

# Mutagenesis by Acridines in Bacteriophage T4

Appo Anopolis (a) being a geneticist

(b) the title.

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 and for David Highy: mutants etc, Alice Vogel

"Facts First"

Main Features of acridine mutagenesis

formula for acridines



1 only in phage; so far

2 mutants at different sites from B.A. mutants.

3 reverse mutations. two main classes. etc.

4 mutants non-leaky.  $r_{II}$   $h$   $r \circ$   $ly_{2037} me.$

\* ~~not~~ not requires data on acridine v BA.  
 for intensive study of  $r_{II}$  P13

preliminary data only

$r_{II}$  system

(on board.)  $\rightarrow$

	B	K(12)A
+	+	±
"leaky +"	"+... r"	✓
r	r	o

- two cistrons.

- mapping: deletion mapping. (like deletion map)

P13 (prob) made with programme: i.e. reversion with acridines.

reversions:  $\approx K$  [usual 1 minute]

$\rightarrow$  painted: streaked on B (and F(A)) all for 2 weeks "with presels. wild."  
 crossed with wild, using u.v. gave  $r_i$ .  $r_i$  identified.

all in B1: all non-leaky.

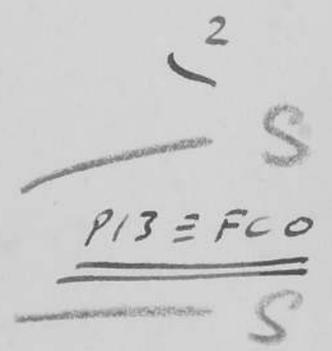
Suppression of suppression.

suppression . . . . . of sup.

Fig 2

P13 = FCO

Fig 6



Analysis for mapping. NOT COMPLEMENTATION

Water will suppress water [41 cases : no 23, 24, 18]

Theory

3 acids add or delete a base.

experiments

- no-leaky
- multiple sites.

1 genetic code no overlapping. evidence.

how to read? hypothesis.

Call mutant + or -.

Fig 2

Prediction

+ ult +

- ult -, Results.

+ ult - ?

two wrong readings  $\therefore$  arrows.

- unacceptable readings

-  $\therefore$  predictions

Table

Why region so large?

1589

complementation test.

A + B cistron separate.

1589 joins together.

summary of results.  
Rigorous theorem

+ +n, n } direction of  
- -n, n } reading.

Slide for triple mutants.

6 (1) cases.



∴ coding reads 3 or multiple of 3.

evidence for 3

4 non-augustin mutants. (Pro +, Pro -)

2 hydroxamic. (augustin recessive) (-, -)

code degenerati

Summarize conclusions about code

prediction about alteration of protein

Lysozyme.

Nirenberg system