June 10, 1955

MATRIX TO TEST TRANSDUCTION MAP SEQUENCES

201

Sequence operators	Codes for multiple exchange types (Operators on donor genotype)				
3-point test					
123	b				
132	c				
213	a				
4-point test					
1234	b	c	ac	bc	bd
1243	b	d	ad	bd	bc
1324	c	b	ab	bc	cd
1342	c	d	ad	cd	bc
1423	d	b	ab	bd	cd
1432	d	c	ac	cd	bd
2134	a	c	bc	ac	ad
2143	a	d	bd	ad	ac
2314	c	a	ab	ac	cd
2413	d	a	ab	ad	cd
3124	a	b	bc	ab	ad
3214	b	a	ac	ab	bd

The complete table can be generated as the permutations of (a'b, cd') where a'b=bb, bc, bd, and bb=b.

Instructions:

1. Write down the donor genotype (differential markers only) in any arbitrary sequence, e.g., W- X+ Y+ Z-.
2. Group the experimental results into the rare and frequent classes.
3. Code these classes as transformations of the donor genotype. The code "a" means "reverse the sign of the first locus written", "b" the same for the second, etc. Thus, (ad)(W-X+Y+Z-) would be W+X+Y+Z+.
4. The table gives the codes for the multiple exchange classes (mec) corresponding to each sequence. Those models are excluded where frequently found types are included in the mec codes, and vice versa.
5. The sequence codes can be translated into maps by writing the donor genotype as W X Y Z and transposing accordingly. Thus, 2314 would be the map XYWZ.
   1 2 3 4
6. For the reciprocal transduction, superimpose the operation abcd, so that, e.g., ac becomes bd; c becomes abd in the mec codes.

J. Lederberg

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Crossing Cont.

	Page
Cross bps to obtain bp+	294
Col_4-F+ x Col_2-F- and neg F	333, 337
Col_4-bp' x Col+ bp+	333

Cont.

Segregations 7- —x 1-6-	319
4- —x 1-6-	319
+ —x 3-7-	320
+ —x 1-6-	320
1-6- —x 2-	321
6- x→x 7-	323, 343, 344
6- x 1-	323
7- —x 1-	327
4- —x 1-7-, 6- —x 1-7-	326, 336
4-x 1-6-, 7 -x 1-6-	327
6- —x 1-7-	332
+ —x 1-7-, 6-7- —x 2-	344
4- xx 6-	345, 346
4-6- —x 2-	346,

Positive Effects

Summary

Segregants			Segregants from Gen +				
Cues	Eco	Stbl	Cues	Eco	Amplif	P.E.	Page
1⁻	4⁻	12/24	12	0	0	0	
4⁻	1⁻	7/24	10 (6)	1 (1)	2 (1)	2 (2)	F⁻ K⁻
14⁻	+	0/24	24	0	0	0	
8⁻	14⁻	?	135	14	3	0	
1⁻	6⁻	16/22	2	4	0	0	
6⁻	1⁻	5/24	8	2	3	6	
16⁻	+	3/23	20	0	0	0	
8⁻	16⁻	?	12	4	0	0	
1⁻	7⁻	19/21 ~~32/42~~	~~1~~ (4)	~~3~~ 4	0 3	0 1	
7⁻	1⁻	4/21	7	4	3	3	
17⁻	+	0/24	24	0	0	0	
8⁻	17⁻	0/30	29	1	0	0	
6⁻	4⁻	3/17	14	0	0	0	
4⁻	6⁻	17/23	3	1	1	0	
46⁻	+	0/16	16	0	0	0	
2⁻	46⁻	?	52	0	2	0	
6⁻	7⁻	15/21	0	4	2	0	
7⁻	6⁻	7/13	5	0	2	4	
67⁻	+	?	15	0	0	0	
2⁻	67⁻	3/24	18	2	1	0	

Revision summary

Page	Endo	Exo	Total	Comment
360	4	4	8	extent given
361	— 4 —	— 4		360-2 (Col 1 – Col
363B	HH=4			W2868
	6 HHH			
364	5	10		10 different heterozygotes
358	— 2 —	1	26 (–add 20 = 26)	total = 77 W2869
291	— 8 —	2		2 different 358-1, 358-2
	— 5 —			
	— 8 —			
	— 4 —			
	— 8 —			3 different heterozygotes
	— 4 —			
		37		
			77	

18 different heterozygotes

	373-1	373-2	373-3	373-4	375-1	375-2	375-3	375-4	375-5	375-6
Lp^+ s	0	25	15	21	34	9	10	0	0	15
ns	0	1	0	0	1	7	2	24	0	2
Lp^L s	9	3	2	3	1	4	6	0	0	5
ns	8	1	0	0	0	2	2	0	0	2
Lp^S s	0	0	3	0	0	0	0	0	0	0
ns	4	[illegible]	0	0	0	0	2	0	24	0
	21	[illegible]	20	24	36	17	22	24	24	24
		36				5wt				

Condensed summary of above ↓

Gm V n	100	6	20	60	20	75	60	125	1000	100	120
	373-1	373-2	373-3	373-4	375-1	375-2	375-3	375-4	375-5	375-6	375-7
Gref	Lp^+ s/Lp^L s/Lp^S s	Lp^+ seq	Lp^+	Lp^+	seq Lp^+	seq Lp^+	seq Lp^+	unseq Lp^+	unseq Lp^s	seq Lp^+	seq Lp^+
Lp^+	0	26	15	21	35	11	12 [4]	24	0	17	22
Lp^R	17	4	2	3	1	6 [2]	8	0	0	7	2
Lp^S	4	6	5	0	0	0	2 [4]	0	24	0	0
	21	36	22	24	36	19	24	24	24	24	24
	4/4	–	–	–	0/1	–	1/2	–	–	12/3	11/3

Segregation from single heterogenotes

(Ref)

No Segregants

Syngenote	Endo	Exo.	Endo	Exo	Single	Total
365B	1⁻ 4⁻	2⁻	11	2	0	13
364	4⁻	2⁻	13*	7*	0	20
	* 3/7 Exo homogenotes; 0/13 Endo "		29	8	0	37
			42	15	0	57
362 (W2868) see 361, 298, 292A	4⁻ s	2⁻ R	s: 3, R: 0	s: 13, R: 34	s: 1, R: 0	51
359B (W.λ)	2⁻	7⁻	7ζ → {7	0	0	7}
			4ζ → {6	0	0	6}
			2ζ {5	0	0	5}
			3	4	0	7
			6	1	0	7
			5	1	0	6
			2ζ {6	0	1	7}
			ζ 1	0	0	1

P.E.

1 x x 4

(211)

	Ref.	F	Endo	Hp	Hel. Hp ∅	Stbl	Endo	Exo	Amphi	P.E.
(285-1)	348	+	1	S	~~R/S~~	12/24	12	0	0	0
	368-2	-	1	S	R/S	18/22	3	0	0	1
(285-2)	331	+	1	S	R/S	13/22	6	1	0	1
	368-1	-	1	S	+	9/15	3	2	0	1
						52/83 (0.63)	24	3	0	3
	366-1	F-	4-	S	+	11/24	6	1	1	2
	329	F+	4-	S	+	7/24	10	1	2	2
	360-2	F+	4-	R	R/S	12/24	4	4	3	1
	366-2	F-	4-	S	R/S	6/20	3	4	2	2
	360-3	F+	4-	R	R/S	9/19	1	3	3	3
						45/111 (0.41)	24	13	11	10

Hp- Hp+

A A x A A

b b B B

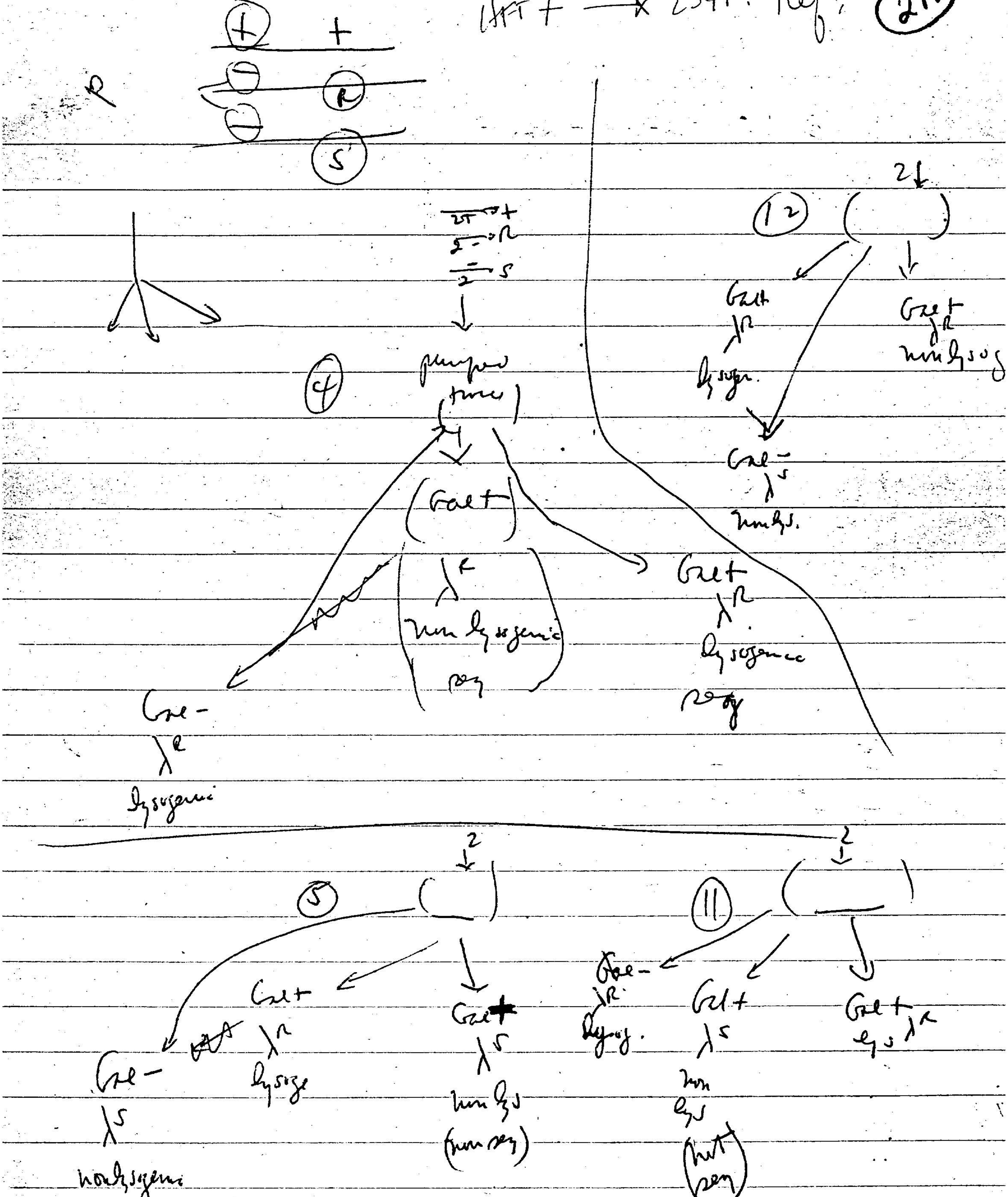
a	A
b	B

A A — b b — Hp-/Hp+

A A — B b — x

A A — B B

HFT + → x 2341. Ref: (212)



Reversion Study

Lp^S Gal- → Gal+

2341 Lp^R/Lp^S → Lp^S + Lp^R 297

1 Lp^R/Lp^S 8/8 reversion seq

1 Lp^S 6/6 reversion not seq

257c6 4- 2+ Lp^S // 4+ 2- Lp^R 292

3 2- rev Lp^S (purple reverted) - (1) non seq.

1 4+ neg Lp^S (") - (1) non seq.

12 2-/2- neg Lp^R/Lp^S (purple) - 11/12 seq.

257c6 · 5 2- Lp^R (five reversion) - ~~5~~ 5 clones of 2/2 reversion seq 298

257c-6 → { 1 2- Lp^R (2/2 reversion unstable) 292A

292-1

292-22 → { 3 2- Lp^R (3/3 reversion unstable)
5 2- Lp^S (5/5 reversion stable)

285-2 1+ 4- Lp^S // 1- 4+ Lp^R 303

↘ (+) + + $Lp^?$ _ of 17 Gal+ obtained
- - ?

9 λ^R were also seq

3 λ^S were not seq.

2279 x— HFr C- 323
Gal-

↘ Lp^R/Lp^S 6-/6+ 1+/1- → 1 Gal_6 - Lp^S → 3/2 Gal+ reversion stable

↘ 1 Gal_6 - Lp^R → 1/6 Gal+ reversion stable

Reversions - Other loci - Diploidy

2341 Lys^R/Lys^S $2^-/2^-$ 288

to see if diploidy for V_1 has occurred. V_1^S/V_1^R would be sensitive. Obtain V_1^R from 2341, if diploidy for V_1, all V_1^R should be λ^S

21 V_1^R obtained, 20 were Lys^R, 1 Lys^S

202-16, 241-14, 241-19 } Lac$^-$ Gal_2^-/Gal_2^-, Lac^R were found stable. 291

241-14, 202-16A } λ_2^R should not be possible 300

2 mal- HFT 2$^-$ obtained 241-14

1 " " " 202-16A

2307X — HFT2$^-$ 309

Xyl$^-$ ara$^-$ Gal_2^- → Xyl$^-$ ara$^-$ Gal_2^-/Gal_2^- No value

2350X — Gal_4^- (NFT) 341

Gal-Lac$^-$Xyl$^-$Ara$^-$ → 1 HFT 2$^-$ obtained - reversions blamed 4/6 Gal$^+$ seg

6/6 Lac$^+$ did not seg

6/6 Xyl$^+$ " " "

6/6 Ara$^+$ " " "

0.2c
566 | 117.0
1132
3800

Lp^R/Lp^+ transl.

Endo	Exo	+/total	Lp^R	Lp^+	Page
4-	2-	39/1312	1	7	223
		7/256			
4-	2-	—	1	0	241
4-	2-	36/2801	3	23	254
4-	2-	2/142	1	1	257
..	..	26/1870	high mult.		259
		108/1279	—		
		117/566	—		
		Lp^R 8/140, Lp^+ 1/426	—		268
		18/199	—		276
		10/215	—		278
4-	1-	2/52	1	1	274
		2/408	—		282
1-	4-	2/356	1	1	285
6-	1-	3/267	—		308
2-	1-	18/428	—		330
7-	6-	9/423	1	1	342
4-	6-	3/295	1	1	342
4-	2-	4/1331 (37c)	—		350
		9/150 (31c)	—		350
2-	1-	3/1254 (37c)	—		350
		3/817 (30c)	—		350
1-	2-	~~[illegible]~~ (37c)			350
		5/161 (30c)			350

(206)

Exo	Exo	+/total	Lp^R	Lp^T
1-	2-	1/311	1	0
+	2-	?	1 ← Reconstructed	1
+	1-	?	1 Reconstructed from Lp^T	
+	4-	?	0	1
~~2~~	+	9/595-	0	8
			13	45-

0.22
58) 13.0
11 6
1 40

~~[illegible]~~

Hsds
*4- hap 20/2- ← 2/90 cdis 4-/4-
2- 2/2- Syn } (2/24) (10/114 HFT)
2- hap }
4-2- hap 1/24

4- 5 — 3
2- R/S — 6 — 19
2 - 5 — 2 — 4 — 6
4- 2- 5 — 1 — 1

Exo

pages in need

Homogenote Summary

Homogenote	Observation	Ref.
[2-] (D1)	518 × 892 mix (153)	
	D1 → × 2050 → solid smear (157) D1 → × 518, 902, 2050 → solid smear (161) D1 titer (164) D1 → × 750 D1 → × 2050	
	D1 → × 518 → dendritic solid (165) D1 → × 2175 (165b) D1 ⊗ 902, 892, 1436 (166) 2050 → × D1, 750 → × D1 (167)	
	D1 {clone Gal₂⁻ Gal+ᴿ unstable 7/10 (168) D1 Gal+ᴿ → (−) neg dom.² (169, 170) D1 × 902 (172, 174, 175) D1 Gal+ᴿ 3/p (179)	
	D1 × 1673 D1 → × 1485 → Gal₂⁻ (178, 183) ~~[illegible]~~ (185) D1 → × 1485 (186)	
	D1 one step, single burst (188) ; 4P5ED1 → Gal₂⁻ seq (190) D1 → × 1924 (2.0×10⁷/ml) (193) D1 vs anti serum (197)(199)	
[2] (D4)	Gal+ᴿ stable (168) D4 × 902 (172, 174, 175) D4 Gal+ˢ (179) D4 → × 518 HFT (181)	
~2343 Gal₁⁻ prototroph 902 × [1-] (N1)	Gal₁⁻ (192B) N1 & sat HFT (192B) N1 × 902 (Sᴿ P) (192B) N1 × 2251 Sᴿ P (mA) (192C) 2 Gal+ᴿ non HFT × 811 (192C)	
	N1 × 1485 → Gal₁⁻ (203) 2 Gal+ᴿ stable (203) LOST (219)	
2343 Gal₁⁻ prototroph 902 × [1-] (N7)	Gal₁⁻ (192B) N7 & sat HFT (192B) N7 × Gal₁⁻ Gal₂⁻ SᴿP (192B) N7 × 2251 SᴿP (mA) (192C) 2 Gal+ᴿ non HFT × 811 (192C)	
	3 Gal+ᴿ stable (203)	
2343 Gal₂⁻ prototroph 902 × [2-] ALSO KNOWN AS [2342] (N16)	Gal₂⁻ (192B) N16 × 902 (SᴿP) (192B) N16 → LFT seq & sat (192C) N16 LFT seq ᴸL⁻? (192C) N16 HFT (192C)	
	N16 → × 1924 (3×10⁸/ml) (201) N16 → × 1673 → Gal₁⁻ Gal₂⁻ (W2432) (203) 9/10 colonies HFT (219) N16 → × 2252 (2341) (244)	
	12/p Gal+ᴿ unstable (227)	

ALSO KNOWN AS [202-16]

(2⁻) (S16) 902–x 811, Gal₂⁻ (202) x 1436, 902 (202) Lac^R stbl (290) tested HFT (299) Mal-λ_2^R (300) one step Mal-λ_2^R deriv. (306)

(4⁻) (S18) 902–x 811 Gal₄⁻ (202) HFT / Gal₁⁻, Gal₂⁻ Gal₃⁻, wt Fil, 1924 (216)

ALSO KNOWN AS [2346]

(1⁻) (NA-4) 902–x 750, Gal₃⁻ (230) NA-4–x 1765 (241) –x 2252 (2345) (244) 4/5 Gal+$^R_{UV}$ not stbl (267) LFT eg Gal₃⁻ 8/8 Gal+^R stbl (270)

[2⁻] (241-14) 902–x 750, Gal₂⁻ (241) 8/10 cell. tested HFT (270) 12/12 Gal+^R unstbl (270) LFT eg Gal₂⁻, 12/12 Gal+^R stbl (270) (298) Lac^R stbl spontaneous λ HFT (299) tested HFT (299) one step (300)

[2⁻] Mal-λ_2^R (303) UV mod. Mal- λ_2^R deriv. λ (316) spont λ Mal- λ_2^R HFT (340) HFT yield/cell (352) HFT λ yield (368)

(241-19) 902–x 750, Gal₂⁻ (241) 5/10 cel. tested HFT (270) 12/12 Gal+^R unstbl (270) LFT eg 1⁻2⁻ (270)

(291) Lac^R stbl

one step (376)

[4⁻] (247B-1) 811 → x 1210, Gal_4^- (247B-1). 9/10 LFT seg [illegible] Gal_4^- $Galt^R$ seg [illegible] (247B-1)
→ x 2252 (276)

[2⁻] (257-2) 902 → x 750, Gal_2^- (257) LFT seg Gal_2^-, $Galt^R$ stable (257)

[2⁻] (257-4) 902 → x 750, Gal_2^- (257) LFT seg Gal_2^-, $Galt^R$ stable (257).

Reexamine

[4⁻] (293-12 etc) and other HFT seg from same trand. clone — 811 → x 2175 (293) lysate HFT (349) tested (365) ↓ [illegible] 3/6 $Galt^R$ unstable (365) (different from [illegible]) 1/6 $Galt^R$ unstable (a different)
(293-12 [illegible]) (365) 2/4 $Galt^R$ unstable (366) (a different →) 1/1 $Galt^R$ unstable (766) (a different →) 2/4 $Galt^R$ unstable (766) (a different →) tested (366)

[2⁻] (293-1A) 811 → x 2175 (293) tested, (339) HFT 4/4 $Galt^R$ unstab. (339) LFT seg 2⁻ (339)

[2⁻] (293-2A) 811 → x 2175 (293) tested (339) 2/3 $Galt^R$ unstab. (339) LFT seg 2⁻ (339)

[2⁻] (293-2B) 811 → x 2175 (293) tested (339) 2/3 $Galt^R$ unstab (339) LFT seg 2⁻ (339)

[2⁻] (293-11A) 811 → x 2175 (293) tested (339) 3/4 $Galt^R$ unstab (339) LFT seg 2⁻ (339)

[1⁻4] (295-1) (ALSO 295A-1,2,3,4) 283-1 → x 1210 (295A)

4/6 Gal+ unstbl

HF [7] (309-1) 2342 → x 2307 (302) obtained ↑ (309) UV mad of gnte (359) (359A) (359B)
7/8 Gal+ unstbl (363B) UV mad. (364) LFT neg 7- (390) 0/7 Gal+ LFT neg (390)

[6-] (311-2) 2070λ+ → x 2175 (311) 2/2 Gal+ seg (363B) LFT neg 6- (363B) 0/2 seg (390)

[2-] (341-9) 811 → x 2580 (335) 4/6 Gal+ unstbl (341)

[2-] (341-12) 811 → x 2580 (335)

[2-] (364A1) 2342 → x 518 (364) 2/2 Gal+ unstbl (364)

[2-] (364B2) 2342 → x 518 (364) 1/2 Gal+ unstbl (364) 4/6 Gal- seg = Gal- (364)

Observations on Homogenotic cultures.

Table 8

Homogenote			LFT Segregant	
Phenotype	Derived from:	Fraction Gal+ Reversions Segregating	Phenotype	Fraction of Gal+ Reversions Segregating
Gal_1^-	Gal+ 1⁻2⁺ / 1⁺2⁻	—	—	0/4
	Gal+	—	—	0/6
	2146	4/5	Gal_1^-	0/8 (1)
Gal_2^-	293-1A 2⁻4⁺ / 2⁺4⁻	4/4	Gal_2^-	—
	293-2A	2/3	Gal_2^-	—
	293-2B	2/3	Gal_2^-	—
	293-11A	3/4	Gal_2^-	—
	341-9	4/6	—	—
	2B82 1⁻2⁺ / 1⁺2⁻	12/12	Gal_1^- Gal_2^-	none obtained (2)
	241-14	12/12	Gal_2^-	0/12 (3)
	341-14	12/12	Gal_1^- Gal_2^-	none obtained
	257-2	—	Gal_2^-	0/1 (minimum)
	257-4	—	Gal_2^-	0/1 (minimum)
	D1 2⁺4⁺ / 2⁻4⁺	10/18	Gal_2^- (mm 4^+)	—
	D4	—	—	0/2 (minimum)
	302-16	—	—	—
	241-12	—	—	—
	3641A1	2/2	—	—
	3641B2	1/2	Gal_2^-	—
Gal_4^-	S18 4⁻2⁺ / 4⁺2⁻	—	—	—
	2478-1 8⁻4⁺ / 4⁻8⁺	—	Gal_4^-	0/1 (minimum)
	243-12S 2⁻4⁺ / 2⁺4⁻	—	—	—
		(1) 1/6	—	—
		(2) 1/6	—	—

223

(3) 2/4

(4) 1/1 — —

(5) 3/4 — —

GdI_6^- $3II^2$ $2^-6^+/2^+6^-$ 2/2 GdI_6^- $-0/3$

GdI_7^- $3II^1$ $2^+7^-/2^-7^+$ 2/8 GdI_7^- $-0/7$

$GdI_1^-GdI_4^-$ $8^-1^+4^+/8^+1^-4^-$ — — —

Table 5

The frequency of transductions unstable for galactose fermentation

Recipient cells		Gal (+)	Lysates Gal_1-	Gal_2-	Gal_4-
Gal_1-	Lp^s	9/22(41)	-	0/11(0)	0/29(0)
	Lp^+(1)	23/24(96)	-	23/24(96)	0/27(0)
	Lp^+(2)	17/24(71)	-	24/24(100)	-
Gal_2-	Lp^s	28/48(58)	63/72(88)	-	64/72(89)
	Lp^+(1)	22/24(92)	19/24(79)	-	16/24(67)
	Lp^+(2)	16/24(67)	21/24(88)	-	22/24(92)
Gal_4-	Lp^s	13/24(54)	0/72(0)	21/24(88)	-
	Lp^+	20/24(83)	0/96(0)	19/24(79)	-
	Lp^r	29/48(60)	-	18/24(67)	-

The figures shown are the fraction of cultures unstable for galactose fermentation. Percentages are shown in parenthesis.

487 unstable
613 total

Locus

Ashburner and Mathis - the position occupied by a gene on a chromosome, with regard to its linear order.

· Woodruff (31) ..... a series of allelomorphic factors (the positions they occupy is their "locus"); .....

· Sinnott, D, + D (217) .... the term locus is used both to indicate the location of a gene on a chromosome map and also to designate the unit, variants of which are alleles."

· Calkins (11) "The name of a mutant and its symbol represent the locus name and the locus symbol respectively."

(15) "The chromosome theory of heredity states that the genes are situated at definite loci in linear order on the chromosomes."

— Knight (90) "The fixed position of a gene on its chromosome."

· Cole (367) "the position on a chromosome occupied by a gene or any of its alleles"

· Riley (17) In other words, on each homologous chromosome there is a gene at a particular place or locus .....

· Klein (166) position occupied by a gene on a chromosome.

· Strickberger + Brachet (94) ..... every gene occupies a fixed position on a chromosome .... such a position is known as a locus ... "

· Jennings (166) The position of a gene on the map or on the chromosome is known as its locus."