Table –

Segregational Behavior of Reversions of hp^S and hp^R Segregants

Expt.	Segregant Phenotype	Segregant Number	No. Reversions Per Segregant	Total Number Found Segregating
287	$Gal2^- hp^R$	2	8	8
	$Gal_2^- hp^S$	1	6	0
292	$Gal_2^- hp^R$	12	1	11
	$Gal_2^- hp^S$	3	1	0
	$Gal_4^- hp^S$	1	1	0
292A	$Gal_2^- hp^R$	1	2	2
	$Gal_2^- hp^R$	3	1	3
	$Gal_2^- hp^S$	5	1	0
298	$Gal_2^- hp^R$	5	2	10
323	$Gal_6^- hp^R$	1	6	1
	$Gal_6^- hp^S$	1	2	0

Heterogenote, 287, $Gal_2^- hp^S // Gal_2^+ hp^R$

292, 292A, 298 $Gal_2^+ Gal_4^- hp^S // Gal_2^- Gal_4^+ hp^R$

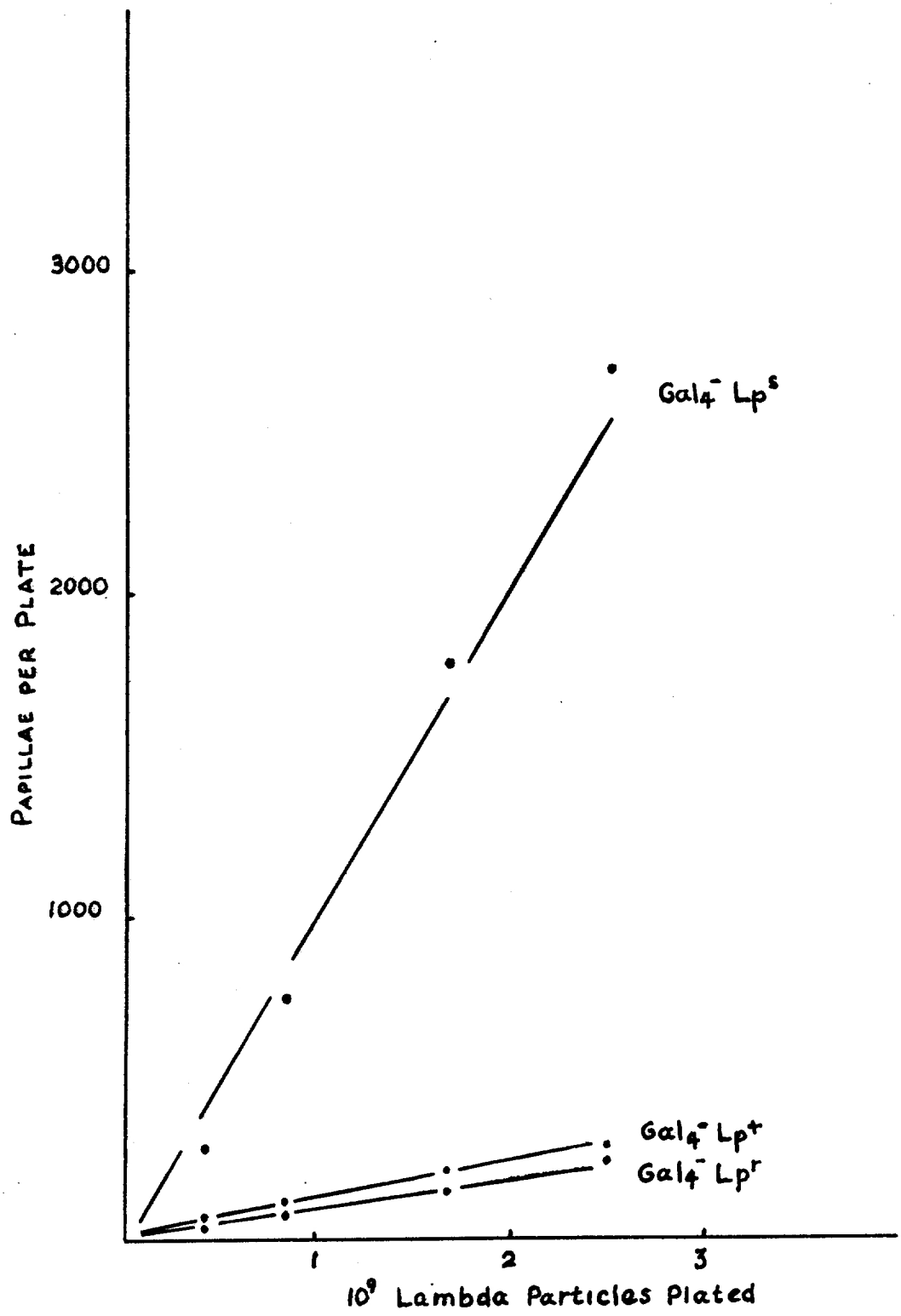
323, $Gal_6^+ Gal_1^- hp^S // Gal_6^- Gal_1^+ hp^R$

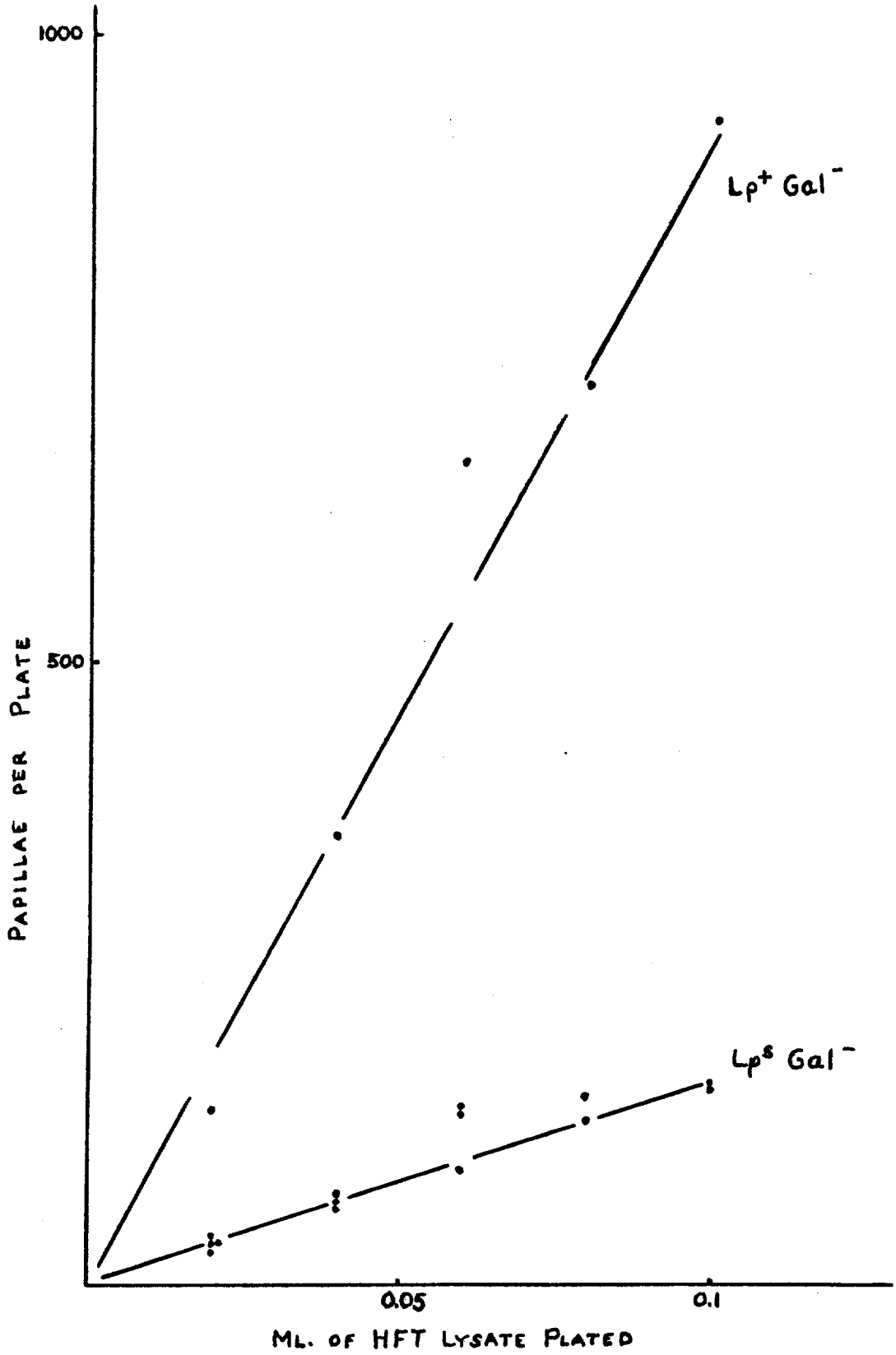
MGI Genetics Soc. Pitch State Coll. Sept. 1955

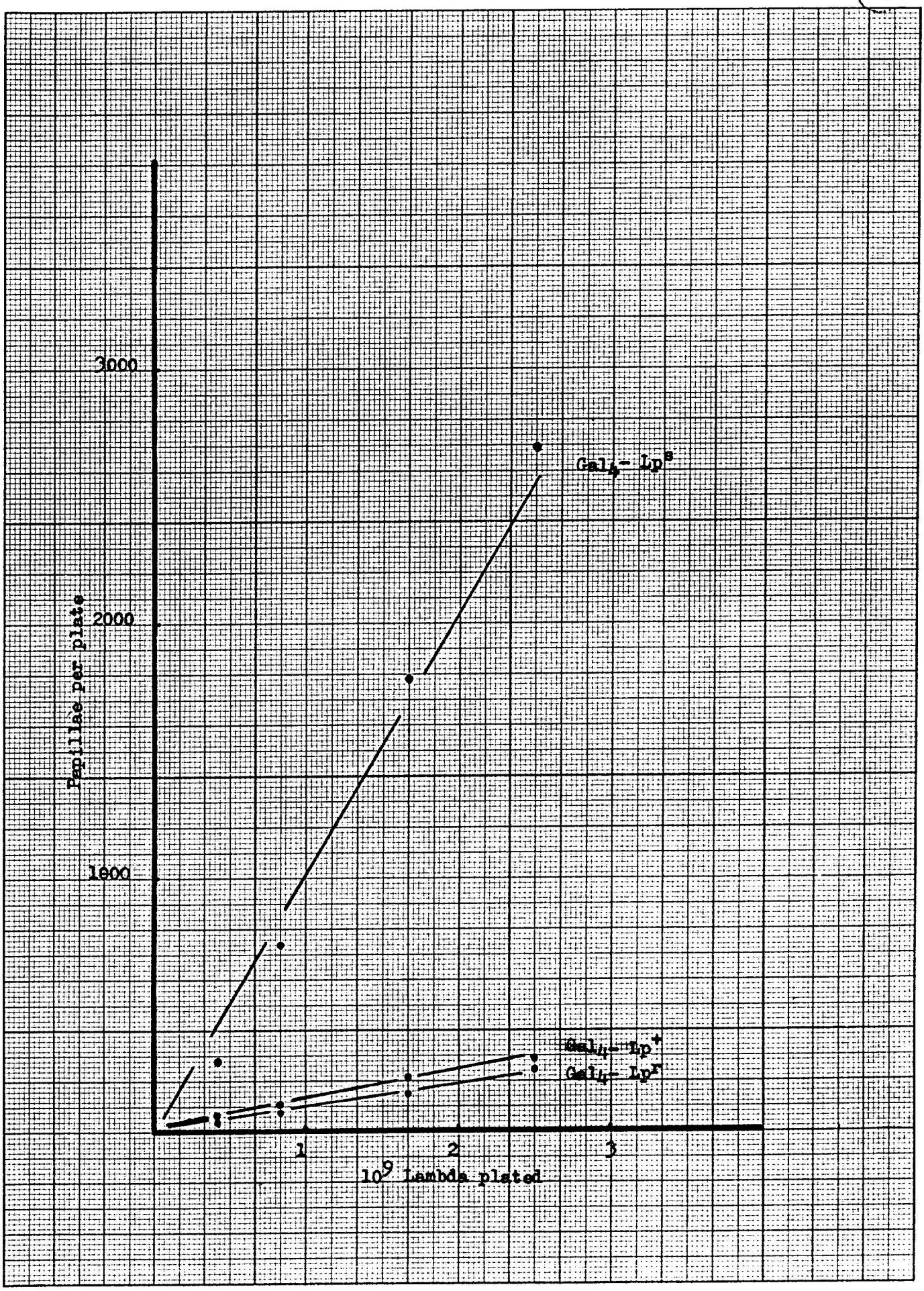
(227)

Cis-trans position effects in transduction heterogenotes of Escherichia coli

—— The phage lambda can transduce a fragment which includes a cluster of genes for galactose fermentation. Most of the transformed clones are "diploid" or heterogenotic for the transduced genes. Many combinations of non-allelic Gal- mutants give galactose positive heterogenotes as readily as Gal+/Gal-. However, some combinations of Gal- gave smaller and delayed yields of positive clones. Further analysis disclosed a cis-trans position effect between certain loci. For example, while the cis ++/— heterogenotes formed by transduction from Gal_1^+ Gal_4^+ to $Gal_1^-Gal_4^-$ are positive, the trans +-/-+ heterogenotes from the transduction from $Gal_1^-Gal_4^+$ to $Gal_1^+Gal_4^-$ are phenotypically galactose negative. In the negative clones, positive heterogenotes are later formed by crossing over in occasional cells. Further segregation results in all possible haploid combinations, +-, -+, ++, and —. The delayed yields that were observed initially are based on these secondary events. Reciprocal transductions have given identical phenotypes, so that in heterogenotes the genes in the fragment are functionally equivalent to the homologous genes in the chromosome. The galactose positive phenotype thus requires that + alleles be in adjacent positions either in the fragment or the chromosome.


3000
2000
1000
PAPILLAE PER PLATE
Gal4⁻ Lp^s
Gal4⁻ Lp^+
Gal4⁻ Lp^r
1
2
3
10^9 Lambda Particles Plated


1000
500
PAPILLAE PER PLATE
Lp+ Gal−
Lp^s Gal−
0.05
0.1
ML. OF HFT LYSATE PLATED



4. Transduction to Lp^s recipients

It has been stated previously that transductions to Lp^s recipients cells with LFT lambda result in lysogeny of the clone. Nearly all of these lysogenizations are Lp^+, but rarely a clone with Lp^r phenotype results. With HFT lambda there is a higher frequency of the Lp^r type, a result which may only be owing to the lower chances of secondary infection with HFT lysates. Of 58 syngenotes isolated as single colonies, 13 (22 percent) were of Lp^r phenotype. These syngenotes were made with different lysate preparations, and are derived from different homogenotes, and there is no indication, as yet, of an association of Lp^r clone formation with either a locus or a lysate preparation.

The Lp^r clones described previously in this report are carriers of a "defective" prophage (Appleyard, 1954), but plaque-forming lambda, in small quantities, may be obtained from them after irradiation with ultraviolet. The Lp^r clones obtained with HFT lambda have not given lambda after UV treatment, and differ from previously described Lp^r cultures in segregating for Lp, yielding Lp^s. Thus they appear to be syngenotes of the form Gal^- Lp^s //Gal^+ Lp^r. Segregation yields Gal-Lp^s, or Gal^+Lp^s haploid segregants. No non-segregating Lp^r clones have been observed. This last observation suggests that the lambda "defect" in these cases is with lysogenization as well as with production of plaque-forming particles.

Obvious segregation at Lp was not observed when Gal+ segregated from Lp^s recipients, and it was not possible with these syngenotes to relate the function of the prophage to the genetic material. Lp^r _//Lp^s heterogenotes permit study of this relationship. If the chromosomal fragment is independent of the Lp genotype, Lp^s segregant cultures may be homogenotic. Gal+ reversions of segre ants from Lp^r_//Lp^s syngenotes were examined for their segregational behavior. Under conditions where the reversion test indicated 23/23 Lp^r Gal− segregants to have been homogenotes, 10/11 Lp^s Gal− segregants were found haploid(table 10). Although it is not possible to determine the adequacy of the data, the indication is that the Lp^r allele has a centromeric function, that $Lp^{\pm}$ probably does not, and that the Lp^s allele cannot so function. Failure to obtain segregation of the Lp^+ allele in transductions to Lp^s recipients may only be an indication that the heterogenotes studied are not the primary product of lambda-sensitive cell interaction.

Table 10

Segregational behavior of Gal+ reversions of Lp^s and Lp^r segregants

Experiment	Segregant Phenotype	Segregant Number	Number of Reversions per segregant	Number reversions found segregating
287	Gal_2^- Lp^r	1	8	8
	Gal_2^- Lp^s	1	6	0
292	Gal_2^- Lp^r	12	1	11
	Gal_2^- Lp^s	3	1	0
	Gal_4^- Lp^s	1	1	0
292A	Gal_2^- Lp^r	1	2	2
	Gal_2^- Lp^r	3	1	3
	Gal_2^- Lp^s	5	1	0
298	Gal_2^- Lp^r	5	2	10
323	Gal_6^- Lp^r	1	6	1
	Gal_6^- Lp^s	1	2	0

Heterogenotes. 287; Gal_2^- Lp^s _// Gal_2^+ Lp^r

292,292A,298; $Gal_2^+ Gal_4^-$ Lp^s _// Gal_2^+ Gal_4^+ Lp^r

323; Gal_6^+ Gal_1^- Lp^s _// $Gal_6^-Gal_1^+$ Lp^r

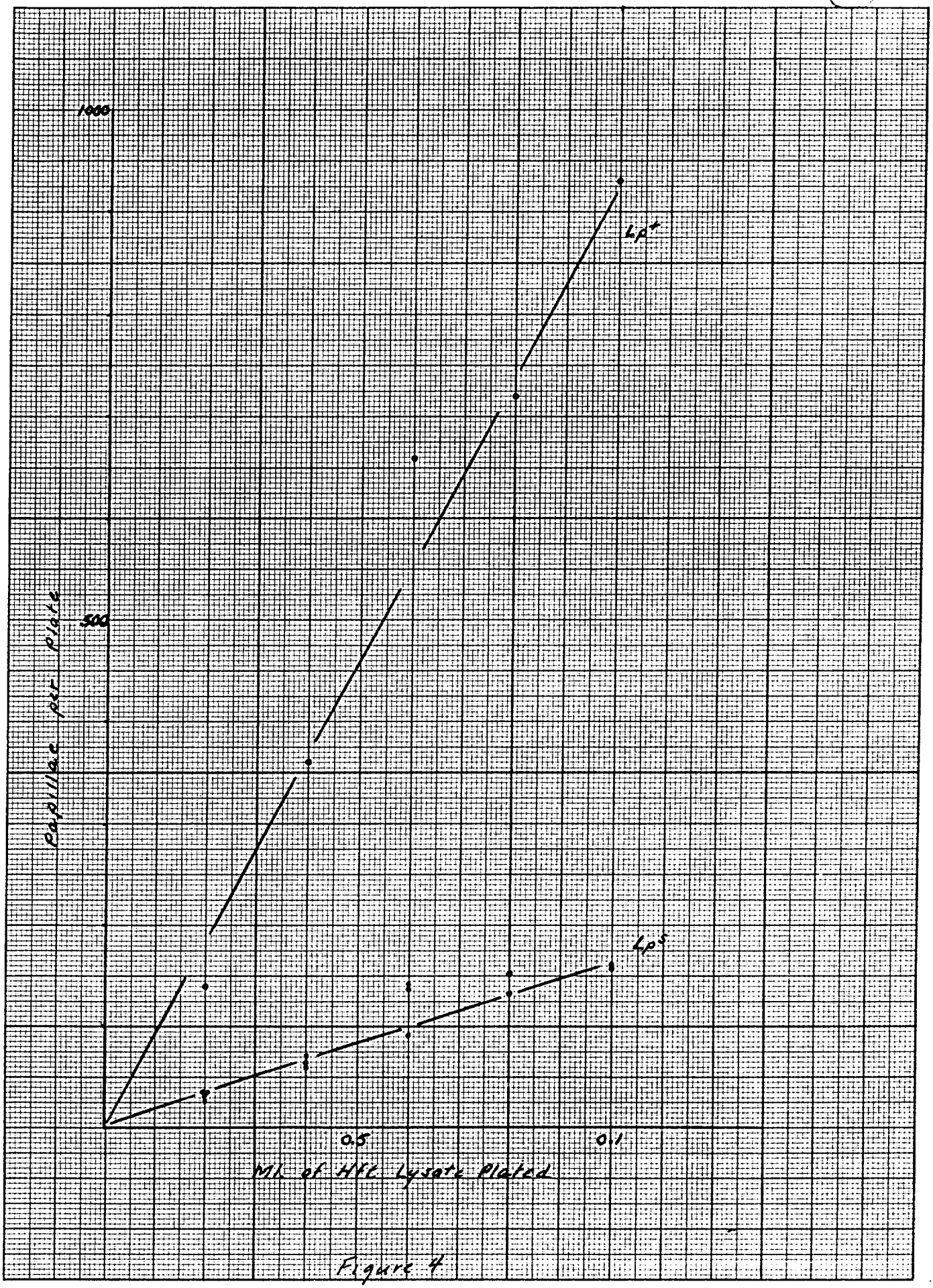
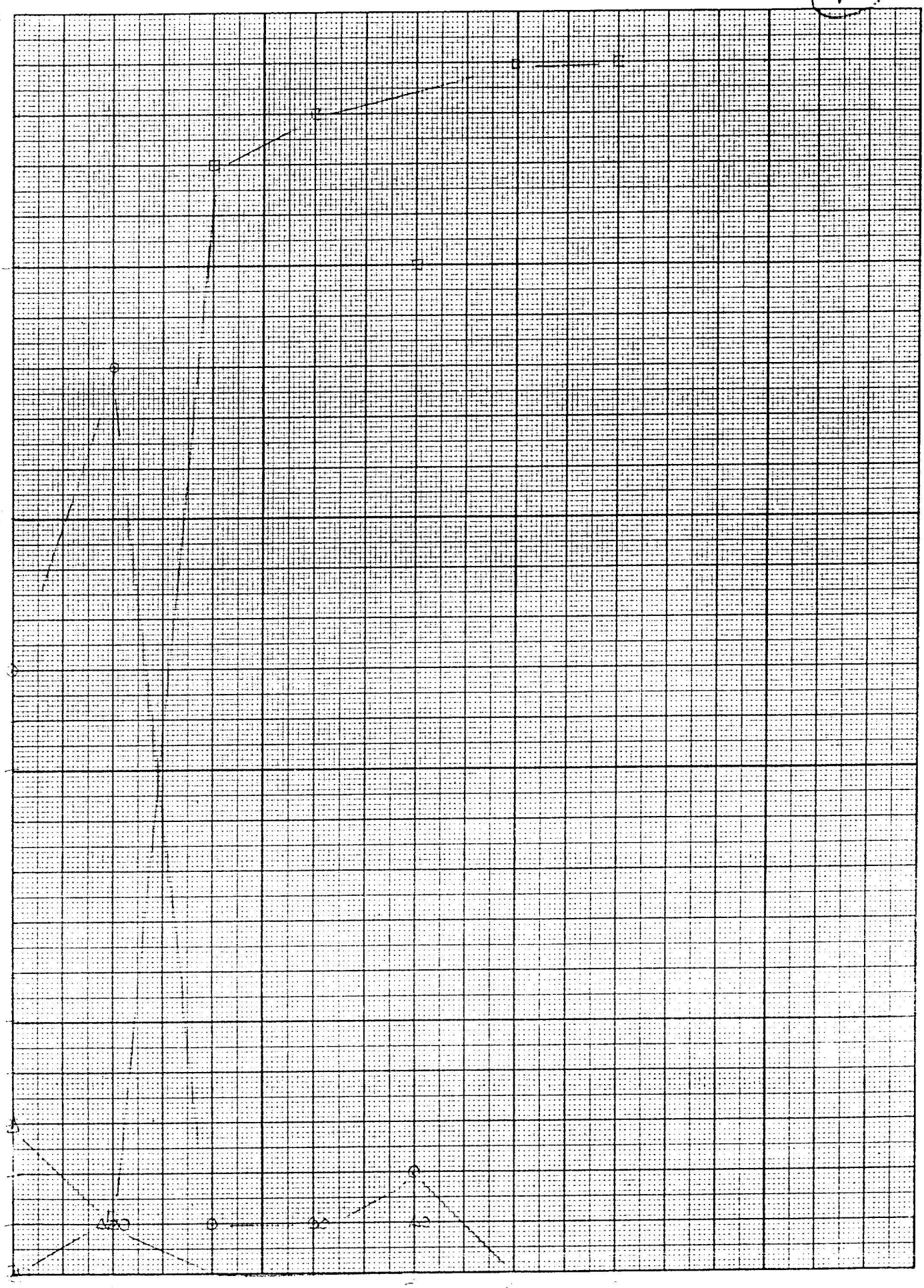
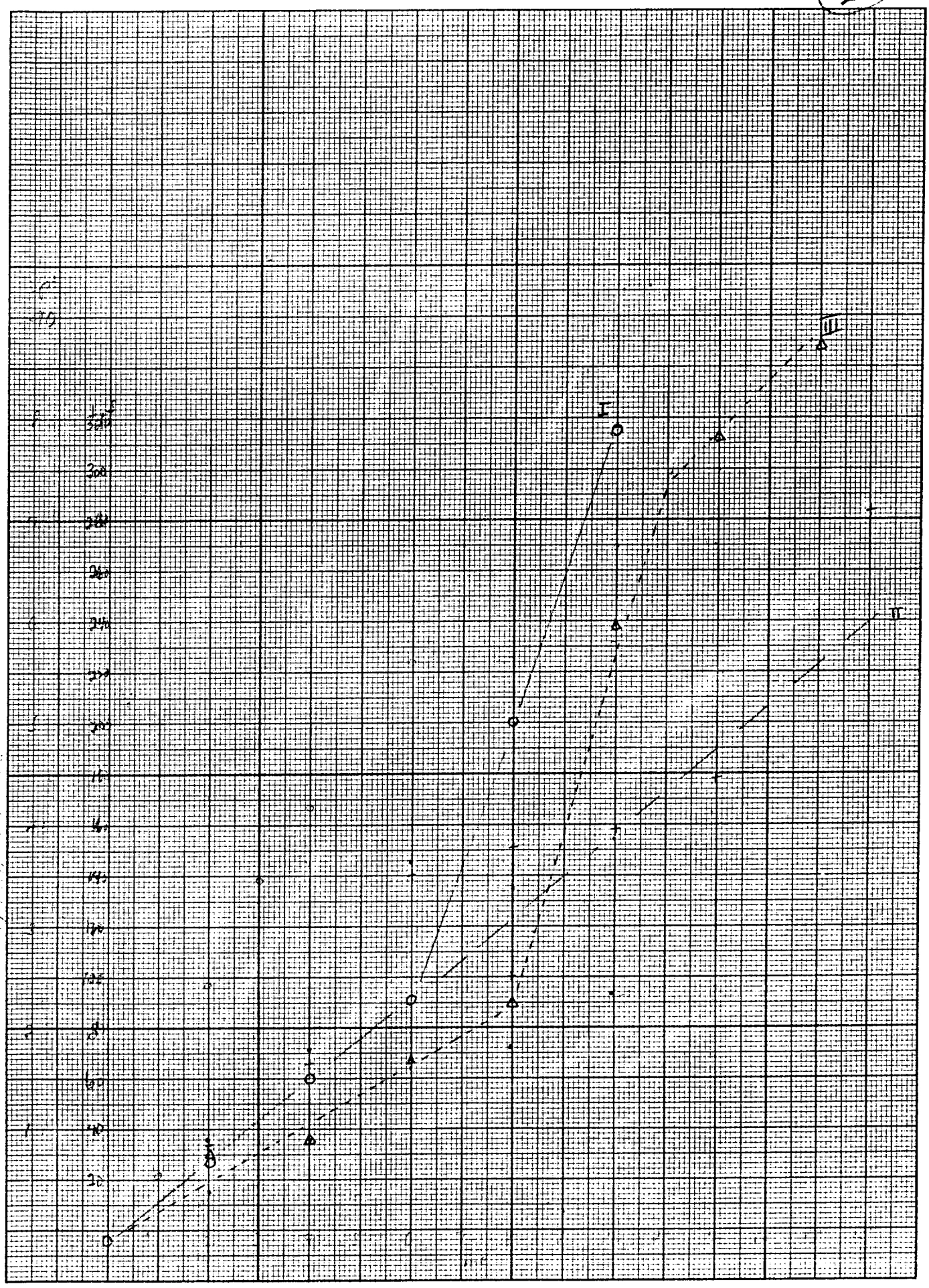


Figure 4





392

285
288
433
327
471
829
649

1804/5 = 361

361) 739 = 2.0
722
170

180/2 = 90 = 739

412

103
117
85
113
108
74
94
70
77

9) 843

93

93) 177 = 1.9
93
840
837

170
183
177

399

27
47
135
100 OD .55
115 % survival = 5.5
176
191
123
76

1018/9 = 112

135
140

112) 138 = 1.2
112
260

400

45
34
37
39
40 OD = 0.58 % survival = 39
42
46

283/7 = 40

27
24
25
20
96/4 = 24

40) 24 = 0.6

410

16
14
20
26
5

5) 81
16

10
4
18
28
28

108/5 = 21

16) 21 = 1.3
16
50

397

84
101
92
104
121
87

589/6 = 98

66
28
106
76
117

443/5 = 89

OD = 0.58 % survival = 13%

98) 89.0 = 0.9
882

determ. from B gel scaling only ↓

Expt	Begin Rise	B. S	Transl. particles Transl. center	Effctl length	% Cell distortion
412	100'	ca. 25	1.9	180'	<1.0
410	90'	ca. 17	1.3	180'	<1.0
399	90'	ca. 20	1.2	120'	5%
397	85'	ca. 30	0.9	125'	15%
392	ca. 85'	—	2.0	180'	—
HFT 400	90'	ca 13	0.6	150'	40.

(Time = 5 hours) from Page 354

Crossing over in P.E. heterozygentes.

Reciprocal on next page

Het.	Dom.	Recip.
342E2	6⁻	4⁻

Multiplicity / 0.1 ml = 0.71

Culture with:	No growth	Gal +
	3	6

Clone size: 7000, – 34

Non-diff. Clones	Diff. clones			
total	(+)	total	Est. no. pol.	
1406	ca. 1000	ca 3000	—	
ca 3000	4	5144	1.3×10^{-4}	
1544	2	6728	5.3×10^{-5}	
3088	5	2266	4.0×10^{-4}	
ca 150	1	5925	3.0×10^{-5}	
5144	ca 1000	ca 3000	—	
ca 4000				
8728				
2266				
ca 7000				
2245				
748				
34				

clone size 5900.

Using null method $\frac{2\text{-}3}{5900}$ log $\frac{1}{\frac{13}{11}} = 7.0 \times 10^{-5}$

See 354 for computation using new clone size

(240)

original see page 354

Crossing over (Time (3.25 hrs.))

Het Donor Recip

4- 6-

Mult. 5.8/0.1 ml

Cultures work.	No. growth	No. Het	Het
	0	17	3

Von dey. clones	Dey. Clones		
2080	(+)	Total	Estimate Freq. Het.
660	2	1004	4×10^{-4}
688	1	185	
640	1	1249	1.4×10^{-4}
392			
640	Using null method, clone size 1200		
728	$a = \frac{2.3}{1200} \log \frac{1}{\frac{17}{20}} = 2.16 \times 10^{-4}$		
644			
1192			
496	Total cells = $\frac{16778}{20} = 838$/clone		
664			
1096	$a = \frac{2.3}{838} \log \frac{1}{\frac{17}{20}} = \frac{(2.3) \log 1.2}{8.38 \times 10^{2}} = \frac{(2.3)(0.08)}{8.38 \times 10^{2}}$		
592			
720			
1216	$= \frac{0.18}{8.38 \times 10^{2}} = \frac{1.8 \times 10^{-1}}{8.38 \times 10^{2}}$		
688			
496	(2.2×10^{-4})		

$a = 0.602r/N \log N$

241

These experiments indicate washing technique not adequate

368-1 4⁻ -x /-

multiplicity = 0.45/sample of 0.01⁻ Elapsed time = 4.66 hours.

Samples with:	No growth	Gal+	Gal+
	6	3	1

Duplicate cultures. Ratio +/- / total = 1/7/265

Gal+	Gal-	Total
1	345	858
0	ca 300	ca 600
0	ca 300	ca 600
0	549	549

$a = 0.602(1)/858 \log 858$

$= 0.602/294(858)$

$= 0.602/2520$

$\frac{6.02\times10^{-1}}{2.52\times10^{-3}}$

$= 2.4\times10^{-4}$

Those eliminated (washed) 376 on

$a = \frac{2.3}{600} \log \frac{1}{3/4}$

$a = 0.38 \log 1.33$ 4.1×10^{-2}

$a = 0.38\,(0.124) = 0.047$

368-2 mult. = 0.34 ratio $10^+/3/201$

No growth	No Gal+	Gal+	Gal+	Gal-	Total
4	5	1	376	0	ca 500
			0	8	794
			0	1	379
			0	ca 300	ca 600
			0	0	208

per 376

$a = \frac{2.3}{600} \log \frac{1}{5/6}$

$a = 0.38 \log 1.2$

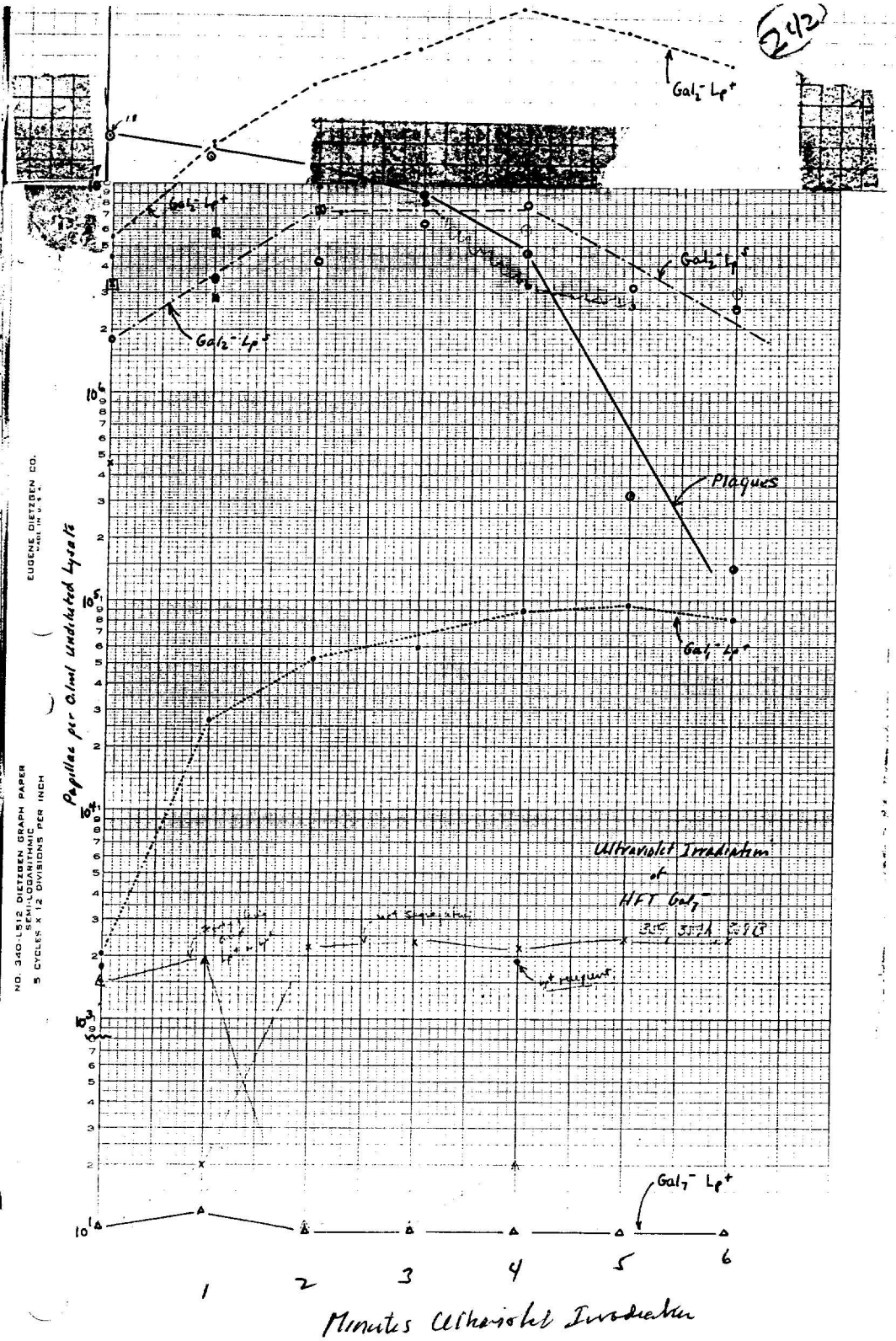
$= 0.38\,(0.079) = 0.030$

$= 3.0\times10^{-2}$

Because of the failure of the washing method in the past, incubation on Bgal attempted without respreading. Inc. 5.5 hours.

368-1 mult.: ratio +/- / total = 0/27/173

No growth	No Gal+	Gal+	Gal+	Gal-	Total
1	6	0	0	6	42
			6	5	314
			0	2	71
			0	226	229
			0	0	2
			0	0	9
			0	0	51


(2/2)
Gal₂⁻ Lp⁺
Gal₂⁻ Lp⁺
Gal₂⁻ Lp⁺
Gal₂⁻ Lp⁺
Plaques
Gal₇⁻ Lp⁺
Ultraviolet Irradiation of HFT Gal₇⁻
Gal₇⁻ Lp⁺
Plaques per 0.1ml Undiluted Lysate
Minutes Ultraviolet Irradiation
1
2
3
4
5
6
EUGENE DIETZGEN CO.
NO. 340-L512 DIETZGEN GRAPH PAPER
SEMI-LOGARITHMIC
5 CYCLES X 12 DIVISIONS PER INCH

Defective Heterogenote Number	Gal⁻ Segregants	
	Lambda Sensitive	Lambda Defective
292	24	36
323	4	2
331	6	0
336	12	0
343	5	1
346	5	1
365	20	1
368	3	0
374	9	0
382	14	1
415A	16	1
420	16	2
420A	9	4
Totals	143	49

Table 1

Expt. 316 2/1/54

Procedure: Ultraviolet irradiation of HFT 2⁻, lysate diluted 1-100 in D(M), 0.1 ml. sample removed and added to 10 ml. Penassay. HFT 2⁻ stock = 241-14, mql- derivative. Distance from lamp, 50 cm.

UV Dose in Seconds

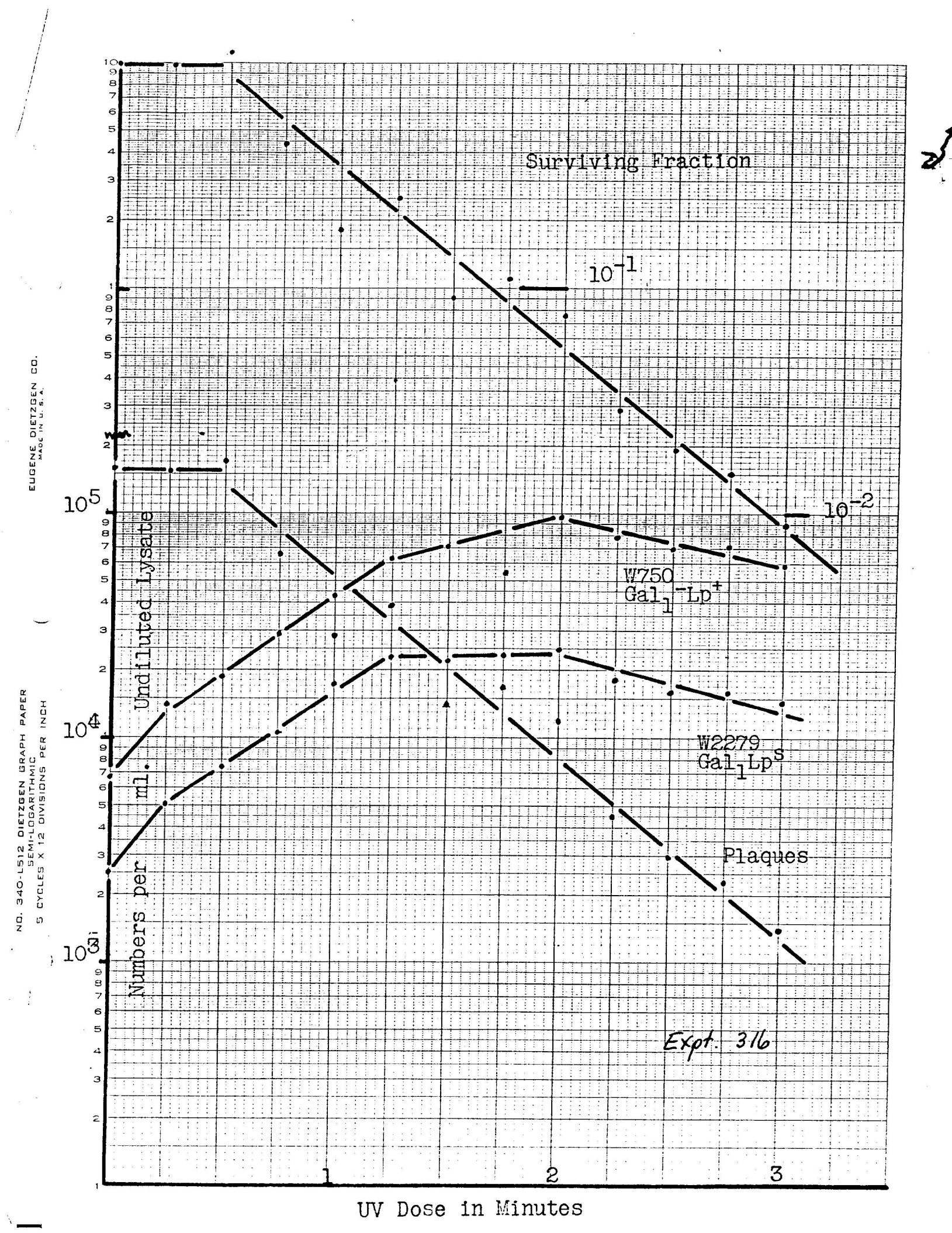
Trnsd. x 10^3 on:	0	15	30	45	60	75	90	105	120	135	150	165	180
$Gal_1^-lp^S$ W2279	2.5	5.1	7.5	10.5	17.3	22.7	21.8	23.4	24.9	18.1	16.0	16.0	14.5
$Gal_1^-lp^+$ W750	6.7	14.0	18.4	29.3	43.4	63.8	71.1	53.6	95.8	79.1	69.9	71.7	58.9
Plaques x 10^3	155	151	172	66	28	39	14	17	12	4.5	3.0	2.3	1.4
Fraction Surviving	1.0	0.97	1.1	0.43	0.18	0.25	0.09	0.11	0.077	0.029	0.019	0.015	0.009

Table 2

Analysis of Transduction on $Gal_1^-Lp^S$ Recipient

UV Dose in Seconds

	0	15	30	45	60	75	90	120 to 180
No. of Trnsd. Tested	1	18	18	18	18	18	18	18
No. Seg.	0	6	1	0	I	1	1	0
% Seg.	0	33	6.0	0	6	6	6	0
Lp_S Gene Types of Segregating Gal+								
Lp^S	-	-	-	-	-	-	-	-
Lp^+	-	-	-	-	-	-	-	-
Lp^R	-	6	1	-	R	R	R	-
Lp_S Gene Types of Non-Segregating Gal+								
Lp^S	-	7	14	17	16	16	17	-
Lp^+	-	2	0	0	0	1	0	-
Lp^R	-	3	2	1	1	0	0	-
% Lp^S	-	58	88	94	94	94	100	-


Surviving Fraction
10^{-1}
10^{-2}
W750
$Gal_1^-Lp^+$
W2279
Gal_1Lp^s
Plaques
Expt. 316
Numbers per ml. Undiluted Lysate
10^5
10^4
10^3
1
2
3
UV Dose in Minutes
EUGENE DIETZGEN CO.
MADE IN U.S.A.
NO. 340-L512 DIETZGEN GRAPH PAPER
SEMI-LOGARITHMIC
5 CYCLES X 12 DIVISIONS PER INCH

Lysate diluted D(M) 1-100 ? 10 ml → 0.1ml samples to broth

(2279) (750)

Page 316 - Diluted HFT lysate (241-14 mal-) —x Gal-Lp^s, Gal-Lp^+

Dose	0	15	30	45	60	75	90	105	120	135	150	165	180
Spont Exit; 0.1ml of 1-10 dilution →3 Lp^s	25	51	75	105	173	227	218	234	249	181	160	160	145
x10^3 titer/ml UVd tube	2.5	5.1 / 2.6	7.5 / 5.0	10.5 / 8.0	17.3 / 14.8	22.7 / 20.2	21.8 / 19.3	23.4 / 20.9	24.9 / 22.4	18.1 / 15.6	16.0 / 13.5	16.0 / 15.5	14.5 / 12.0
0.1ml of 1-100 tube → Reassay x10^3 (t=0)	1	15 / 14	22 / 21	25 / 24	22 / 21	19 / 18	24 / 23	37 / 36	31 / 20	2.0 / 1.0	—	—	—
plaques x10^3	155	151	172	66	28	39	14	17	12	4.5	3.0	2.3	1.4
	1.5x10^5 ·100 ·100 = 1.5x10^9 plaques/ml; 6.7x10^3 ·10^4 = 6.7x10^7 transd./ml												
No. papillae 40 picked	1	18	18	18	18	18	18	18	18	18	18	18	18
Seg =	—	33%	6.0%	0	6.0	6.0	6.0	0	6.0	0	0	0	0
No. stable	1	12	17	18	17	17	17	18	17	18	18	18	18
Gal stable phenotype	R	24 7S 3R	14S 2r	17S 1R	16S 1R	16S	17S	~~[illegible]~~ →					
% = 0		0.58	0.875	0.94	0.94	.94	100						
x10^3 Lp^+ (Lp^s)	6.7	14.0	18.4	29.3	43.4	63.8	71.1	53.6	95.8	79.1	69.9	71.7	58.9
	0	7.3	11.7	22.6	36.7	57.1	64.4	46.9	88.1	72.4	63.2	66.0	52.2

) Ignore?

~~0 15 30 45 60 75 90 105 120~~

Raw data

HFT 7 S unadulterated lysate.

Technic. ~~dilute 1-10 with 10(?), UV and 0.1ml added to 10ml~~

Bat.	Dilution	0	1	2	3	4	5	6
				min UV				
Transd Assay /2580	x10⁷ 2X10⁵	4.7 235	14.0 707	—	—	—	—	—
/2790	x10⁷ 2X10⁵	0.46 23	3.5 176	4.2 213	4.5 227	—	3.2 161	2.7 134
purified cult. → /2790 preworned plate.	x10⁷ 1X10⁵	1.8 189	2.8 280	9.8 977	—	—	—	—
/2915	x10⁷ 1X10⁵	3.3 330	5.9 588	6.5 653	—	—	—	—
/750	x10⁵ 1X10³	0.2 21	2.7 273 ~~252~~	5.2 517 ~~496~~	5.9 593 ~~572~~	8.8 883 ~~864~~	9.5 950 ~~9~~	8.1 809
/2307	1-20	5	6	-2	-2	2	3	3
Abfass /2580	x10⁷ 1X10⁶	4.4 44	18.3 183	34.7 347	54.5 545	68.9 689	53.2 532	38.1 381
/2341	x10⁷ 1X10⁶	3.5 35	—	—	—	25.3 253	—	—

Ave lys: 5.6/3 = 1.8 12.2/3 = 4.1 20.5/3 = 6.8

	Dilution	0	1	2	3	4	5	6
Plaques /2790	x10⁷ 2x10⁵	500+	500+	11.7 584	8.7 436	4.7 234	0.32 16	0.14 7
preworned plate, purif cult. /2790		—	—	ca 1000				
/2915	x10⁷ 10⁵	16.5 1650	11.8 1176	6.5 653				

Testing Abgesdudni

	⓪	①	②	③	④	⑤	⑥	
No. sampled	24	24	23	24	24	24	24	
/2790	9 Sens-ns	3s ns	22 all ns	22s 22ns	21s-21ns	24s-ns	24s-ns	The streaks of the last two doses /λ were restreak on B gal. No evidence of seg suggesting that addition of λ does not restore seg. behavior
	3+ s	2+ 1ns 1s	0	0	1 - ns	0	0	
	12r s	19r 1ns 18s	1r-seg	2 1ns 1s	2 1ns 1seg	0	0	
Spont. present	9.6 s	1.7	1.4	—	—	—	—	

/2915				Richeck
No.	36	34	47	This last by odd. Streak showed
	0 s	0	38s 38ns	38 ns
	8+ 2w 6s	2 - 2 seg	0	—
	28r 0w 28s	32r 31s 1ns	9r 9s	9 seg 8 ns 1

Totals over

359 - 359A - 359B

248

Testing Transd	0'	4'
Picked	24	24
/2580 Lpt	24	24
Seg	18	19
ND	6	5
Sp. reversions	9.8	1

4' dose 2580

on retest not weak 10 single colonies of it tested found none Lpt organisms

		Nature of Segregants	Endo Lpt	Endo Lp^R	Exo Lpt	Exo Lp^R	Amphi Lpt	Amphi Lp^R
→	x	Transd. 1	3	0	4 1wk	0	0	0
	c	2	6	0	0	0	1	0
→ 5a = Tendo	x	3.	5 1wk	0	0	0	0	0
5b = 6endo	a	4.	7	0	0	0	0	0
5c = 6endo lamphi	a	5.	7	0	0	0	0	0
	b	6.	6	0	0	0	0	0
	b	7.	6	0	0	0	0	0
	a	8.	7	0	0	0	0	0
	b	9.	6	0	0	0	0	0
	x	10.	6	1	0	0	0	0
→	x	11	5 1wk	0	1	0	0	0
→	b	12	6 1wk	0	0	0	0	0
	c	13.	6	0	1	0	0	0
	a	14.	7	0	0	0	0	0
	d	15.	5	0	0	0	0	0
	b	16.	6	0	0	0	0	0
	c	17.	6	0	0	0	1	0
	a	18.	7	0	0	0	0	0

Exo 10%

Summary - Analysis of Transductants

Dose	0	1	2	3	4	5	6
Cal_2 – Lp^s Recip. %							
Lp^+	22 ~~216~~	7 ~~64~~	0	0	4	0	0
Lp^R	78 ~~784~~	93 ~~864~~	14	8	8	0	0
Lp^s	0	2 ~~16~~	86	92	88	100	100
$Lp^+ + Lp^R$	100	98	14	8	12	0	0
% Seq.	94 ~~944~~	93 ~~952~~	14 ~~142~~	4	9	0	0
% not seq.	6 ~~56~~	7 ~~46~~	86 ~~860~~	96	91	100	100

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Table 1

Expt. 316 2/1/54

Procedure: Ultraviolet irradiation of HFT 2⁻, lysate diluted 1-100 in D(M), 0.1ml samples removed and added to 10ml Penassay. HFT. 2⁻ stock = 241-14, mal- derivative. Distance from lamp, 50 cm.

Trnsd. Doses x 10³ on:	UV Dose in Seconds 0	15	30	45	60	75	90	105	120	135	150	165	180
Gal$_1^-$ Lp^s W2274	2.5	5.1	7.5	10.5	17.3	22.7	21.8	23.4	24.9	18.1	16.0	16.0	14.5
Gal$_1^-$ Lp$^+$ W750	6.7	14.0	18.4	29.3	43.4	63.8	71.1	53.6	95.8	79.1	69.9	71.7	58.9
Plaques X10^3	155	151	172	66	28	39	14	17	12	4.5	3.0	2.3	1.4
Fraction Surviving	1.0	0.97	1.1	0.43	0.18	0.25	0.09	0.11	0.077	0.029	0.019	0.015	0.009

Table 2

Analysis of Transductions on Gal$_1^-$ Lp^s Recipient.

No. of Trnsd. tested.	UV Dose in Seconds 0	15	30	45	60	75	90	180 to 180
	1	18	18	18	18	18	18	18
No. Seg.*	0	6	1	0	1	1	1	0
% Seg	0	33	6.0	0	6	6	6	0
Lp Genotypes of Segregating Gal+								
Lp^s	—	—	—	—	—	—	—	—
Lp$^+$	—	—	—	—	—	—	—	—
Lp^R	—	6	1	—	1	1	1	—
Lp Genotypes of Non Segregating Gal+								
Lp^s	—	7	14	17	16	16	17	—
Lp$^+$	—	2	0	0	0	1	0	—
Lp^R	—	3	2	1	1	0	0	—
% Lp^s	—	58	88	94	94	94	100	—

Table 1

Expt. 359-359A-359B 8/17/55

Procedure: Ultraviolet irradiation of HFT 7⁻, undiluted lysate in Penassay. Distance = 50 cm. Irradiation in petri dish, 15 ml volume, 1.0 ml samples removed at varying times. HFT 7 stock = W3067

Assays ① Plaques on B gal on W2915, W2790

Dose →	0	1	2	3	4	5	6
10^7 plaques /ml lysate	16.5	11.8	9.2	8.7	5.7	0.32	0.14
Fraction surviving	1.0	0.72	0.55	0.53	0.35	0.019	0.009

② Transduction on B gal vs. the following cultures

Recipient Culture		Dilution	0	1	2	3	4	5	6
$Gal_2^-Lp^+$ W2580	(1)	10^7	4.7	14.0	—	—	—	—	—
	(2)	10^7	4.4	18.3	34.7	54.5	68.9	53.2	38.1
$Gal_2^-Lp^s$ W2915		10^7	3.3	5.9	6.5	—	—	—	—
W2790	(1)	10^7	1.8	2.8	9.8	—	—	—	—
	(2)	10^7	0.46	3.5	4.2	4.5	—	3.2	2.7
$Gal_2^-Lp^{R/S}$ W2341		10^7	3.5	—	—	—	25.3	—	—
$Gal_1^-Lp^+$ W780		10^5	0.2	2.7	5.2	5.9	8.9	9.5	8.1
$Gal_7^-Lp^+$ W2307		1-20	5	6	-2Ⓐ	-2	2	3	3

Ⓐ All values given have been corrected for spontaneous reversions of the indicator culture. In the assays on W2307 figures given are papillae on lysate addition plate − spontaneous reversions papillae. None of these papillae were checked for Galactose stability.

Table 3

(B) Transductions to Gal_2^- Lp^s Recipients. Total

Dose →	0	1	2	3	4	5	6
% Lp^+	22	7	0	0	4	0	6
% Lp^R	78	91	14	8	8	0	0
% Lp^S	0	2	86	92	88	100	100
% $Lp^+ + Lp^R$	100	98	14	8	12	0	0

Table 4

(A) Transductions to Gal_2^- Lp^+ Recipient. W2580

	UV. Dose (min) 0	4
Number tested	24	24
No. Lp^+	24	24
No. seg.	18	19
No. Not. Seg	6	5
No. Sp. Rec. in Sample	9.8	1

(B) Analysis of the transductions produced with lambda irradiated 4 minutes, survival = 2.0×10^{-2}. 18 different transductions analyzed, about 7 segregants from each tested for lp genotype and Gal allele.

Number of transductions with the following seg. pattern	Endogenotic Lp^+	Endogenotic Lp^R	Exogenotic Lp^+	Exogenotic Lp^R	Amphidiploic Lp^+	Amphidiploic Lp^R
~~5~~	7	0	0	0	0	0
~~4~~	6	0	0	0	0	0
2	6	0	0	0	1	0
1	5	0	0	0	0	0
1	6	0	1	0	0	0
1	3	0	1 *	0	0	0
1	5 w	0	0	0	0	0
1	6	1 **	0	0	0	0
1	5 w	0	1	0	0	0
1	6 w	0	0	0	0	0
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w = one of these segregants gave slight lysis of Lp^s tester

* This seg. gave slight lysis of Lp^s tester. Streaked out and 10 colonies retested. All found Lp^R

were performed on a pure colony from the 1st streaking from the transduction plate, which was also streaked on B gal to observe segregation for galactose fermentation.

Table 2

Expt 359 - 359A - 359B 5/17/55

(25)

Analysis of the transductions formed with UV'd lysate. At this time a number of spontaneous reversions of the indicators were examined and found stable for galactose fermentation and unchanged for lambda reaction. ~~[illegible]~~ Lp genotypes were determined from tests against both lambda + a lambda sensitive ~~[illegible]~~ culture. Those tests

(A) Transductions to Gal_2^- Lp^s W2790 . (s = segregating, ns = not segregating)

UV Dose →	0	1	2	3	4	5	6
No. trnsd. examined →	24	24	23	24	24	24	24
No: Lp^s →	9 ns	3 ns	22 ns	22 ns	21 ns	24 ns	24 ns
" Lp^+ →	[illegible] 3 s	6 ns 1 s	0	0 [illegible]	1 [illegible]	0	0
" Lp^R →	12 s	18 s 1 ns	1 s	1 s 1 ns	1 s 1 ns	0	0
Spontaneous reversions present in sample	9.6	1.7	1.4	negligible →			

(B) Transductions to Gal_2^- Lp^s W2915

UV Dose	0	1	2	3	4	5	6
No. examined →	36	34	47				
No. Lp^s	0	38 ns	38 ns.				
" Lp^+	6 s 2 ns	2 s	0				
" Lp^R	28 s	31 s 1 ns	8 s 1 ns.				

SEPARATE PAGE

Table 3

(A) Totals for Gal_2^- Lp^s Recipients

UV Dose	0	1	2	3	4	5	6
Segregating	49	52	10	1	2	0	0
not segregating	2	4	60	23	22	24	24
% Seg	94	93	14	4	9	0	0
% not seg.	6	7	86	96	91	100	100

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Introduction

The transfer of genetic material between bacterial cells by temperate bacteriophages has been shown for certain Salmonella and for Corynebacterium diphtheriae. In each of these cases the transduction of genetic factors singly has been demonstrated. This mechanism of genetic recombination is in contrast with the complete sexual mechanism of recombination in which the whole genetic material of the cell participates at one time. The study of these two mechanisms and their interrelationship is difficult in biological systems in which only one has been found to operate. The present report summarizes a study of E. coli K-12 where the independent occurrence of sexual recombination (Tatum and Lederberg, 1947) and transductive recombination has been demonstrated.