				F. HUNGATE (1946)
D	263 <i>pyr</i>	5	227	5.72	
	35405 <i>pyro</i>	8	182	6.86	
	37803 "	10	262	10.3	
	39106 <i>pyro-p</i>	2	30	3.3	
	39706 "	2	27	7.4	
	44602 "	4	70	11.4	
	46904 "	2	30	1.6	
	44204 "	4	80	10.5	
	1298 <i>pyr</i>	2	27	14.8	
	37301 "	11	234	15.8	
	37815 <i>pyr-t</i>	8	255	11.2	
	44101 <i>pyr</i>	7	118	4.7	
	44302 "	1	18	5.5	
	45502 "	6	104	0.96	
	67602 "	6	171	10.5	
	67701 "	1	16	6.2	
	9666 <i>meth</i>	1	20	12.5	BUSS (1944)
	34486 <i>chol</i>	1	20	22.5	
	34542 "	4	119	25.2	
	37903 "	2	49	19.4	
	5531 <i>pan</i>	11	257	26.2	
	34556 "	1	15	20	
	38502 <i>pyr</i>	6	94	31.4	
E	33933 <i>lys</i>	3	52	4.8	GRANT (CALHOUN) (1945)
	16117 <i>isol-val</i>	12	235	8.9	
	47101 " "	1	20	5	
	35810 " "	1	18	8.3	
	39709 " "	1	12	12	
	46807 " "	1	14	10.7	
	36104 <i>meth</i>	1	20	30	BUSS (1944)
	37401 <i>inos</i>	9	196	22.7	
	83201 <i>inos-t</i>	2	142	31.7	
F	E15172 <i>sfo</i>				S. EMERSON unpublished
Unknown	C84 <i>hist</i>	1	10	15	
	517 <i>fut (1)</i>	1	23	2.2	
	1633 <i>pab</i>	4	81	29.6	
	1752 <i>fut (1)</i>	1	13	34.6	
	14789 <i>nitr</i>	1	15	33	

TABLE 6—(continued)

GROUP	MUTANT	NUMBER OF CROSSES	NUMBER OF ASCI	CENTRO- MERE DISTANCE	LINKAGE FIRST DEMONSTRATED BY
28610	<i>ad</i>	4	81	14.2	
28815	"	1	18	33	
32213	<i>un-t</i>	1	18	36	
33026	<i>val</i>	1	20	5	
34547-10	<i>tryp</i>	1	33	18.1	
35301	<i>ad</i>	2	33	15.2	
39401	<i>nic-tryp</i>	6	118	23.3	
40008	<i>tryp</i>	1	14	14.3	
44008	"	1	18	11.1	
44104	<i>thr</i>	2	35	18.5	
44411	<i>ad</i>	5	85	34.1	
44504	<i>pyr</i>	1	22	6.8	
44601	<i>un</i>	1	21	0	
45004	<i>ad</i>	1	20	20	
45208	<i>un-t</i>	2	18	30	
45304	<i>tryp</i>	2	43	9.3	
45612	<i>un</i>	1	19	2.6	
46407	<i>prol</i>	1	15	23	
51505	"	1	16	28	
46705	<i>ad</i>	1	16	25	
47102	<i>pyr</i>	1	15	3.3	
47305	<i>un-t</i>	1	18	27	
47904	<i>chol</i>	5	71	31.3	
66210	"	1	15	36.6	
48504	<i>ad</i>	1	20	20	
49001	<i>pyr</i>	1	17	5.8	
50005	<i>thi</i>	1	20	27.5	
63902	<i>pyr</i>	1	18	19.4	
63904	"	2	43	14	
68305	"	1	20	10	
68902	"	1	22	20.4	
71103	<i>un</i>	1	18	19.4	
75001	<i>tryp</i>	1	19	13.1	
83106	<i>un-t</i>	1	18	13.8	

Note: The data referred to, of BELL, BUSS, DOERMANN, GRANT, HUNGATE, REGNERY and SRB, are not included here.

17084 and 56501 show linkage to 18558 but in the case of 17084 much closer linkage is indicated. The two adenineless strains 27663 and 70004 behave as alleles, but 27663 shows much closer linkage to 44206 (the only crossovers observed were among random spore isolations) than does 70004.

Attempts to correlate LINDEGREN'S (1939) Group II with these linkage groups were not successful, possibly because the medium used was apparently not suitable for classification of most of the LINDEGREN mutants which were tried. *Fluffy* was used successfully but no linkage to the biochemical mutants

crossed to it was observed. Since it is not known whether any of the linkage groups which appear here correspond to LINDEGREN's chromosome II, letters rather than numbers have been used as designations. Group A corresponds to LINDEGREN's (1936) chromosome I. Group C was established by F. HUNGATE and REGNERY and is referred to by HUNGATE (1946) as chromosome III.

Genetic data which have appeared in earlier publications of the authors, and in the unpublished M.A. dissertation (Stanford University) of HOULAHAN, are included here.

SUMMARY

Data are presented from 330 crosses involving 118 mutants of *Neurospora crassa*. Spores were isolated, in order, from 8,549 asci, and in 6,905 of these germination was sufficiently complete to allow classification. Types of segregation observed are tabulated for each cross. Sixty-nine genes, representing at least 35 different loci, have been placed in linkage groups of which five are represented.

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