A PRELIMINARY MAP OF GENOMIC SITES FOR F-ATTACHMENT IN ESCHERICHIA COLI K12

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In presenting a segmented-genomic model for E. coli K12, Matney and Felkner (1962) predicted that the linkages between segments might be identified as specific sites which have an affinity for the fertility episome, F. The limited number of F-attachment sites predicted by the segmented model has been established experimentally by demonstrating that several Hfr mutants, isolated by different investigators, appear to involve the same F-attachment site, i.e., have the same origin and sequence of marker transmission (Matney et al., 1963). The present paper presents a preliminary map of 17 F-attachment sites involving 44 distinct Hfr mutants.

The Hfr donor strains are listed chronologically in Table 1. They are positioned according to F-attachment site in Fig. 1. The arrows signify both the origin and polarity of chromosomal transmission. Each F-attachment site is assigned a number that signifies its clockwise map distance in minutes from the Hayes site. This starting point was chosen since the resulting 60 minute hemispheres appeared to contain an unequal distribution of clockwise and counter-clockwise donors.

The hemisphere on the right side of Fig. 1 contains 28 counter-clockwise Hfr's and only 3 clockwise donors. This "counter-clockwise" hemisphere also corresponds to the area containing UV-inducible prophage sites (Jacob and Wollman, 1961). The other hemisphere contains 12 clock-

wise males and 4 counter-clockwise donors. This "clockwise" hemisphere has been shown to contain only non-UV-inducible prophage sites (Jacob and Wollman, 1961).

It is difficult to precisely map characters residing between $\underline{arg}_6$ and $\underline{his}$, the so-called "dark region". The elucidation of the transmission - polarity hemispheres shown in Fig. 1 suggests that it is highly improbable that a stable Hfr will be found which transmits this region proximally.

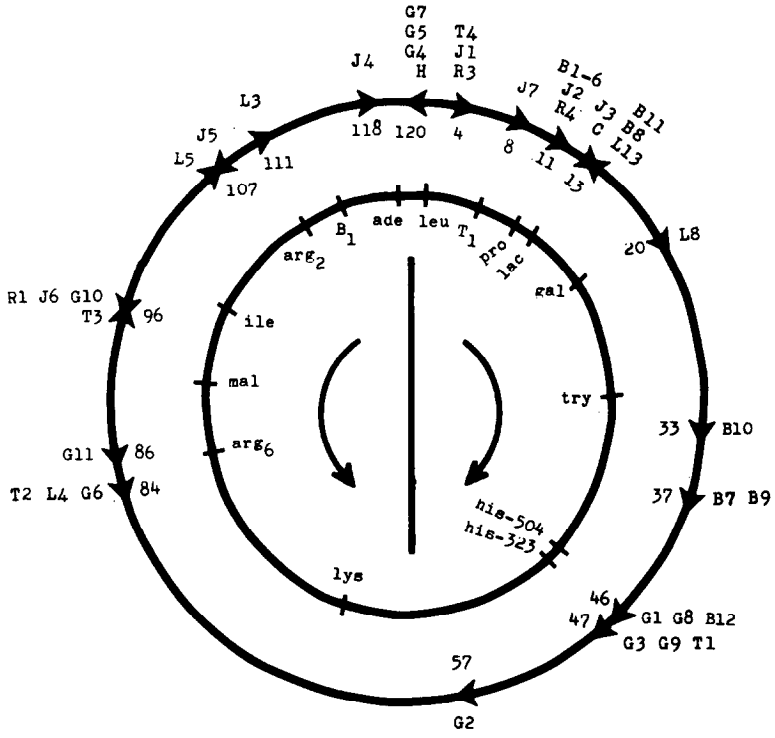

Fig. 1. A Composite Map of F-attachment

Fig. 1. Schematic representation of the linkage group of E. coli K12. The inner circle represents the order of characters. In general, distances are based on timed data using the G4 and G6 males. The arrows on the outer circle represent the origin and direction of transfer exhibited by different Hfr mutants.

Symbols correspond to synthesis of leucine (leu), proline (pro), tryptophan (try), histidine (his), lysine (lys), arginine (arg), isoleucine (ile), thiamine (B_1) and adenine (ade); the fermentation of lactose (lac), galactose (gal), maltose (mal); resistance to phage T_1.

TABLE 1

HFR MUTANT STRAINS OF *E. COLI* K12

MAP SYMBOL	STRAIN	COMMENT
C	CS101	Cavalli-Sforza (1950)
H	HfrH	Hayes (1953)
R1	-	Isolated by Reeves (Hayes, 1964)
R3	-	Isolated by Reeves (Hayes, personal communication)
R4	-	Isolated by Reeves (Hayes, 1964)
J1-7	Hfr_1-Hfr_7	Described by Jacob and Wollman (1961)
T1	AB-311	Taylor and Adelberg (1960)
T2	AB-312	Taylor and Adelberg (1960)
T3	AB-313	Taylor and Adelberg (1960)
T4	AB-453	Taylor (personal communication)
L3	Hfr_3(W2924)	Richter (1961)
L4	Hfr_4(W4321)	Richter (personal communication)
L5	Hfr_5	Richter (personal communication)
L8	Hfr_8(W3208)	Sneath (1962)
L13	Hfr_{13}(W3213)	Sneath (1962)
G1-11	-	Our laboratories
B1-12	-	Isolated by Broda (Hayes, 1964)

F-sites 13, 96 and 107 appear to be represented by contradirectional Hfr types. Strains such as T3 and G10 which are identified as occupying a common site, 96, but with contradirectional transmission, have not been conclusively demonstrated to have the same F-attachment site. They are specified in this way since no common terminal or proximal marker has been found for these strains.

The G-series of Hfr strains has been studied in our laboratories. G1 and G8 appear to have origins of transmission within the histidine region.

G2 displays a low fertility despite attempts to pick more fertile clones. G3 and G9 admit the entire histidine region first. G4 loses fertility and must be frequently re-isolated. G5 contains a transposition involving lead markers. G6 is extremely stable. G10 has given rise to an F'-mal^+ derivative. The origins of G6 and G11 are about one minute apart and this segment contains the $\underline{arg}_6$ locus.

We suggest that a more rational system for naming Hfr strains could be based on the map position of the origin and the direction of insertion of the chromosome. The following examples will illustrate such a scheme:

Hfr 4k (T4)

Hfr 84c (L4)

Hfr 37k (B7)

where "c" stands for clockwise and "k" stands for counter-clockwise. We are not suggesting that the present designations be discarded completely since strains which are identical for origin and transmission direction may have other genomic differences.

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