

Diagram referenced as "Genetic map of the Lac region of E coli"

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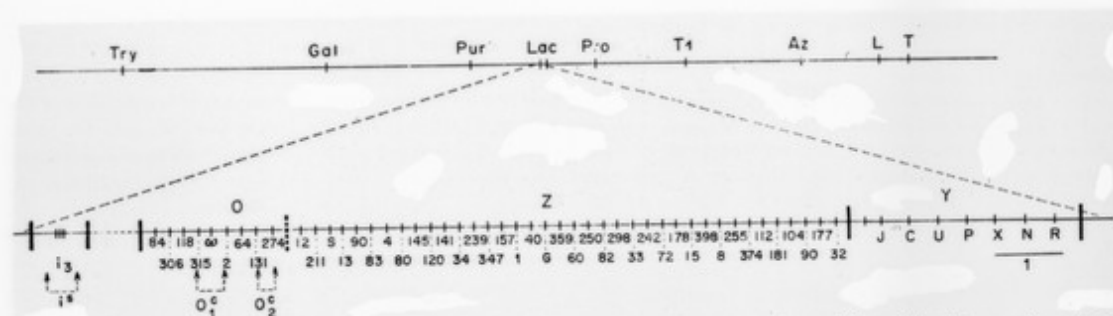
(*) The high levels observed in i^+ / i^- heterozygotes are due to the presence of a sex factor F (see Fig. 3). They affect to the same extent the synthesis of all the known components of the system (Pardee, Jacob, and Monod, 1959). Similar mutants have been found for a series of inducible systems, such as penicillinase of *B. cereus* (Kogut, Pollock, and Tridgell, 1956); amylomaltase (Cohen-Bazire and Jolit, 1953); glycuronidase (Stoeber, 1961); and the enzymes of galactose utilization in *E. coli* (see Buttin, this Symposium; Kalekar, this Symposium).

This table summarizes the results of many experiments. The three activities are given in per cent of those obtained with fully induced haploid, wild type. Note that the activities found in heterozygotes are two to three times greater than those found in haploids. This is probably due to the presence of several F factors per chromosome. i : regulator gene (i^+ : inducible; i^- : constitutive). z and y : structural genes for β -galactosidase and galactoside permease respectively. F : sex factor of *E. coli* K12. Δ_{ozy} : deletion of the *Lac* region.

Genotypes	Non-induced			Induced		
	β -galactosidase	galactoside-permease	galactoside-transacetylase	β -galactosidase	galactoside-permease	galactoside-transacetylase
i^+ / i^-	100	100	100	100	100	100
i^- / i^-	100	100	100	100	100	100
i^+ / i^- (with F)	200	200	200	200	200	200
i^- / i^- (with F)	200	200	200	200	200	200

Among repressible systems, mutations affecting a regulator gene, located far from the cluster of structural genes of the tryptophan pathway, result in constitutive (derepressed) synthesis of all the enzymes of the pathway in *E. coli* (Cohen and Jacob, 1959). Similar situations have been observed in the arginine pathway (see Gorini, this Symposium; Maas, this Symposium).

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Genetic map of the *Lac* region of *E. coli*. The upper line represents the position of the *Lac* region among linked characters in the bacterial chromosome. The lower line represents an enlargement of the *Lac* region, with the two structural genes z and y and the regulator gene i . The operator o appears to correspond to the extremity of the z gene.

ably recessive to wild type; moreover, deletion of the gene also results in a constitutive phenotype, proving the latter to correspond to an inactive state of the gene, or gene product.

These observations identify a regulator gene as a determinant which, in the active state, controls negatively the transcription of certain specific structural genes without itself contributing any structural infor-