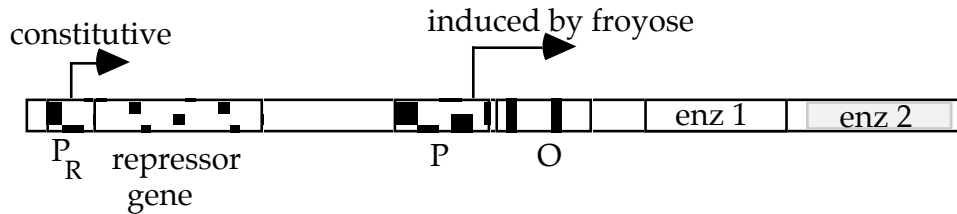


7.012 SECTION PROBLEM: PROKARYOTIC GENE REGULATION- SOLUTIONS

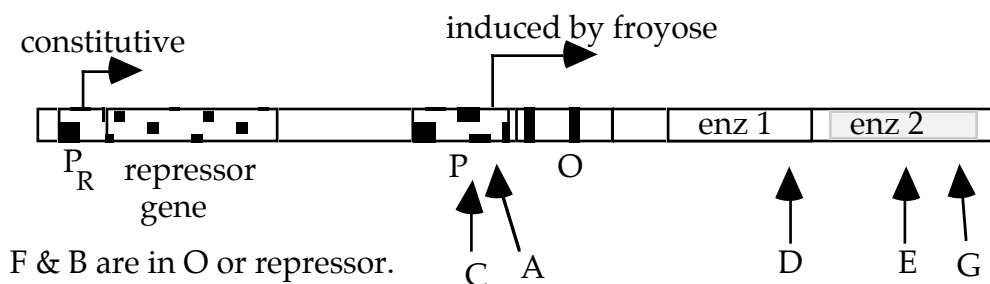
The operon could be diagrammed like this:

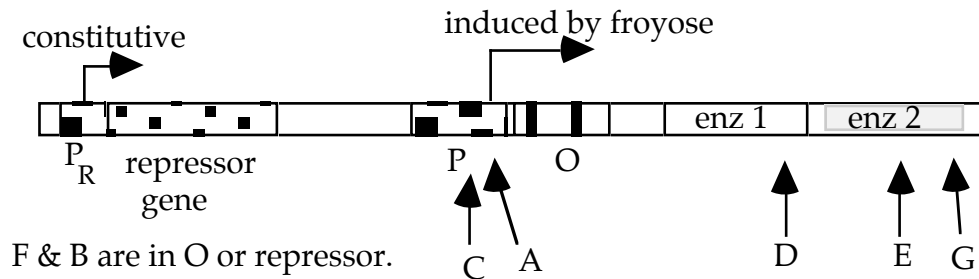


One way to solve this type of problem is to write out the expected phenotype for the particular mutation and then match the prediction to the data. Remember that we are assuming that these are loss of function mutations (no super repressors, etc.).

- 1) A strain with a mutation in enzyme 1 would give LLLH. Strain D⁻ has this phenotype.
- 2) A strain with a mutation in enzyme 2 would give LLHL. Strains E⁻ and G⁻ have this phenotype.
- 3) A strain with a mutation in the promoter would give LLLL. Strains A⁻ and C⁻ have this phenotype.
- 4) A strain with a mutation in the repressor or the operator would give HHHH. Strains F⁻ and B⁻ exhibit this phenotype.

This gives the map:





5) Using the notation from the diagram:

- Diploid strain 1: D and E strains have mutations in different genes, therefore you see complementation in the diploid and a return to wild-type control.
- Diploid strain 2: E and G strains have mutations in the same gene, enzyme 2 does not get produced (is always low), enzyme 1 shows appropriate control.
- Diploid strain 3: strain A has a mutation in the promoter. Because promoters act *in cis*, a wild-type promoter upstream of mutant copies of the genes for enzyme 1 and 2 cannot restore normal control.
- Diploid strains 4 and 5 deal with mutations in the operator or repressor. In this case, it is easier to predict the outcome and match it to the data:

If the mutation is in the operator (operators act *in cis*), you cannot restore normal control with a wild-type operator upstream of mutant copies of the genes for enzyme 1 and 2.

If the mutation is in the repressor (repressors act *in trans*), you can restore normal control with a wild-type repressor upstream of mutant copies of the genes for enzyme 1 and 2.

Therefore: the F strain has a mutation in the repressor

the B strain has a mutation in the operator