201

MATRIX TO TEST TRANSDUCTION MAP SEQUENCES

	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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7⁻ —x 2⁻	
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6- x 1-7- 332

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4-6- x 2- 346,

Position Effects

Summary

Syngenetic Endo	Syngenetic Exo	Stable	Segregants from Cross Endo	Exo	Amphi	P.E.	Page
1⁻	4⁻	12/24	12	0	0	0	
4⁻	1⁻	7/24	10 (6)	1 (1)	2 (1)	2 (2)	F-X
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 5	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	Ecto	Total	Comment	
360	4	4	8	extent given	360-2 (Gal$_{1,2}$-Gal$_{4}$
361	— 4 —		4		W2868
363B	~~IIII~~ = 4				
	6 ~~IIIII~~		10	10 different heterogenate	
364	5	1	26	(−add 20 = 26)	total = 77 W2869
358	— 2 —		2	2 different	358-1, 358-2
291	— 8 —				
	— 5 —				
	— 8 —				
	— 4 —				3 different heterogenate
	— 8 —				
	— 4 —		37		
			77		18 different heterogenate

	Lp^R	Lp^+	Lp^+	Lp^+	Seq Lp^+	Seq Lp^+	Seq Lp^+	non Seq Lp^+	non Lp^S	Seq Lp^+	
	373-1	373-2	373-3	373-4	375-1	375-2	375-3	375-4	375-5	375-6	
Lp^+ s	0	Lp^+ seq 25	15	21	34	9	10		0	15	
ns	0	ns 1	0	0	1	7	2	24	0	2	
Lp^R s	9	Lp^R seq 3	2	3	1	4	6	0	0	5	2
ns	8	ns 1	0	0	0	2	2	0	0	2	0
Lp^S s	0	Lp^S seq	3	0	0	0		0	0	0	0
ns	4	ns 6	0	0	0	0		0	24	0	
	21		20	24	36	17	22	24	24	24	
		36				5ut					

Condensed summary of above ↓

Conv 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^+	seq Lp^+	Lp^+	Lp^+	Seq Lp^+	Seq Lp^+	Seq Lp^+	non-seq Lp^+	non-seq Lp^S	seq Lp^+	seq Lp^+
Lp^+	0	Lp^+ 26	15	21	35	11	12	24	0	17	22
Lp^R	17	Lp^+ 4	2	3	1	6	8	0	0	7	2
Lp^S	4	Lp^S 6	5	0	0	0	2	0	24	0	0
	21	36	22	24	36	19	24	24	24	24	24
	4/1	–	–	–	6/1	–	1/2	–	–	12/3	11/3

Segregation from single heterogenotes

(210)

(Ref)

No Segregants

Synogenote	Endo	Exo	Endo	Exo	Amphi	Total
365B	1⁻4⁻	2⁻	11	2	0	13
364	4⁻	2⁻	13*	7*	0	20
		* 2/7 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 (UV.λ)	2⁻	7⁻	7 of → {7	0	0	7}
			4 of → {6	0	0	6}
			2 of {5	0	0	5}
			3	4	0	7
			6	1	0	7
			5	1	0	6
			2 of {6	0	1	7}
			1	0	0	1

P.E. 1⁻xx4⁻ (211)

	Ref	F	Endo	Lp	Het. Lp Ø	Stbl	Endo	Exo	Amphi	P.E.
(285-1)	348	+	1⁻	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

Lp⁻ Lp⁺

A A × A A

b b B B

a | A

b | B

A A / b b

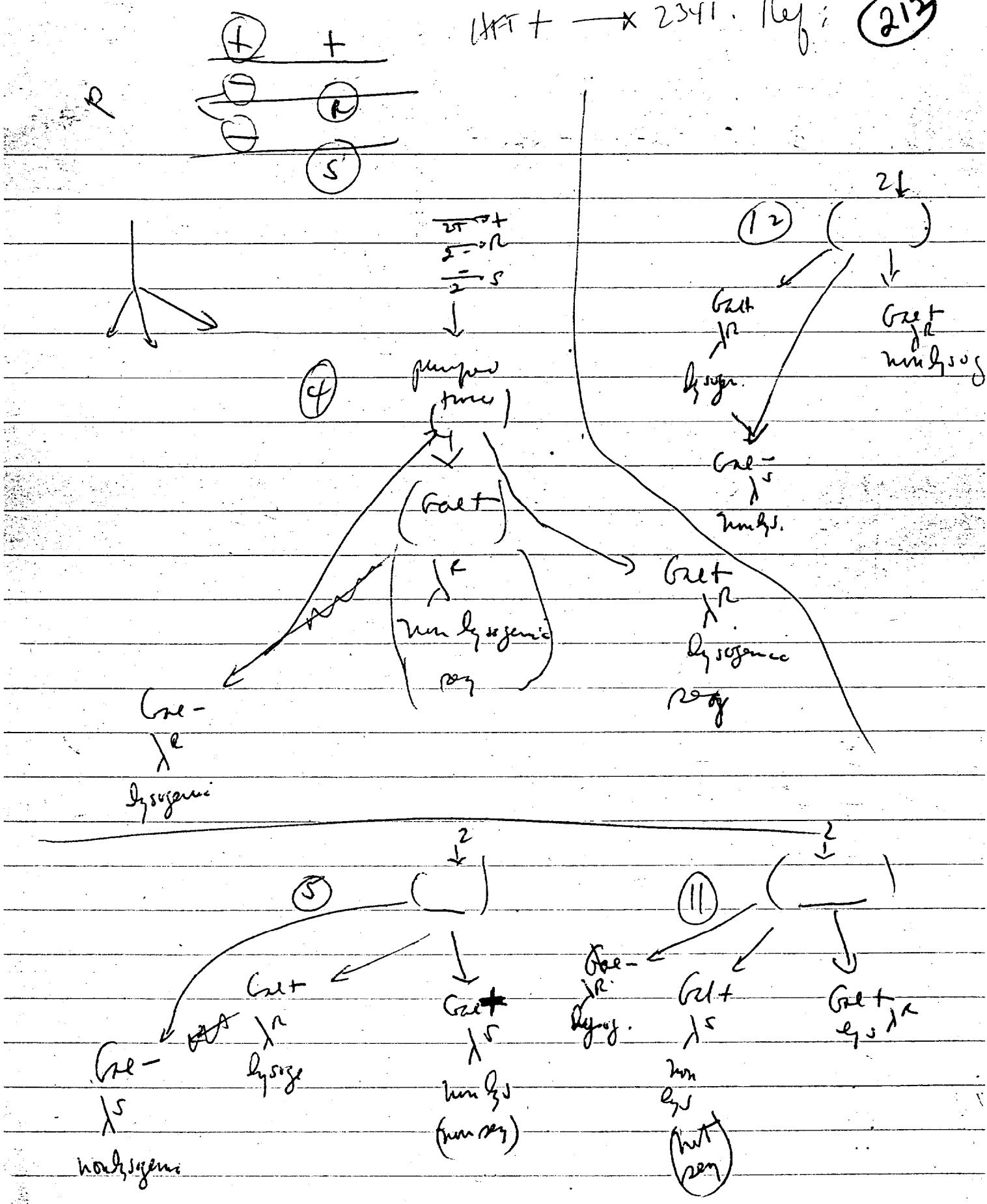
A A / B b

A A / B B

Lp⁺/Lp⁻

x

HFT + → x 2341. Ref: (212)



Reversion Study

Lp^S Gal- → Galt ~~287~~

2341 Lp^R/Lp^S → $Lp^S + Lp^R$ 287

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

1 Lp^S 6/6 reversions not seg

257C-6 $4^- 2^+ Lp^S$ // $4^+ 2^- Lp^R$ 292

3 2^- seg Lp^S (single reversed) - (1) non seg.

1 4^- seg Lp^S (") - (1) non seg.

12 $2^-/2^-$ seg Lp^R/Lp^S (single) - 11/12 seg.

257C-6 5 $2^- Lp^R$ seg (two reversions) - 5 cases of 2/2 reversion seg 298

257C-6 { 1 $2^- Lp^R$ (2/2 reversions unstable) 292A

292-1

292-22 → { 3 $2^- Lp^R$ (3/3 reversions unstable)

5 $2^- Lp^S$ (each seg not known 5/5 reversions stable)

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

↘ (+) $\frac{+}{-}\frac{+}{-}$ $Lp^?$ - of 17 Galt obtained

9 λ^R were also seg

3 λ^S were not seg.

2279 x — HFT 6^- 323
Gal_1 -

↘ Lp^R/Lp^S $\frac{6^-}{6^+}$ $\frac{1^+}{1^-}$ → 1 Gal_6 - Lp^S → 2/2 Galt reversion stbl

↘ 1 Gal_6 - Lp^R → 1/6 Galt reversion stbl

Reversions - Other loci - Diploidy

2341 Lp^R/Lp^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 Lp^R, 1 Lp^S

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

241-14, 202-16A } Argument similar to 2341 V_1^R above. Selection of λ_2^R should not be possible 300

2 mal- HFT 2^- obtained 241-14

1 " " " 202-16A

2307X — HFT 2^- 309

$Xyl^-Ara^-Gal_2^-$ → $Xyl^-Ara^-Gal_2^-/Gal_2^-$ no value

2380X — Gal_4^- (NFT) 341

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

6/6 Lac^+R did not seg

6/6 Xyl^+R " " "

6/6 Ara^+ " " "

0.20
566) 117.0
113 2
3800

215

Lp^R / Lp^S transl.

Endo	Exo	+/total	Lp^R	Lp^+	Page
4-	2-	39/1312	1	7	223
		7/256			
4-	2-	—	1	0	241
4-	2-	26/2801	3	23	254
4-	2-	2/142	1	1	257
..	..	26/870	high mult.		259
		108/1279	—		
		117/566	—		
		Lp^S 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)	—		
		9/150 (31c)	—		
2-	1-	3/1254 (37c)	—		
		3/817 (30c)	—		
1-	2-	14/481 (37c)			
		5/161 (30c)			350

Ends	Exo	t/total	Lp^R	Lp^t
1⁻	2⁻	1/311	1	0
+	2⁻	?	1 ← Reconstructed	1
+	1⁻	?	1 Reconstructed from Lp^v	0
+	4⁻	?	0	1
2	+	9/595	0	8
			13	45

0.22
58) 13.0
11 6
140

~~[illegible]~~

Endo
4⁻/4⁻
*4⁻ hap 20/2⁻ ← 2/90 cdiv
2⁻
2/2⁻ syn } (2/24) (10/114 HFT)
2⁻ hap }
4-2⁻ hap 1/24

4⁻ 5
2⁻ R/S
2⁻ 5
4⁻ 2⁻ 5

3
19
6
1

Exo

pages in red

(217)

Homogenate Summary

Homogenate	Observation	Ref.
2- D1	518 x 892 mix (153)	155
	D1 → x 2050 → solid smear (157) D1 → x 518, 902, 2050 → solid smear (161) D1 titer (164)	
	D1 → x 518 → dentrin solid (165) D1 → x 750, D1 → x 2050, D1 → x 2175 (165b) D1 ⊗ 902, 892, 1436 (166) 2050 → x D1, 750 → x D1 (167)	
	D1 {class. Gal2- Gal+R unstable 7/10 (168) D1 Gal+u → (-) seq class. 2- (169, 170) D1 x 902 (172, 175, 174) D1 Gal+u 3/8 (179)	
	D1 x 1673 D1 → x 1485 → Gal2- (178, 183,) ~~[illegible]~~ (185) D1 → x 1485 (186)	
	D1 one step, single burst (188) : 485 ED1 → Gal2- seq (190) D1 → x 1924 (2.0x10⁷/ml) (193) D1 vs antiserum (197) (199)	
2- D4	Gal+R stable (168) D4 x 902 (172, 175, 174) D4 Gal+S (179) D4 → x 518 HFT (181)	
2343 Gal1- prototroph 902 → x 1- N1	Gal1- (192B) N1 lysate HFT (192B) N1 x 902 Gal1- (SRP) (192B) N1 x 2251 SRP mA) (192C) 2 Gal+R non HFT → x 811 (192C)	
	N1 x 1485 → Gal1- (203) 2 Gal+R stable (203) LOST (219)	
2343 Gal1- prototroph 902 → x 1- N7	Gal1- (192B) N7 lysate HFT (192B) N7 x Gal1- Gal2- SRP (192B) N7 x 2251 SRP mA) (192C) 3 Gal+R non HFT → x 811 (192C)	
	3 Gal+R stable (203)	
2343 Gal1- prototroph 902 → x 2-	ALSO KNOWN AS 2342	
N16	Gal2- (192B) N16 x 902 (SRP) (192B) N16 → LFT seq lysate (192C) N16 LFT seq 1-2-? (192C) N16 HFT (192C)	
	N16 → x 1924 (3x10⁶/ml) (201) N16 → x 1673 → Gal1- Gal2- (W2432) (203) 7/10 colonies HFT (219) N16 → x 2252 (2341) (244)	
	12/12 Gal+R unstable (227)	

ALSO KNOWN AS 202-16

2⁻ S16 902-x811, Gal_2^- (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-x811 Gal_4^- (202) HFT / Gal_1, Gal_2^- Gal_3^-, not 811, 1924 (210)

ALSO KNOWN AS 2346

1⁻ NA-4 902-x 750 Gal_1^- (230) NA-4-x 1765 (241) -x 2252 (2345) (244) 4/5 $Gal+^R$ UV stbl (267) LFT seg Gal_1^- 8/8 $Gal+^R$ stbl (270)

2⁻ 241-14 902-x750, Gal_2^- (241) 8/10 col. tested HFT (270) 12/12 $Gal+^R$ unstbl (270) LFT seg Gal_2^-, 12/12 $Gal+^R$ stbl (270) (291) Lac^R stbl Spontaneous λ HFT (299) tested HFT (299) one step (300)

2⁻ Mal-λ_2^R (300) 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, Gal_2^- (241) 5/10 col. tested HFT (270) 12/12 $Gal+^R$ unstbl (270) LFT seg 1⁻2⁻ (270)

(291) Lac^R stbl

one step (370)

4⁻ 247B-1 811 → x 1210, Gal4⁻ (247B-1). 9/10 LFT seg found Gal4⁻ Gal+R seg found stable (247B-1)
→ x 2252 (276)

2⁻ 257-2 902 → x 750, Gal2⁻ (257) LFT seg Gal2⁻, Gal+R stbl (257)

2⁻ 257-4 902 → x 750, Gal2⁻ (257) LFT seg Gal2⁻, Gal+R stbl (257).

Reexamine

and other HFT seg from same trnsd. clone ↓ Mal2⁻ (different from R.S.) ← different

4⁻ 293-12 etc 811 → x 2175 (293) lysate HFT (349) tested (365) 1/6 Gal+R unstbl (365) 1/6 Gal+R unstbl
← different → ← different → ← different →
(293-12 mal-) (365) 2/4 Gal+R unstbl (366) 1/1 Gal+R unstbl (766) 3/4 Gal+R unstbl (766) tested (366)

2⁻ 293-1A 811 → x 2175 (293) tested, (339) HFT 4/4 Gal+R unstb. (339) LFT seg 2⁻ (339)

2⁻ 293-2A 811 → x 2175 (293) tested (339) 2/3 Gal+R unstbl. (339) LFT seg 2⁻ (339)

2⁻ 293-2B 811 → x 2175 (293) tested (339) 2/3 Gal+R unstb (339) LFT seg 2⁻ (339)

2⁻ 293-11A 811 → x 2175 (293) tested (339) 3/4 Gal+R unstb (339) LFT seg 2⁻ (339)

(ALSO 295A-1,2,3,4)

1-4⁻ 295-1 283-1 → x 1210 (295A)

6/6 Galt^R unstbl

HFT 7 (309-1) 2342 —x 2307 (302) obtained (309) UV mod of lysate (359) (369A) (359B)
2/8 Galt^R unstbl (363B) UV mod. (364) LFT seq 7- (390) 0/7 Galt^R LFT ~~seq~~ (390)

6- (311-2) 2020λ+ —x 2175 (311) 2/2 Galt^R seq (363B) LFT seq 6- (363B) 0/3 seq (390)

2- (341-9) 811—x 2580 (335) 4/6 Galt^R unstbl (341)

2- (341-12) 811—x2580 (335)

2- (364A1) 2342 ~~[illegible]~~ —x518 (364) 2/2 Galt^R unstbl (364)

2- (364B2) 2342—x518 (364) 1/2 Galt^R unstbl (364) 6/6 Gal- seq = Gal2- (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^- lost	$1^- 2^+ / 1^+ 2^-$	–	–	0/4	
lost		–	–	0/6	
2346	[illegible]	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	–	–	
2342	$1^- 2^+ / 1^+ 2^-$	12/12	$Gal_1^- Gal_2^-$	none obtained	(2)
241-14		12/12	Gal_2^-	0/12	(3)
241-19		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^- (from +)	–	
D4		–	–	0/2 (minimum)	
302-16		–	–	–	
341-12		–	–	–	
364A1		2/2	–	–	
364B2		1/2	Gal_2^-	–	
Gal_4^- 518	$4^- 2^+ / 4^+ 2^-$	–	–	–	
247B-1	$8^- 4^+ / 4^- 8^+$	–	Gal_4^-	0/1 (minimum)	
293-12S	$2^- 4^+ / 2^+ 4^-$	–	–	–	
	(1)	1/6	–	–	
	(2)	1/6	–	–	

223

		(3)	2/4		
		(4)	1/1	—	—
		(5)	3/4	—	—
Gal_6^- 311-2	$2^-6^+/2^+6^-$		2/2	Gal_6^-	— 0/3
Gal_7^- 309-1	$2^+7^-/2^-7^+$		2/8	Gal_7^-	— 0/7
Gal_1^- Gal_4^-	$8^-1^+4^+/8^+1^-4^-$		—	—	—

Table 5

The frequency of transductions unstable for galactose fermentation

Recipient cells		Lysates Gal (+)	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 Mather – the position occupied by a gene on a chromosome, with regard to its linear order.

· Woodruff (31) ....a series of allelomorphic factors (the position 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.....

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

· Sturtevant + Beadle (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."