Diploid studies: The preceding evidence points to a chromosomal localization of the Lp lysogenicity determinant closely linked to a series of Gal loci. Evidence for the segregation of a prophage linked to the Gal_4 locus ruled out the possibility of a random distribution of cytoplasmic particles in cells carrying λ(10). These observations have since been extended to Gal_2 and Gal_4 hybrids (all heterozygous Lp^+/s), and also $Gal_4^+Lp^+/Gal_4^-Lp^r$ diploids (table 10). A study of such diploids segregating out distinguishable λ types is in preparation. Preliminary evidence also has been obtained elsewhere from crosses with lysogenic parents, one carrying a mutant λ (or one "doubly lysogenic") the other doubly sensitive, which yielded Gal/Lp progeny in parental couplings (1).

The mutational independence of Gal and Lp was also examined in the doubly homozygous diploid. Comparable experiments with the closely-Lac_1 and V_6 loci have already been reported. Lac^+ reversions were selected in $Lac^-V_6^r/Lac^-V_6^s$ diploids. The resulting doubly heterozygous diploids were of two types: $Lac^+V_6^r/Lac^-V_6^s$ and $Lac^-V_6^r/Lac^+V_6^s$, and with equal frequency (11).

A double homozygote $Gal_2^+Lp^s/Gal_2^-Lp^s$, also segregating a few other markers, (and unfortunately also Lp_2) was prepared by stepwise exposure of

the double heterozygote to U-V (14) and the isolation of suitable "reorganized" diploids. The resulting diploid, H-331 was infected with λ. Several $Gal_2^-Lp^+/Gal_2^-Lps$ isolations, A to G, were then allowed to papillate on EMS galactose agar. Independently occurring Gal^+ were selected, and the segregation pattern of Lp and Gal_2 of the resulting double heterozygotes was tested. The incidence of mutation to Gal^+ on the Lp^+ chromosome (coupling phase, or cis configuration) was compared with that on the Lp^s chromosome (repulsion phase, or trans-configuration). The analysis included a single Gal^+ and a single Gal^- segregant from a large number of diploids, (pair analysis) and the examination of many segregants from a single mass diploid culture (random analysis). From diploid B, 5 cis configurations and 6 trans configurations were scored. The conclusion from this evidence (table 11) is that the condition of the Lp locus, whether lysogenic or sensitive, has no significant bearing on which one of the 2 Gal^- alleles will mutate to Gal^+. (These preliminary data will be expanded, and also extended to a corresponding study of diploids first made heterozygous $Gal_2^-Lp^s/Gal_2^+Lp^s$, and then infected with λ.)

The above studies provide two kinds of Lp^+/Lp^s; Gal^+/Gal^- diploids: λ coupled on the one hand with Gal^+ (cis) and on the other, with Gal_2^- (trans) If the activity of from "trans" bacteria is confined to non Gal_2^- recipient cells, a chromosomal but not nuclear limitation to λ specificity is indicated. All Gal^- including Gal_2^- is expected to respond to cis λ. A difference in λ from these diploids which are phenotypically identical, and genetically identical except for the arrangement of component parts established a "position effect." So far, only λ from the trans-type diploid has been prepared. Table shows that while Gal_4^- ($Gal_2^+Gal_4^-$) cells are subject to transduction, only rare Gal_2^+ transductions were recovered. The development of an adequate diploid culture to satisfy the nutritional prerequisites for U-V induction in K-12 (3,5) and an intermediate growth period necessarily permits some selection for haploid segregants. The yield of λ obtained very probably includes a limited portion derived from $Gal_2^-Lp^+$ and $Gal_2^+Lp^+$ haploids. The latter crossover types may account for those transductions which were found. The data so far allow the tentative conclusion of a position effect hypothesis and strengthen the concept of an intimate relationship of λ and Gal at a specific action site on the chromosome. Transductions of the double homozygote H-331 and lysogenic

derivatives has apparently been obtained. The analysis is complicated by the fact that diploid-haploid instability can be confounded with transduction instability.

COMPARATIVE GENETICS OF Lp AND Gal IN OTHER LINES

Among the independently isolated crossable strains of E. coli (12) the wild type of three lines (28,47, and 51) were sensitive to λ carried by line 1. A fourth, line 31, threw off rough variants which were all λ sensitive. These strains occurred in nature as F^- but could be altered to F^+ by growth with K-12 or suitable derivatives. So far, at least one Gal^- mutant is subject to transduction. Preliminary intra-line-47 crosses established an Lp locus like that of K-12, and a Gal-Lp linkage. Very little mapping work has been completed among these strain, and the emphasis so far in these studies has been the genetic behavior of λ in outcrosses with K-12.

Sensitives of each line are readily lysogenized by K-12 λ but these lysogenics show a reduction of eop on K-12 sensitive indicators. This system is entirely analagous to host modification demonstrated for T2 (19) and λ produced by strain C (2). The terminology established for these systems will be used to describe the properties of our strains.

Thus lines 28,31, and 47 can be designated as λ* lysogenic or λ* sensitive. Line 1 sensitives are more resistant to λ* than to type λ. λ* can be introduced at low rates into λ sensitive hosts, but normal rather than λ* is recovered. Similarly, normal λ is converted to λ* after a single passage in λ* sensitive hosts. The four phenotypes are readily distinguishable in cross-brush tests as follows:

Example	Type	Reaction with: λ-sens. C bacteria	λ*-sens. B bacteria	λ	λ*
line 1 lysogenic	A	+	+	R	R
line 47 sensitive	B	-	-	S	S
line 1 sensitive	C	-	-	S	R
line 47 lysogenic	D	-	+	R	R

+/- = lysogenic or not; R/S = resistant or sensitive

Two major hypotheses can be tested by intercrossing these types:

I Lp controls all reactions: the types A-D are determined at a single locus.

II Lp controls lysogenicity/ sensitivity; another locus, Mp, controls resistance or sensitivity to λ*.

(a) Both λ and λ* are fixed at Lp in phenotypes A and D.

(b) λ is fixed at Lp in type A; λ* is fixed at Mp in type D.

The consequences of these hypotheses are shown in table 12. The critical crosses for I and II are A x B and C x D. The only decisive cross for II a vs. II b is A x D. II b would be favored by the recovery of sensitive recombinants as well as a novel genotype whose phenotypic effects are unpredictable. Since there is a possibility that Lp and Mp are closely linked a large sample of progeny many be required. One must bear in mind, in reviewing these intercross data that the prototrophs represent recombination of as yet unmapped nutritional factors. In addition, chromosome and other irregularities correlated with interstrain hybrids have not been analysed.

Effective transductions have been achieved in these strains. Gal-in lines 47 and 31 have been used as recipients, for λ produced by line 1, 28, 31, and 47. A reduction in the effectiveness of transduction to line 1 recipients is parallel with the reduced effectiveness of lysogenization. In general no important differences with the K-12 mechanism have been demonstrated. Hypothesis II b is doubtful.so far. The differentiation of the λ* of different lines is still to be tested. A single intercross shows no genetic difference so far.

In preparing this report, it has been necessary to make numerous references to the unpublished work carried on in this laboratory by Professor J. Lederberg, Mr. M. L. Morse, and others, under other auspices. These are cited by number to the bibliography.

Table 1

Characteristics of F (compatibility factor) and λ (virus)

Criterion	F status	λ (effects)
(1) Yield of recombinants	Decisive	None
(2) Type of recombinants	Decisive	None
(3) Transmission to recombinants	100%	Segregated according to linkage with selected nutritional markers; behaves as a genetic locus.
(4) Transmission by infection	Rapid and fixed	Results in mixed clones (3).
(5) Cell-free preparations	Not yet accomplished	Easily filtered.
(6) Effect of antiserum	Slight if any	Blocks adsorption
(7) Role in Gal^+ transduction	None	Decisive

Table 2

The Effect of λ on % Gal^- Progeny

M^-Gal^- parent x	$T^-L^-Th^-Gal^+$ parent lysogenic	immune
lysogenic	8.0	7.1
immune	6.3	6.3
sensitive	6.7	10.1

Table 3

Linkage of Gal, Lp, and Hfr

W-1895 x W-2308

Part A:

Genotypes recovered[1]			Total
Gal	Lp	F	
+	+	+	14 *
−	s	−	29 *
+	s	+	5
−	+	−	0
+	s	−	4
−	+	+	0

Part B: 2 x 2 contingencies

	Gal^+	Gal^-	Total	F^+	F^-	Total
F^+	20*	0	20			
F^-	9	31*	40			
Lp^+	15*	0	15	13*	5	18
Lp^s	11	29*	40	6	33*	39
Lac^+	26*	5	31	22*	9	31
Lac^-	4	26*	30	7	27*	34
V_1^r	1*	9	10	1*	9	10
V_1^s	28	21*	49	23	20*	43
Xyl_2^+	9*	1	10	7*	2	9
Xyl_2^-	20	30*	50	16	7*	23

* Parental combination

1 Selected as Gal^+ and Gal^- prototrophs.

Table 4

Lysogenization in Transduced and Nontransduced Lp^s

Part A: Gal^+ and Gal^- from single papillae

Gal^+/Gal^- Pair type	Number
Lp^+/Lp^+	13
Lp^+/Lp^s	15
Lp^s/Lp^+	3
Lp^s/Lp^s	2
Lp^r/Lp^s	2
% Gal^+ sensitive	15.2
% Gal- sensitive	47.2

	Gal^- Lp^s	Gal^- Lp^+
Gal^+ Lp^s	2	3
Gal^+ Lp^+	17	13

Part B: Lysogenization of transduced and inserted Gal^+

Lp^s strains	Av. No. Gal^+ recovered Control	Treated*	Types in mixture	No. tested	% lysogenic
Gal^+Lac^+	109	92	Gal^+Lac^+ (inserts)	46	68.5
Gal^-Lac^-	11**	432	Gal^-Lac^- (original)	40	72.5
Mixture***	106.5	419	Gal^+Lac^- (transductions)	103	100.

* 10^9

** Spontaneous reversions per 10^8 inoculum

*** 10^8 Gal^-Lac^- and 109 Gal^+Lac^+.

Table 5

Transductions to Gal_4^- Immune-I: Segregation Patterns

Exp. 385: Strain 1924: 27 Gal^+

Colony generation	Number lysogenic (lys)	Number semilysogenic (semi)	Number nonlysogenic (non)
	1 #24	1 #7	25 #1
L	1 Gal^- non : 19 Gal^+ lys : 4 Gal^- lys	18 non (Gal^+ and Gal^-) / 1 Gal^+ semi	1 Gal^+ semi / 18 Gal^- and Gal^+ non
II	Gal^- non : Gal^+ lys : Gal^- non / Gal^- lys	2 Gal^+ lys / 2 Gal^- non / 19 Gal^+ non	2 Gal^+ lys / 2 Gal^- non / 19 Gal^+ non
III	Gal^+ lys / Gal^- non / 43 lys / 3 non / 1 semi		
IV	lys / non		
V	lys / non / non		
VI	lys / non		

Exp. 431: Strain 2110: 38 Gal^+: 28 non, 1 semi (#23), and 9 lys

Segregation patterns of lys	all Gal^+ lys, all Gal^- non: 2
	all Gal^+ lys, all Gal^- lys: 5
	all Gal^+ lys, Gal^- lys and non 2
	both Gal^+ and Gal^- non: #23

Table 6

Survival and Transduction with Irradiated λ

	No phage	Untreated phage	U-V[1]	X-ray[2] (x 10^3 r) 50	100	150	200
Av. plaques/ml x 10^5	0	127,000	16.9	41,667	3,975	377	100
% survival	-	100	0.013	32.8	3.13	0.297	0.008
Lp^S bacteria							
No. Gal^+ papillae	20	1,000	170	250	85	30	30
% " "	0.5	100	34	25	17	6	6
Lp^r bacteria							
No. Gal^+ papillae	39	60	-	135	115	31	20
% " "	65	100		225	191.7	5.2	3.3

1 20 minutes, sterilamp

2 10^3 r/min. at 250 K.V., courtesy A. Novick, Radiobiology Inst., U. of Chicago.

Table 7

Segregation of Gal, Lp,... diploids

A. H-324 Segregation of Lp_2, B_1, not tabulated.							B. H-325 Segregation of V_6, Mtl, Lp_2, B_1 not tabulated.	
Gal_2-	Gal_2+	Lp	Mal	Xyl	M	T,L	Gal_1-	Gal_1+
1	47	+	+	+	-	-	1	49
0	1	+	+	-	-	-	0	0
0	1	+	+	+	-	+	2	0
0	0	+	+	+	+	-	0	1
1	0	+	+	+	+	+	0	0
2	0	+	+	-	+	+	0	0
25	0	s	-	-	+	+	13	0
9	1	s	+	+	-	-	13	1
3	0	s	-	-	-	-	0	0
6	0	s	+	+	-	+	7	0
1	0	s	-	+	+	+	0	0
2	0	s	+	+	+	+	3	0
0	0	s	-	-	-	+	12	0
50	50	Total tested					51	51

Table 8

Allelic Specificity of the Gal - λ Transduction at the Gal 1, Gal 2, and Gal 4 loci.

λ- donor bacteria			Recipient cells		
Gal 1	Gal 2	Gal 4	1-2+4+	1+2-4+	1+2+4-
+	+	+	+	+	+
-	+	+	-	+	+
+	-	+	+	-	+
+	+	-	+	+	-
diploids:					
+	-	+ Lp^+	No data	± (21)*	+ (300)*
+	+	+ Lp^s (trans)			
+	+	+ Lp^+ (cis)		No data	
+	-	+ Lp^s			

* Gal + papillae per 10^9 λ

Table 9

Summary of Current Allelism Tests

Exp. No.	Gal^- type	F^- parent	F^+ parent	Total** progeny	No. Gal^+	Maxim., % Gal+
535*	1 x 4	W-750 Lp^+	W-2234 Lp^s	5000	17	0.3
563*				2000	15	0.75
534*	2 x 4	W-1210 Lp^+	W-2234 Lp^s	6000	25	0.4
563*				1600	11	0.68
580*				2400	8	0.3
535	4 x 3	W-518 Lp^s	W-2315 Lp^+	807	6	0.74
582	4 x ?3	W-518 Lp^s	W-2315 Lp^s	5000	0	0
				6700	5	0.06
583	1 x ?	W-2291 Lp^s	W-583 Lp^+	7603	2	0.026

* All Gal^+ recombinants in these experiments are Lp^s.

**Estimated total.

Table 10

Behavior of Gal and Lp in Lac +/- Diploids

Type of cross		Parents: F	(T L Th)	M	Lac_1	Lac_4	Gal_1	Gal_4	Lp	Diploid progeny: Gal	Lp
1. Het diploids	(a)(Het)	+	-	+	+	+	+	+	+	+/-	+/• or -/• 1/ 5/
		+	+	-	-	+	+	-	s		
	(b)(Het)	+	-	+	+	+	+	+	+	+/• or -/•	not segregating
		+	+	-	-	+	-	+	+		
2. Lacl- x Lac_4-	(a)	-	-	+	+	-	+	+	+	Mostly +/•	Mostly +/• 2/
		+	+	-	-	+	+	-	s		
	(b)	+	-	+	+	-	+	+	+	Mostly -/•	Mostly s/• 2/
		-	+	-	-	+	+	-	s		
3. Haploid x auxotrophic diploid	(a)	- 4/	-/•	+/-	+/-	-/+	+	+/•	+/•	$Gal^+ Lp^+$ / Gal-Lp^s (linked) 3/	
		+	+	-	-	+	+	-	s		
	(b)	same, except M- parent is Lp^r								$Gal^+ Lp^+$ / Gal-Lp^r (linked)	

1/ In Het crosses, Lp does not segregate. Gal 1 and Gal 4, two closely linked loci also differ: Gal 4 segregates, but Gal 1 does not.

2/ Diploids resulting from delayed disjunction revealed by heterozygotes of two Lac pseudoalleles show no segregation of Gal or Lp. Reversal of F status reverses the polarity of the Gal, Lp segregation.

3/ The only successful demonstration of heterozygosity of Gal and Lp.

4/ Aeration phenocopy.

5/ +/• indicates purity for +, whether hemizygous or homozygous.

Table 11

Segregation Patterns of Gal^+ Reversions in $Gal_2^-Lp^s/Gal_2^-Lp^+$ Diploids

Diploid number	Total segregants	Gal^+		Gal^-		Gal^+		Gal^-		Gal^+		Gal^-		Inferred type of diploid
		Lp^+	Lp^s	Lp^+	Lp^s	Lp_2^r	Lp_2^s	Lp_2^r	Lp_2^s	Mal^+	Mal^-	Mal^+	Mal^-	
A 1	161	76	6	3	76	45	0	39	0	1	53	17	36	cis
B 1	121	2	58	60	1	52	8	60	1	38	22	61	0	trans
B 2	73	0	40	41	0	32	7	31	0	33	7	33	0	trans
B 3	76	61	4	1	10	65	0	57	5	65	0	44	18	cis
C 1	48	1	23	24	0	23	1	24	0	9	15	24	0	trans
E 1	60	30	0	3	27	26	4	24	6	30	0	16	14	cis
E 2	24	0	12	12	0	12	0	12	0	6	6	12	0	trans
E 3	23	12	0	0	11	12	0	11	0	12	0	3	8	cis
F 1	66	32	1	2	31	31	2	30	3	32	1	21	12	cis
F 2	40	20	0	1	19	20	0	20	0	20	0	7	13	cis
F 3	23	12	0	0	11	12	0	10	1	12	0	3	8	cis
F 4	18	11	0	1	6	10	1	0	7	11	0	7	0	cis

Table 12

Genetic Determination of Host Modification: line 1 lines 28, 31, 47

		Genotypes Under				
		Hypothesis I Lp locus with alleles	Hypothesis IIa fixed at Lp, modified by Mp		Hypothesis IIb fixed at Lp in line 1, at Mp in other lines	
Phenotypes	Symbol	Lp	Lp	Mp	Lp	Mp
lysogenic	A	+	+	r	+	r
sensitive*	B	s*	s	s	s	s
sensitive	C	s	s	r	s	r
lysogenic*	D	+*	+	s	s	+
A X B		None	C, D		C, D	
B X C		None	None		None	
C X D		None	A, B		A, B	
A X D		None	None		B and Lp^+Mp^+	

EXPTL. RESULTS:	Lines crossed	Type	A	B	C	D	Gal char.
Expt. No. 419	1 x 28	A Gal^- x <u>B</u>	0	46	1	0	+
			18	0	0	0	-
		C Gal^- x <u>D</u>	0	0	0	34	+
			2	8	18	3	-
418	1 x 31	A Gal^- x <u>B</u>	3	43	26	1	No record
420		A Gal^- x <u>B</u>	4	22	28	12	Gal^+ only
423		A Gal^- x <u>B</u>	8	2	1	37	+
			0	1	0	0	-
423		C x <u>D</u> Gal^-	28	1	3	0	(and 28 Lp_2^r) B or C
444		C Gal^- x D	2	2	19	0	mostly Gal^-
502		B Gal^- x C	0	15	13	0	+
			0	13	68	0	-
443	31 x 31	B x A	0	26	0	1	
468	1 x 47	A x <u>B</u> Gal^-	51	0	0	6	+
			0	2	2	3	-
527		<u>A</u> Gal^- x B	4	7	1	9	+
			41	0	0	2	-
528		B x <u>C</u> Gal^-	0	13	17	0	+
			0	8	24	0	-
529		<u>C</u> Gal^- x D	3	2	2	21	+
			2	2	28	0	-
523		<u>A</u> Gal^- x D	8	0	0	52	+
			37	0	0	19	-

F^- parent underlined.

Table 13

Genetic Control of the Semiresistant Phenotypes:

Nonlysogenic (W-2147) and Lysogenic (W-2172)

Part I

Hypothesis I: A new allele at Lp_2:				Hypothesis II: A 3rd locus, Lp_3, is involved:		
Phenotype symbol	Lp_1	Lp_2	Example	Lp_1	Lp_2	Lp_3
A	+	s	Type lysogenic	+	s	s
B	+	r	Immune-2 lysogenic	+	r	s
C	+	p	W-2172 mutant	+	s	p
D	s	s	Type sensitive	s	s	s
E	s	r	Immune-2	s	r	s
F	s	p	W-2147 mutant	s	s	p

B x F Yields: B, F, E, C progeny — Yields B, F, E, C, A, D
C x E

Results: No. of Progeny

	B x F						C x E					
	A	B	C	D	E	F	A	B	C	D	E	F
Mal^+	55	1	1	1	0	1	22	2	1	26	0	1
Mal^-	0	58	0	0	1	0	0	0	0	0	59	0

Part II Linkage of Lp_3 to Lp_1--Gal and Lp_2--Mal ?

Parents	No. of Progeny			
	$Mal^+ Lp_1^s$	$Mal^+ Lp_1^+$	$Mal^- Lp_1^s$	$Mal^- Lp_1^+$
F Mal^+ x B Mal^-	4	56	1	58
C Mal^+ x E Mal^-	27	25	59	0
	$Mal^+ Lp_2^s$	$Mal^+ Lp_2^r$	$Mal^- Lp_2^s$	$Mal^- Lp_2^a$
F Mal^+ x B Mal^-	59	1	0	59
C Mal^+ x E Mal^-	51	2	0	59
	$Mal^+ Lp_3^s$	$Mal^+ Lp_3^p$	$Mal^- Lp_3^s$	$Mal^- Lp_3^p$
F Mal^+ x B Mal^-	57	3	59	0
C Mal^+ x E Mal^-	50	2	50	0
C Gal^+ x D Gal^-	$Gal^+ Lp_1^+$	$Gal^+ Lp_1^s$	$Gal^- Lp_1^+$	$Gal^- Lp^s$
	60	0	0	28
	$Gal^+ Lp_3^s$	$Gal^+ Lp_3^p$	$Gal^- Lp_3^s$	$Gal^- Lp_3^p$
	37	23	37	26

The above data are consistent with the hypothesis that an Lp_3 locus separable from Lp_1 and Lp_2 modifies the reaction to λ-1 and λ-2. This locus is not linked to Lp_1--Gal or Lp_2--Mal.

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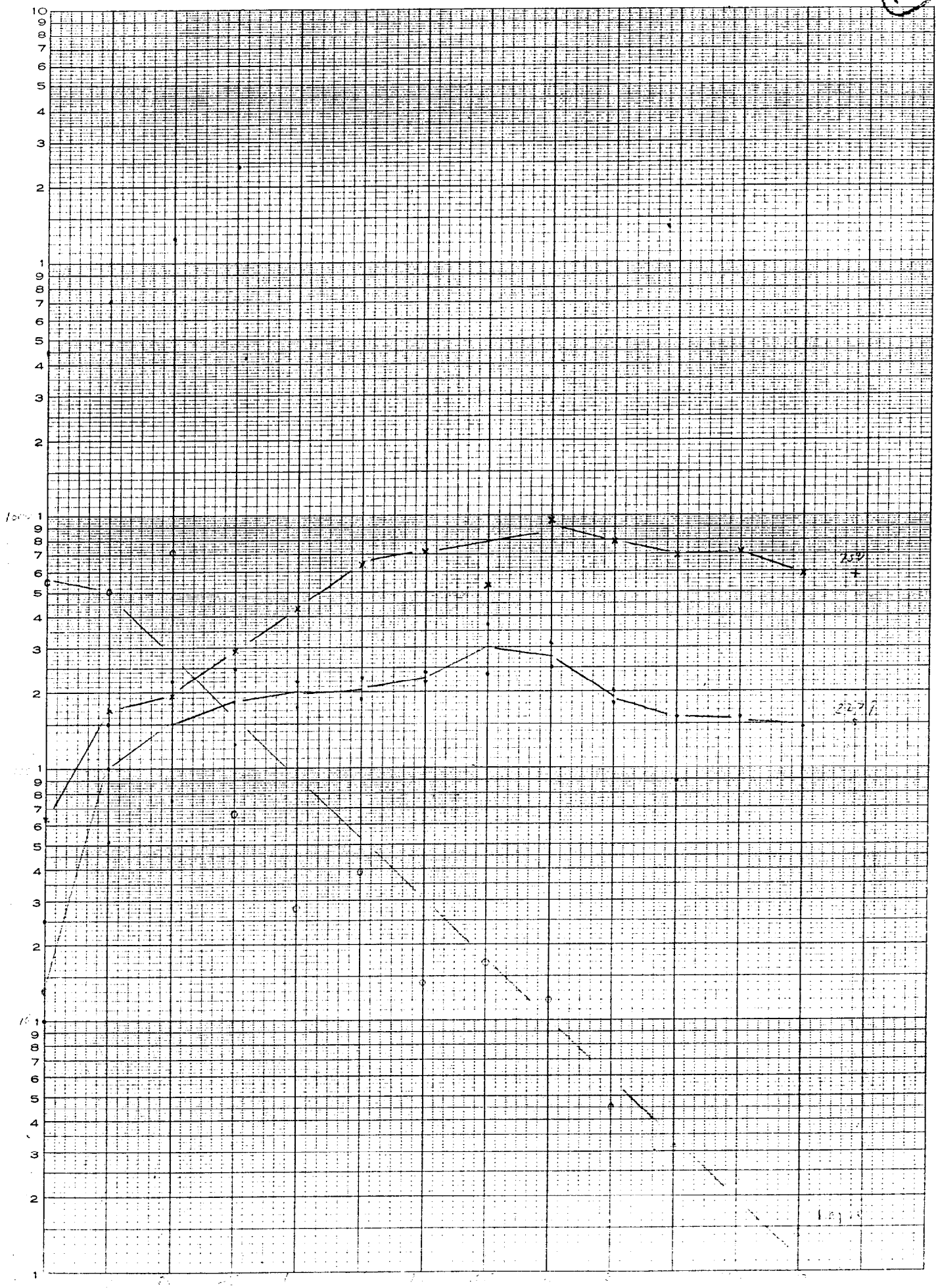

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SEMI-LOGARITHMIC
5 CYCLES X 12 DIVISIONS PER INCH

Keysort cards carry 68 bits. The following scheme is tentatively suggested for organizing the stockbook. Further suggestions urgently requested.

	bits
Stock number and series (3 digits only)	11
Line: (1; 2-10; 11-20; 21-40; 41-..;) and E. coli not wg; Not E. coli; .....;	3
Event and agency:	3

"Mutation"	Not "mutation":
spontaneous, sporad.	new isolate or receipt
spont; selected	segreg. orrecombinant (sex or —x)
UV	Infection (F or lambda...)
X-rays or other mutagen	"Cure" " " "

	bits
Kind of locus changed:	3

Not indicated	auxotroph
Lp_1 or_x	fermentation
Gal (by transduction)	Sm
F	Other resistance

20

Genotype: 1 bit each for:

Gal 1, 2, 4, x	4	S (incl S^d)	2
Lac 1, x	2	Other resist. (lv fut)	2
Mal 1, x	2	Fla	
Xyl, Mtl, Stl, Ara, Stl, Glu, Suc, Cell, Rh, X	10		
M, (T,L)	2	misc.	5
Other aux: AA, Vit, Pur, etc.	3		64
Hfr; F	2		
Het	1	lyophil	1
Heterogenote or heterozygote	1		
any suppressor	1	who entered	3
any temp.-sens.	1		68
Lp or other phage	3		
V_1 V_6 V_x Lp_2 Lp_x	5		
	35		

Incidence of Homogenotes

Type	Ende	Exo	No. Tested		
341	2⁻	4⁻	17	(3 sep seg from done each)	2 HFT 2⁻ / 3×17 = 52 ✓
	4⁻	2⁻	5	(about 9 seg from each)	0 HFT / 9 × 5 = 45
311	2⁻	6⁻	30	(single seg)	1 HFT 6⁻ / 30 (no tests of 2⁻) ✓
309	7⁻	2⁻	5	(6 seg from each)	1 HFT 7 / 30 (no tests of 2⁻)
295	2⁻	1⁻4⁻	152	(single seg) only 1⁻4⁻ tested	1 HFT 1⁻ 1⁴/14 (no tests of others)
293	2⁻	4⁻	5	(sep. seg)	1 HFT 2⁻/11 | 2 HFT 2⁻/11 | 0/11 | 1 HFT 2⁻/11 | 7 HFT 4⁻/12 | 0/10) |
291	8⁻	4⁻	3	(sep. seg)	0/20 | 0/22 | 0/8 |
248	1⁻	+	4	single	0/4
247B	8	4	1	single	1/1 HFT 4⁻
247A	8	+	4	single	0/4
243	1	8	3	single	0/3
242	4	8	1	single	0/1
241	1⁻	2	24	single - done against 1⁻, 2⁻	2 HFT 2⁻/24
236C	8	4	1	single	0/1
212	4	+	4	single	0/4
209	2	1	2	"	0/2
205	4	+	3	"	0/3
202	4	2	18	"	1 HFT 2⁻ 1 HFT 4⁻ / 18 |
198	4	2	16	"	0/16
196	2	+	4	"	0/4
192B	1	2	9	"	2 HFT 1⁻ 1 HFT 2⁻ / 9 |
192A	1	+	4	"	0/4

24/385 (199)

0/300 24/ca 200

Corrected Combinations of Homogenate Frequency

range	2⁻	1⁻	4⁻	6⁻	7⁻	8⁻
341	2/47 (I)		0/5 (A)			
	0/4 (A)		0/41 (I)			
311				1/3 (A)		
309					1/27 (I)	
293	1/10 (I)		0/1 (A)			
	2/10 (I)		0/1 (A)			
	0/10 (I)		0/1 (A)			
	1/10 (I)		0/1 (A)			
	0/9 (I)		0/1 (A)			
291						0/46 (I)
278		0/4 (I)				
247B			1/1 (A)			
247A						0/4 (I)
243						0/3 (A)
242						0/1 (A)
241	2/2 (A)	0/22 (I)				
236c		0/1 (A)				
212		0/4 (I)				
209	0/2 (A)					
205		0/3 (I)				
202	1/3 (A)	1/14 (I)				
192		0/16 (I)				
196	0/13 (I)					
192B	1/5 (A)	2/4 (I)				
184		(I)				

	2⁻	1⁻	4⁻	6⁻	7⁻	8⁻
I	4/14	2/54	1/78			
A	6/81	9/2	1/12			

General

	2⁻	1⁻	4⁻	6⁻	7⁻	8⁻
	10/114	2/36	2/91	1/3	1/27	0/54
	0.09	0.06	0.02	0.33	0.03	0.00

16

6/11 0.33

2⁻ 0.09

1⁻ 0.06

7⁻ 0.03

4⁻ 0.02

8⁻ 0.00

Obtained from

Exogenote (0.04) 10/240

Endogenote (0.19) 6/31

10HFT/240 -

6/31 1-

-/+ 0/23

	Page		F+	F−	(+)	total	% +
1X3	200		M− Gal$_1$− Lp+ (750)	TLB$_1$− Gal$_3$− Lp+ (2238)	2	ca. 1600	0.13 ✓
1X2	214	(1)	M− Gal$_1$− Lp+ (750)	TLB$_1$ ≡ Gal$_2$− Lp+ (2251)	4	1957	0.2 ✓
1X2		(2)	"	"	4	ca. 6517	0.06 ✓
4X2			M− Gal$_4$− Lp+ (811)	TLB$_1$ ≡ Gal$_2$− Lp+ (2251)	0	1039	0 - ✓
8X2		(1)	M− Gal$_8$− Lp^s (2281)	TLB$_1$ ≡ Gal$_2$− Lp+ (2251)	3	ca 6840	0.04 ✓
8X2		(2)	"	"	0	ca 9640	0. ✓
8X2			"	"	0	ca. 1872	0. ✓
1X2	199		M− Gal$_1$− Lp+ (750)	TLB$_1$ ≡ Gal$_2$− Lp+	2	ca 1500	0.13 ✓
1X4	210		M− Gal$_1$− Lp+ (750)	TLB$_1$− Gal$_4$− Lp^s F+ (1436)	6	4588	0.13 ✓
1X2	240		M− Gal$_1$− Lp+ (750)	TLB$_1$ Gal$_4$− Lp^s (2251)	1	3606	0.03 ✓
2X4	171		M− Gal$_4$− Lp^s (578)	TLB$_1$ Gal$_2$− Lp+ (962)	5	1289	0.38 ✓
2X4	171a		" Lp+ (811)	"	0	706	0.0 ✓
2X4	174		"	"	0	200	0.0 ✓
2X4	175		"	"	1	358	0.28 ✓
Fraternal 2X4	337		M− Gal$_4$− Lp+ (1402) F−	TLB$_1$− Gal$_2$− Lp+ F+	7	3771	0.18

		(+)	total	% +
1X2	(1)	1.	1957	0.2
	(2)	4	ca 6517	0.06
	(3)	2	ca 1500	0.13
	(4)	1	3606	0.03
			Ave 8/13680	0.06%
1x3	(1)	2	ca 1600	0.13%
1x4	(1)	6	4588	0.13%

both F+ ↑

2X4	(+)	total	% +
	0	1039	0.
	5	1289	0.38
	0	706	0.
	0	200	0.
	1	358	0.28
	6	3592	0.17
4X2	7	3771	0.18

	+	total	% +
8X2 (1)	3	ca 6840	0.04
(2)	0	ca 9640	0
(3)	0	ca 1872	0