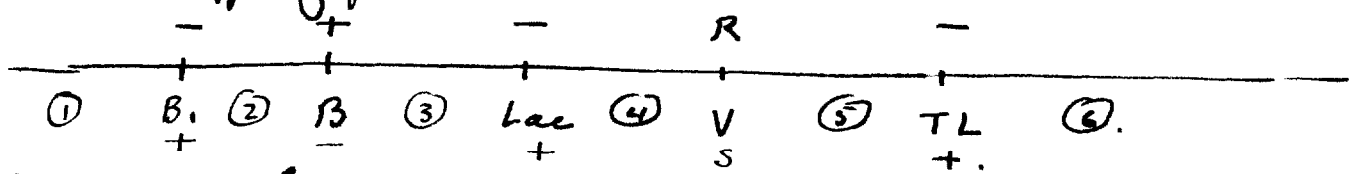
Mapping genes on the chromosome:



BX × TLB₁ V^R Lac – :

	X	B₁	B		TL
	+	–	+	– R	–
X in region ①	–	+	–	+ S	+

++ ① · ② [3,4,5]. Dist. as in BM × TLB₁

X⁻ > X⁺ 2 · [3,4,5]. do.

B₁⁻ > B₁⁺ [3,4,5] as in BM × TLB₁.

B⁻ > B⁺ 1.[3,45] (probably Φ, C).

		B₁	~~X~~ B		TL.
X in region ②		–	+ +	– R	–
		+	– –	+ S	+

++ 2L · (345) Dist. as in BM × TLB₁

B₁⁻ >> B₁⁺ (345)

X⁻ ≪ X⁺ 2R (345)

B⁻ ≪ B⁺

		B₁	B	X	~~df~~ TL.
X in region ③		–	+ +	– R	–
		+	– –	+ S	+

++ 2 · 3R45 Dist..., except that + S ≪ than BM++TLB₁

B₁⁻ >> B₁⁺ 3R45 do.

X⁻ ≪ X⁺ 2 · 3L Mostly + S.

		B₁	B	Lac	X	V	TL
X in region ④		–	+	–	+	R	–
		+	–	+	–	S	+

++ 2 · 4R5 No + S; < – S; Mostly – R

X⁻ = X⁺ 2 · 34L

5⁻ 34L · 45R → Mostly + S; < – S; No – R.

X in region 5

B, B	Lac	V	X	TL
− +	−	R	+	−
+ −	+	S	−	+

++	2·5R	all − R (barring doubles). Like B P.
$X^- > X^+$	2·345L	Less − R. otherwise like BM x TLB,
B ~~=~~ >	345L·5R	do.

X in region 6.

B, B	Lac	V	TL	X
− +	−	R	−	+
+ −	+	S	+	−

++	2·345·6	as BM x TLB,
$B^- >$ ++	6	all + S barring doubles
$X^- > X^+$	2·345	as ++

X between TL (assume Het order).

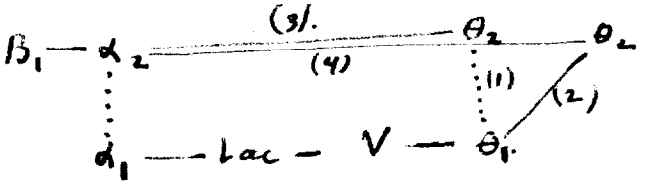
B,	B	Lac	V	T	X	L
−	+	−	R	−	+	−
+	−	+	S	+	−	+

7L 7R.

++	2·345·7L·7R.	as in BM x TLB,
$B^- >> B^+$	7L·7R	all + S.
$X^- >>$	2·345	like ++

Compare 4, 5.

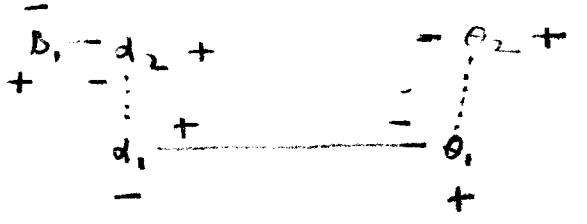
1. Since B_1^- is more frequent than B_1^+ it is linked to α_1 and is either on a different chromosome from α_1 or exterior to it:



Also θ_2 is linked (2) or spon. linked (1) with θ_1.

It may also be linked to α_2.

(1)

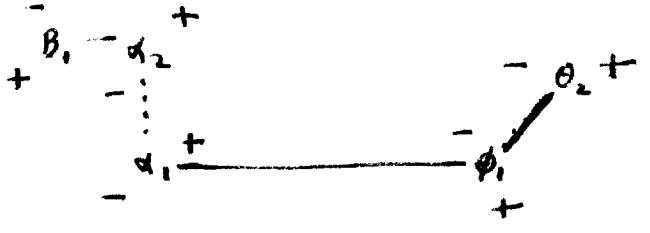


$\alpha_2^- = B_1^- > +$ $\quad \alpha_2 \overset{?}{=} M$

$\alpha_1^- = \theta_1^- \geqq +$ $\quad \alpha_1 \overset{?}{=} M$ F

$\theta_2^- = \theta_2^+$ $\quad$ F

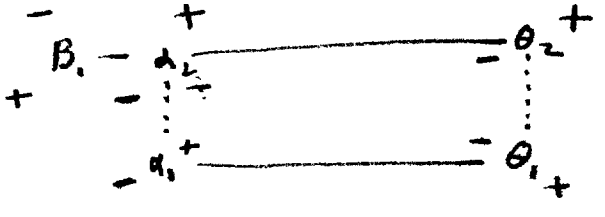
(2).



$\alpha_1^- \geqq +$ $\quad \alpha_1 \overset{?}{=} M$

$\alpha_2^- = B_1^- > +$ $\quad \alpha_2 \overset{?}{=} M.$

(3)

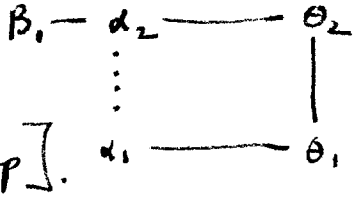


$\alpha_1^- = \theta_1^- \geqq +$ $\quad$ F $\alpha_1 = M.$

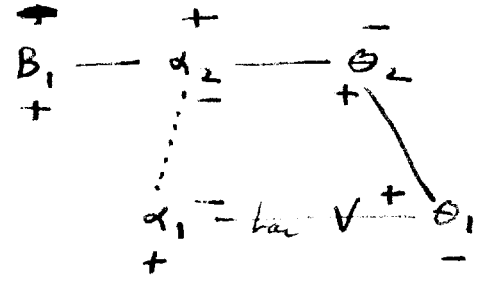
$\alpha_2^- > +$ $\quad \alpha_2 = M$

$\theta_2^- > \theta_2^+$ $\quad$ F

(4.)



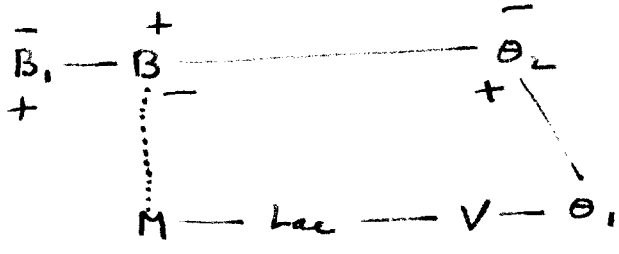
One linkage map].



Both $\alpha_1^- > +$ and α_2^-

The bond ..... is meaningless for the isolation of α_1^-.

As this theory $\alpha_1^- = \alpha_1^+$ ∴ it may be M.



(ϕc) M — Lac — V — Θ_2 — B — B_1 $\quad B- > B+$ s.s.

OK.

∴ f(B) is crucial evidence against sequence linkage

MAXTLB_1^- = α
+S = β
−R = γ

Prot.	B_1^-	B^-	X^-	Position	
α	$>_\alpha$	$\gg_\alpha$	$>\alpha$	1	
α	$>\alpha$	$<\alpha$	$<\alpha$	2	
α′	$>\alpha'$	$<\alpha'$	$<\beta$	3	[α′, +S
γ+S	$>\gamma$	$\geq\alpha''$	$\gg\beta$	4	α″ > +R
γ	$>\gamma$	$>\alpha'$	$>\alpha'$	5	
α	$>\alpha$	$>\beta$	$>\alpha$	6.	
α	$>\alpha$	$>\beta$	$\gg\alpha$	T−x−L.	

① B_1 ② B ③ Ia ④ V ⑤ TL ⑥

1+2, ~~3~~ 4, 5 are not very readily distinguishable.

Routine: Test prototypes, colonies with B.