

Nontransducible Gal_x - W2312

(51)

<u>Exp</u>	<u>No Additions</u>	<u>HFT Lysate</u>			<u>NFT</u>
		<u>Gal₁ -</u>	<u>Gal₂ -</u>	<u>Gal₄ -</u>	<u>wild type lysate</u>
206 (1)	0	0	0	0	-
(2)	0	-	-	-	0
220 (1)	0	0	0	0	0
(2)	0	0*	0*	0*	0*

* = NFT lysate

Action of Lysate of W2312 on Various Gal- Cultures.

<u>Gal -</u>	<u>No Additions</u>	<u>Numbers of Papillae</u> <u>W2312 lysate</u>
Gal ₁ - Lp ⁺	4	37
Gal ₂ - Lp ⁺ (220)	8	7
(221)	19	28*
Gal ₄ - Lp ⁺	17	74
Gal ₁ - Lp ^s	3	121

* 12/11 examined found stable +

<u>Character</u>	<u>Crosses of W2312 with Known Gal -</u>	<u>Number</u>	<u>% (+)</u>
Gal ₂ - F ⁻	(4)	2112	0.5 (0.05)%
Gal ₄ - F ⁺	1	198	0.5

Table 8
Absorption of the Transducing Ability
of Adenovirus

(52)

<u>Adsorbing Cells</u>	<u>Phage titer</u>	<u>Cell titer</u>	<u>1st Adsorption</u>		<u>2nd Adsorption</u>		<u>3rd Adsorption</u>	
			<u>Phage</u>	<u>Transd.</u>	<u>Phage</u>	<u>Transd.</u>	<u>Phage</u>	<u>Transd.</u>
W84 gal ⁻ hp ⁺	1.0×10^{10}	2.6×10^{10}	—	72%	—	56%	—	0
W750 gal ⁺ hp ⁺	2.8×10^8	6.5×10^9	—	45%	—	100%	—	0
W2175 gal ⁺ hp ⁺	1.8×10^{10}	6.0×10^9	—	35%	—	33%	—	0
W518 gal ⁻ hp ⁺ (1)	2.5×10^9	7.1×10^8	60	79	50	41	16	46
W518 gal ⁻ hp ⁺ (2)	3.9×10^9	5.5×10^8	52	33	—	—	—	—
W811 gal ⁺ hp ⁺	1.4×10^{10}	c. 10^{10}	—	79	—	—	—	—
W1736 gal ⁺ hp ⁺	1.4×10^{10}	c. 10^{10}	—	97	—	—	—	—

2837 | 31.00
 2801
 2990

53

Table 10

Exposure	Post Exposure Cue title	Number Colonies Observed			Total
		Gal -	Gal +	Gal - Partially lysed	
Bottle	1.1×10^9	3280	0	0	3280
HFF lyzate	3.5×10^9	2801	31 (1.1%)	54	2286

Table 11

Examination of Colonies after HFF Exposure

Colony	Number	lyt ⁺ pyogenic	Susceptible	lyt ^R
Gal(-)	31	0	31	0
Gal(+)	26	23	0	3

Transductions to Gal-

Culture to

Gal- locus transduced

Recipient Culture and
to genotype
Environment

W1485 h_p^S

Gal₂-

- $h_p^+ h_p^+$

8 distinct ϕ s obtained from single culture.

Gal₂-

- ~~$h_p^+ h_p^+$~~

2 distinct ϕ s obtained from separate cultures.

Gal₁-

- h_p^+
and
 h_p^S

2 distinct ϕ s obtained from separate cultures.

W1673 h_p^S

Gal₂-

- h_p^+ or h_p^R

3 ϕ s obtained not known whether from same clone.

W1765 h_p^S

Gal₁-

W2373

S

3 ϕ s obtained not known whether clonal or not.

W2252 h_p^S

Gal₁-

W2345

$h_p^{R?}$

2 ϕ s obtained from distinct clones.

Gal₂-

W2341

h_p^R

2 ϕ s obtained from separate clones.

Transduction in *E. coli* K-12
 Progress Report Aug 1953
 September

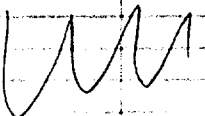
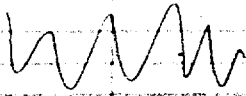
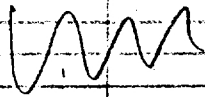
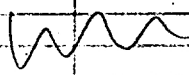

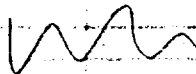
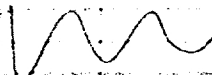
M. L. Morse

1. References

Source

Recipient Cells	K-12 Gal +	W750 Gal ₁ -	W902 Gal ₂ -	W2238 Gal ₃ -	W811 Gal ₄ -
Gal ₁ - prototroph	Experiment M page 190 192A	_____	Experiment N page 190 192B, 192C	not done in progress 221	doesn't go? page 206
Gal ₂ - W2175 (prototroph)	Experiment O page 191 196	Experiment T page 206 209	_____	not done in progress 222	Experiment aside U page 206 207
Gal ₃ - W2247 (prototroph)	not done	page 208	page 208	_____	page 208
Gal ₄ - W578 (prototroph)	Experiment Q page 200D 205	doesn't go? page 189	Experiment R page 191 198	not done doesn't go? 222	_____
Gal ₄ - W811 (prototroph)	Experiment V page 212	doesn't go? page 185	Experiment S page 202	not done doesn't go? 222	_____
Gal ₄ - W1924 (prototroph)	Experiment X page 216	doesn't go? page 208	Experiment W page 213	not done	_____

Lysis

Cells	K72	W750	902 W1210	602 W811 (1607)
W750 lp ⁺	248 + seq anal. complete		by 902 p. 230 + seq anal complete by 1210 p. 243 seq anal complete	Does it go? p 202
W2373 W1765 lp ^s gp ⁺	249D + Do seq anal complete		by 1210 249B + seq anal complete Do by 902 249C + seq anal complete	249A + Do seq anal complete
W1210 lp ⁺	247A + seq anal complete	247C + seq anal complete		247B + seq anal complete
W2281 lp ^s	p. 233 + seq anal complete words almost complete	pg. 236B + seq anal complete		p. 236C + seq anal complete
W811 lp ⁺	Expt. V p. 242 + seq anal complete	doesn't go? 189	by 1210 (do) - + by 902 p. 202 (Expt) seq anal complete	
W518 lp ^s	Expt. Q + p. 207 seq anal complete Expt. anal. almost complete	doesn't go? 194	by 1210 p. 242 + seq anal complete by 902 p. 198 (Expt) seq anal complete	
W1924 lp ⁺	Protein seq. lost.	doesn't go? 208	by 902 p. 213 (Expt W) seq anal complete by 1210 (do)	
W475	Expt. O. 196 complete	Expt. T. page 208 seq anal complete	X	Expt. U. p. 207. seq anal complete
W2342 (W2000m)	Expt. M. 192A + seq anal complete	X	Expt. N. 192B + seq anal complete.	not done

3. Status of the Segregant Analysis

Recipient Cells	Source	Gal ₁ - W750	Gal ₂ - W902	Gal ₃ - W2238	Gal ₄ - W811
Gal ₁ -	K-12	17 17 gal ₁ - 4/4 gal ₁ - 4/4 gal ₁ - (incomplete)	23 18 gal ₁ -, 5 gal ₂ - 5/5 gal ₂ -, 4/4 gal ₁ - 5/5 gal ₂ -, 4/4 gal ₁ - (incomplete)	not done in progress	stable (+)?
Gal ₂ -		20 20/20 gal ₂ - 4/4 gal ₂ - 4/4 gal ₂ - (incomplete)	19 14 gal ₂ -, 3 gal ₁ -, 2 gal ₂ - (double?) incomplete - incomplete -	not done in progress	16 8 gal ₂ -, 7 gal ₁ - incomplete incomplete
Gal ₃ -		not done	stable (+)	stable (+)	stable (+)?
Gal ₄ - Lp ^S		13 13/13 gal ₄ - 4/4 gal ₄ - 4/4 gal ₄ - (incomplete)	21 18 gal ₄ -, 3 gal ₂ - 16/16 gal ₄ -, gal ₂ - incomplete 4/4 gal ₄ - complete gal ₂ - incomplete	not done does it go?	
Gal ₄ - Lp ^T		20 20/20 gal ₄ - incomplete incomplete	19 16 gal ₄ -, 3 gal ₂ - 15/15 gal ₄ -, gal ₂ - incomplete 4/4 gal ₄ - (complete) gal ₂ - incomplete	not done does it go?	
Gal ₄ - Lp ^T		29 29/29 gal ₄ - incomplete incomplete	18 15 gal ₄ -, 3 gal ₂ - incomplete incomplete	not done	

Explanation

17 = no (-) segregants
 17 gal₁ = "allele" by transduction test
 4/4 gal₁ = "allele" by donor lysate test
 4/4 gal₁ = "allele" by cross with gal₁-
 The same segregants as in (-)
 ← what a cell is not transduced by
 ← which "allele" cannot be traced by a lysate of segregant

Segregants from a *E. coli* transduction - One
 ordering the segments is not specified

Random Cell Genotype	Spore Source	Homozygous	Heterozygous	Homo-Hetero	Total
July-	July-	17	2	1	20

Fractin Gal+
 (+) x (-)
 in cross

P	Gal	% +	No. Cells
190	Gal ⁻ x Gal ⁺	12.4	864
	(F-) 2238 x 1655 (F+)		

EML Phase	(F+) Gal ⁻ x Gal ⁺ (F-)	% +
49	750 Y-10	14.7

169	F ⁺ Gal ⁻ x Gal ⁺ (F-)	0.66%	0.300
	750 Y-10		

149	(F+) Gal ⁻ x Gal ⁺ (F-)	3.5	480
	511 Y10		

143	F ⁻ Gal ⁻ Lp ¹ x F ⁺ Gal ⁺	0	71	Galactin Phenocopies
	578 167F			
	F ⁺ Gal ⁻ Lp ¹ x F ⁻ Gal ⁺	0.52	57F	
	51F 1678			
	F ⁻ Gal ⁻ Lp ¹ x F ⁺ Gal ⁺ (Lp ¹)	3.5	29	
	F ⁺ Gal ⁻ Lp ¹ x F ⁻ Gal ⁺ (Lp ¹)	3.8	427	
	51F 1673			

Transduction	Number of Segments	Classification by Transduction	Classification by Lysate	Classification by Crossing over, crossed with			
				Homozygous (+) total prototrophs	Heterozygous (-) total prototrophs		
a d x gal ⁻	4	(1) gal ⁻	gal ⁻	0	896	-	-
		(2) gal ⁻	"	0	918	-	-
		(3) "	"	0	1134	-	-
		(4) "	"	0	863	-	-
<hr/>							
gal ₁ ⁻ x gal ₂ ⁻	4	(1) gal ₂ ⁻	-	0	1037	-	-
		(2) "	-	0	10512	-	-
		(3) "	-	0	110	-	-
		(4) "	-	0	800	-	-
no gal ₁ ⁻ segments found <i>omit</i>							
<hr/>							
gal ₁ ⁻ x gal ₂ ⁻	2	(1) gal ₂ ⁻	-	0	117	-	-
		(2) gal ₂ ⁻	-	0	1096	-	-
		(3) gal₂⁻	-	0	12000	-	-
<hr/>							
	1	(1) gal ₁ ⁻	gal ₁ ⁻	-	-	2+	291
	1	(1) gal ₂ ⁻ gal ₁ ⁻	- <i>omit</i>	-	-	0	12000

Transduction	Number of Segments	Classification by Transduction Key	Classification by Hyate	Classification by Crossing				
				(+) Homotype	(+) Heterotype	(+) Total	(+) Total	
gal ₂ ⁻ x gal ₄ ⁻ hp ⁺	5	(1) gal ₄ ⁻	gal ₄ ⁻	0	2786	3	3183	
		(2) "	"	0	2675	2	3471	
		(3) "	"	0	3485	23	5342	
		(4) "	"	0	5952	1	1665	
		(5) "	"	0	5000	1	891	
	2.	(1) gal ₂ ⁻	gal ₂ ⁻	7	3102	0	1988	
		(2) gal ₂ ⁻	gal ₂ ⁻	10	4364	0	1187	
	gal ₂ ⁻ x gal ₄ ⁻ hp ⁺	4	(1) gal ₄ ⁻	gal ₄ ⁻	0	16164	3	1359
			(2) "	"	0	5730	1	164
			(3) "	"	0	3358	0	202
(4) "			"	0	12848	1	171	
3		(1) gal ₂ ⁻	gal ₂ ⁻	1	11200	0	827	
		(2) "	"	6	10602	0	604	
		(3) "	"	30	6720	0	718	
wild x gal ₁ ⁻		4	(1) gal ₁ ⁻	gal ₁ ⁻	0	426	-	-
			(2) "	"	0	554	-	-
			(3) "	"	0	529	-	-
	(4) "		"	0	391	-	-	
wild x gal ₂ ⁻ (2291)	4	(1) gal ₂ ⁻	gal ₂ ⁻	0	7805	-	-	
		(2) "	"	0	4992	-	-	
		(3) "	"	0	106	-	-	
		(4) "	"	0	4552	-	-	
	2175	4	(1) gal ₂ ⁻	gal ₂ ⁻	0	4071	-	-
			(2) "	"	0	5384	-	-
			(3) "	"	0	2072	-	-
			(4) "	"	0	6988	-	-

Print

(6)

Lysate Assay

<u>Name of Original Transfection</u>	<u>Homotype</u>	<u>Heterotype</u>	<u>Hom-hetro</u>	<u>Total</u>
wild type on gal,-	21/21	0	0	21
gal,- on gal,-	39/39	16	-	55
	60	16		76

Lupinus E

Page	No. Homotype	Heterotype	Total	Wild - x
205	4 (4)	0	4	+
196 2175	4 (4)	0	4	+
192A (4)	4 (4)	0	4	+
<hr/>				9
✓ 192 B (4)	4	5 (902)	9	→ 12
✓ 202 (4)	15	3 (12)	18	→ 5
✓ 198 (4)	16 (400)	3 (902)	19	→ 52
<hr/>				64
✓ 212 (4)	35	0	4	+
✓ 247A (4)	4	0	4	+
✓ 248 (4)	1	-	1	+
<hr/>				
Total 56			11	67
✓ 207 (4)	4	0 (811)	4	→
<hr/>				
Total 60			11	71
✓ 247B (4)	-	1 (811)	1	→
<hr/>				
Total 60			12	72
✓ 236C (4)	-	1 (811)	1	→
<hr/>				
Total 60			13	73
✓ 242 (4)	-	1 (1219)	1	→
✓ 243 (4)	-	2 (1219)	2	→
<hr/>				
Total 60			16	76
✓ 209 (4)	-	2 (1250)	2	

Occurrence of HFT X-

Recip. Cell	K-12	Gal ₁ -W750	Source Gal ₂ -W2175	Gal ₃ -W2238	Gal ₄ -W811
Gal ₁ -	0/4 HFT	_____	<div style="border: 1px solid black; padding: 5px;"> 1/5 gal₂ - HFT 3/4 gal₁ - HFT 2/24 gal₁ </div>	not done	not done Stable(+)?
Gal ₂ -	0/4 HFT	not done 1/1 unstable (+) HFT	_____	not done	not done
Gal ₃ -	not done	not done stable(+)	not done stable(+)	_____	not done Stable(+)?
Gal ₄ Lp ^s	0/4 HFT	not done stable(+)?	<div style="border: 1px solid black; padding: 5px;"> 0/16 gal₄ - HFT gal₂ - not done </div>	not done	_____
Gal ₄ Lp ^t	not done	not done stable(+)?	<div style="border: 1px solid black; padding: 5px;"> 1/15 gal₄ - HFT gal₂ - not done³ </div>	not done	_____
Gal ₄ Lp ^r	not done	not done stable(+)?	not done	not done	_____

Previously - unstable (+) from 518K-12
 750 E 1821 (gal₁ - mixed by gal₄)
 1436E K-12 } examined and not found HFT

Explanation

0/4 - no. lysates found HFT
 no. lysates examined

- 62 Misc obs transduct. not affected by presence of other phage W1736
- 80 50521 road of d (112) W1736
- 89 adaptation of trans. factor W171, W1736
- 99 F- gal⁻ W1574
- 121 peakurization of lysate not possible W 811
- 141 no. cells vs. hand. W 57F
- 177 HFT infection 4.2% W 518
- 178, 168, 169, 170 instability of D1
- 183 (186) (203) HFT (-) infection N16 N1, N6 W1485 W1485, W1673
- 197 (199) anti d sera on HFT D1
- 200A U.V. effect on nat 2175, 750, 811, 1924, 518
- 206 (220) (221 et seq) nontransducible gal 511, 1924, 750, 57F, 2200 2281, 2175
- 217 U.V. on HFT d 1924
- 219a U.V. lysate of ~~4-1~~ ⁴⁻² W 57F
- 223 HFT infection of N16 (3%) also correlation = lysogenicity
- 224 U.V. lysate of ⁴⁻² ~~4-1~~ 1027
- 225 adsorption of d 811
- 226 adsorption of .. 750
- 240 hand. of by gal + R 750 2175

Misc

2

65

②

Topic

Code

→

241

~~① HFT (-) W1765 chs ans ② 750F~~

→

~~② HFT (+) duration
correlation with frequency W178
again~~

244

~~AFT (-) W2252 part 1 -
part 2 -~~

HFT (+) ducts

66

<u>Exp</u>	<u>Relinquish</u>	<u>of</u>	<u>Numbers</u>	<u>% (+)</u>
			<u>(-)</u>	
<u>177</u>	no lypate	0	9.36	0
	HFT lypate	72	1708	4.0
<u>223</u>	no lypate	0	0	-
	HFT lypate	39	1312	3

Expt	Page	(X)	hys	Descript
V	212	1, 10, 12, 1F x 1436		FUEK12
Q	205	4, 6, 8, 10 x 1436	complete	STATK12
247A	-	4, 13, 22, 23 x 902		1210t K12
248	-	1, 7, 9, 11 x -?		750t K12
249D	-	4, 11, 8, 12 ¹⁴ x -?		1765 gal, - t K12
233	-	13 x 902F ⁺	3, 7, 13, 16	22Ht K12
247C	-	11, 13, 22, 24 x 902		1210t 750 (2 hrs)
236 B	-	4, 6, 21 x 902	2, 8, 12	22Ht 750
O	196	complete	complete	2175t K12
M	192A	2, 14, 15, 17x -?	complete	2342 (750pr t K12)
N	192B	2- complete w/o 1- confused	complete	750pr t 902 (2342)
T	209	all	all	2175t 750
230	-	230-5 x 902 3 others	5 + 3 others	250t 902
243	-	3, 6, 7 x 902	3, 6, 7	750t 1210
249B	-	10, 13, 20, 21 x -?	10, 13, 20, 21	1765 gal, - t 1210
249C	-	12 x -?	12	1765 gal, t 902
S	202	4 gals x 1436 complete 14, 15, 17, 19 x 902 5, 9, 16 x 1436, 902 *	4 complete 5, 9, 16	81t 902
242	-	5, 8, 9, 20 x 1436, 902 *	5, 8, 9, 20	578t 1210
R	198	4 Gals - x 1436 complete 4 " x 902 " complete 2 Gal L x 902 complete 2 Gal L x 1436 " complete	complete complete 1, 4, 17 ok	578t 902
X	213	1, 4, 14, 17, 1F x 902 1436 *		1924t 902
249A	-	6 x -?	6	1765 gal, - t 84
247B	-	1, 8, 14, 1F x 902 1436 *	1, 8, 14, 1F	1210t H11
236C	-	6, 10, 14 ¹⁴ x 902, 1436?	6, 10, 14, 23	22Ht t 811
Z	207	1, 3, 7, 13 x -?	1, 3, 7, 13	2175t 84

Gal - mutants induced

Confirmation

$\Sigma = 3$
 $\begin{matrix} 1 & 1 & 4 \\ & 1 & 1 \\ & & 2 \\ & & & 2 \\ & & & & 2 \\ & & & & & 2 \end{matrix}$
 2 mutant
 (18)
 (X) 811 → 7(4)

W	designations	locus (if known)	transduced by	confirmation
206	W1673	-2 (2310)	transd. by 2, not by 1, 4 = double?	✓ ✓
		-4 (2311)	" " " " " " " "	✓ ✓
		-5 (2312)	not " " " " 1, 2, 4 non transducible?	(X) 811 → 7(4)
		-6 (2313)	" " 1, 4 " " 2 = 2- ✓ ✓	
		-7 (2314)	" " 1, 2, 4 _____ = new locus? ✓ ✓	
		-8 (2315)	" " 1, 2, 4 not by 3 = " " " 3-? ✓ ✓	
		-9 (2316)	" " 2, 4 not by 1 = 1-? ✓	
		-10 (2317)	" " 2 not by 1, 4 = double? ✓	
		-11 (2318)	not transd. by 1, 2, 4 = non transducible?	

2312 x 811 → 11/84

220 W2312 not transd. by (HFT) 1, 2, 4, 877(+), 1412
 (MFT) 1, 2, 4, 1412

mode λ+ -lyrate

transd. 1, 4, 6 possibly not gal⁻

W2318 not transd. by 1, 2, 4 (HFT) -

221 W2318 x 811 0+/206

W2312 lyrate of does not transd 2175 but others.

222 W2312 x 902 Σ = 11/2112 = 11/198
 x 811

225 W2312 x 1655 to see if 2 types (→) B transducible only 17 prots (+) obtained

W2312 x 1655F- (with prots added) → 3/11

Gal: mutants induced
W1765

(2)

(69)

Box	orig designation	locus	
238	2 W2645	not + 4 ⁻ , 1 ⁻ , 2 ⁻	un hand. ?
	5 W2646	+ by all	new ? ✓
	6 W2647	+ by all but 1	1 ⁻ ? ✓
	8 W2648	+ by all	new ? ✓
	10 W2649	new ? ✓
	11 W2650	not + by 1 ⁻ , 4 ⁻	1 ⁻ 4 ⁻ ?
	12 W2651	not + by 2 ⁻	2 ⁻ ✓
	13 W2652 2 ⁻	2 ⁻ ✓
cross	of #11	x 578 →	04/6050
		x 750 →	04/2683

Σ

2	2 ⁻
3	x ⁻
1	1 ⁻
1	1 ⁻ 4 ⁻
1	unhand.

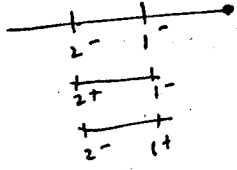
T18 - 2175t 750 = loc + gal₂ - gal₁ - by hand assay

① loc gal₂ - trans loc₁ gal₁

② dominated by mixture of

HFT 1- but not by the amt singly
HFT 2-

③ Proposed



Forward ①

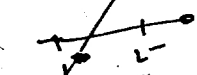
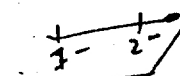
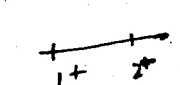
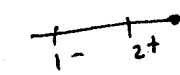
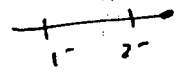
Forward ②

Forward ③

Forward ④

Forward ⑤

Segregants



in loc

slow

slow

+

+

slow

Prox
bandwidth

wt.

1-

2-

2-

1-

Revised
seg graph

wt

wt

wt

yes

yes

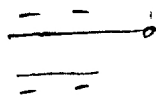
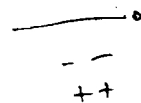
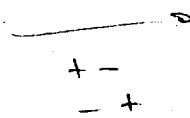
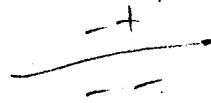
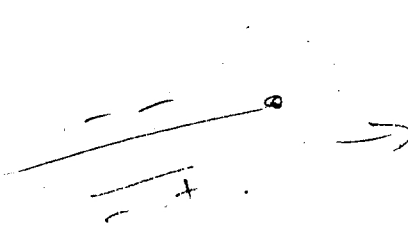
band

Forward ① 1- 2-

Forward ② 1- 2-

③ Update on 2070
2 seg tested

5 1-
2 2-



Double (- -)

237A - 10 = 750 + N16

wt t by N16, N1 (repeated), possibly by SIF
cutter Lp⁵

ly site apparently didn't produce 2175, 200

Crushed with 902 ⁰⁴/1650

209 - 18 2175 + 750

wt t by N1, N16, ~~902~~ but by 1012
SU

ly site yielded to t 750, 2175, 2297, 2070
possibly 84, 578 nearby. - these gave all tubes

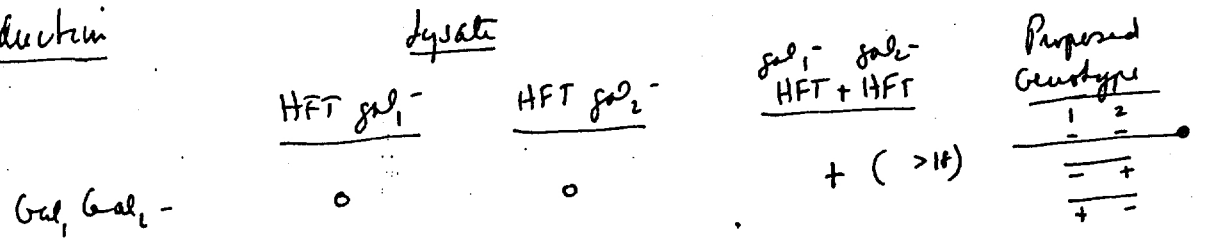
Account
issues and
pay at this
see p. 209

209 - 19 similarly to T18

236C - 202350

$T18 = 2175t.750$

1. The transduction



2. The Segregants. (not possible to distinguish bet pro loci)
 And. Papirose checked in Gal and (-) classified by Transduction:
Transduced by

	<u>Only</u> <u>HFT gal₁⁻</u>	<u>Only</u> <u>HFT gal₂⁻</u>	<u>Neither</u>	<u>Total</u>
<u>Number</u>	5	10	17	32
<u>Genotype</u> (proposed)	Gal ₂ ⁻	Gal ₁ ⁻	Gal ₁ ⁻ Gal ₂ ⁻	-
<u>Structurally</u>				-
<u>Number of</u> <u>Cultures found</u> <u>Giving Gal+ unstable</u> <u>Reversion</u>	0	1	-	-
<u>Possible</u> <u>Reversion</u> <u>Structure</u>	-		-	-

Correlation of h^+ Change with Transduction

73

Recipient Cells

p ³	Lysate	Transduction			Total	Segregant			T(%)
		h^+	h^+	h^+		h^+	h^+	h^+	
Gal ₁	① wild	0	9	0	9	0	9	0	9
	② gal ₁	0	0	0	0	0	0	0	0
	③ gal ₁	0	0	0	0	0	0	0	0

the various Gal⁻ clones negative cell results similar to those shown in table 4 are obtained. With the possible exception of the interactions of Gal⁺ and Gal⁻ each of the plates is capable of evolving Galactose fermenting papillae upon plating (cross with non-homologous negative cells. With the usual h^+ Gal⁺ interactions are erratic some times giving significant differences between control and lysate added plates, sometimes not. This interaction will be dealt with in more detail in a later section, it will be sufficient to state here that

Gal ₂	Lysate	Transduction			Total	Segregant			T(%)
		h^+	h^+	h^+		h^+	h^+	h^+	
① wild	① wild	0	19	0	19	0	19	0	19
② gal ₁	② gal ₁	0	0	0	0	0	0	0	0
③ gal ₁	③ gal ₁	0	0	0	0	0	0	0	0

each interaction does not produce clones that are phenotypically different. The differentiation by lysate interaction corresponds to the differentiation of these loci by recombinational analysis. Reverse mutation restores the ability of lysates of a Galactose

Gal ₂	Lysate	Transduction			Total	Segregant			T(%)
		h^+	h^+	h^+		h^+	h^+	h^+	
① wild	① wild	0	29	0	29	0	29	0	29
② gal ₁	② gal ₁	0	0	0	0	0	0	0	0
③ gal ₁	③ gal ₁	0	0	0	0	0	0	0	0

negative culture to evoke papillae from cells of its own type (table 2). Reversions of the first gene. Reversions of this second class should not be able to evoke papillae from cells of type. Such reversions as the latter have not as yet been investigated.

Examination of the other characteristics of the cells transduced to ability to ferment galactose by lysate exposure has uniformly shown no changes in any of them with the exception of the induction of lysogenicity in the lambda sensitive forms.

tot	h^+
23	20
36	25
22	17
12	11
20	19
24	24
127	116

0.91
116.0
1143
170

Amended Table a Correlation between λ_{phage} + Trans.

74

2-2373

Strain	Phage	Trans.	+4	+4 ^{1R}
249A	30/1	5S, 17+	(12)1	1+
249B	56/0	3S, 18+	3R (2)8	7+
249C	44/1	3S, 7+	2R (1)2	1R
249D	33/1	3S, 20+	9	7+

224

Strain	Phage	Trans.	+4	+4 ^{1R}
229A	46/0	5S, 16R	2/	16R
229B	4/0	4S, 17R	4S	17R
229C	4/0	4S, 17R	4S	17R

578

Strain	Phage	Trans.	+4	+4 ^{1R}
1709	4/0	1R, 18R	1R	18R
146	115/29	4S, 4R	4S	4R
147, 150	247/41	4S, 4R	4S	4R

The number of galactose fermenting colonies is proportional to the amount of lysate added (figure 1). Since each of these mutations is inability to ferment galactose is capable of reverse mutation the data must be corrected in each case. This has been done for the data in figure 1 by subtracting the number of spontaneous reversions as determined from control plating with no added lysate. In addition to indicating proportionality, the data in figure 1 indicate that the cells show the effect as irrespective of the genotype of the cell, and that lambda sensitive cells are more capable of showing the effect of added lysate than lysate cultures.

Page 9
Hyates of Unstable Galactose (+)

Titers .5

Page	Recipient	Hyate	Plaque	Transducing	Plaque #	
271	(2) Gal ₁ -	Gal ₂	1.5 x 10 ⁷	5 x 10 ⁷	7.5 x 10 ⁷	60
284	(5) Gal ₄ -	Gal ₂	1.5 x 10 ⁸	5 x 10 ⁷	7.5 x 10 ⁷	2
284	(1) Gal ₁ -	Gal ₂	1.5 x 10 ⁷	5 x 10 ⁷	7.5 x 10 ⁷	32
284	(4) Gal ₂ -	Gal ₁	1.5 x 10 ⁷	5 x 10 ⁷	7.5 x 10 ⁷	4
286	(3) Gal ₁ -	Gal ₂	1.5 x 10 ⁷	5 x 10 ⁷	7.5 x 10 ⁷	
286	(6) Gal ₄ -	Gal ₂	7.3 x 10 ⁸	2.5 x 10 ⁷	2.8 x 10 ⁵	29

* the highest single assay of transducing activity

Stable

(hand count)

Table 10

Lysals

(75)

Recipient cells

Wild

Gal₁-

Gal₂-

Gal₄-

Recipient cells	Colony	Sp. Sample
Gal ₁ - Lp ^S 33	1	14
Lp ⁺ 46	1	42
Lp ⁺ 143	1	42

Sp. Sample
11
84
92

Sp. Sample
11
4
0

Sp. Sample
30
27

30
%27

Recipient cells	Colony	Sp. Sample
Gal ₂ - Lp ^S 46	0	15
Lp ⁺ 24	17	21
Lp ⁺ 23	4	6

Sp. Sample
21
23
25

Sp. Sample
27
61
0

Sp. Sample
28
29
56

4
52
0

Recipient cells	Colony	Sp. Sample
Gal ₄ Lp ^S 53	19	383
Lp ⁺ 57	41	133
Lp ^R 32	31	127

Sp. Sample
72
96

Sp. Sample
472
23
31

Sp. Sample
20
50

Gal₁- Lp^S

Total	Stable
33	14
11	11
56	20
30	29
130	74

74 57/130

stable observed x transduction's
sample taken

51 x 4
24 x 25