

A microscopic image showing numerous rod-shaped bacteria, likely E. coli, that have been genetically modified to express a blue fluorescent protein. The bacteria are scattered across the field of view, appearing as bright blue, glowing rods against a dark background.

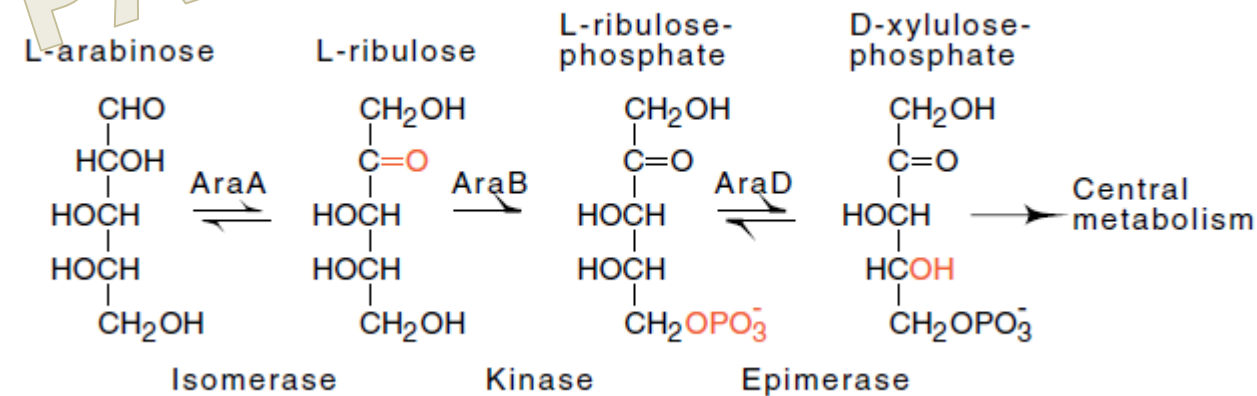
The Arabinose Operon

Parimal K. Khan

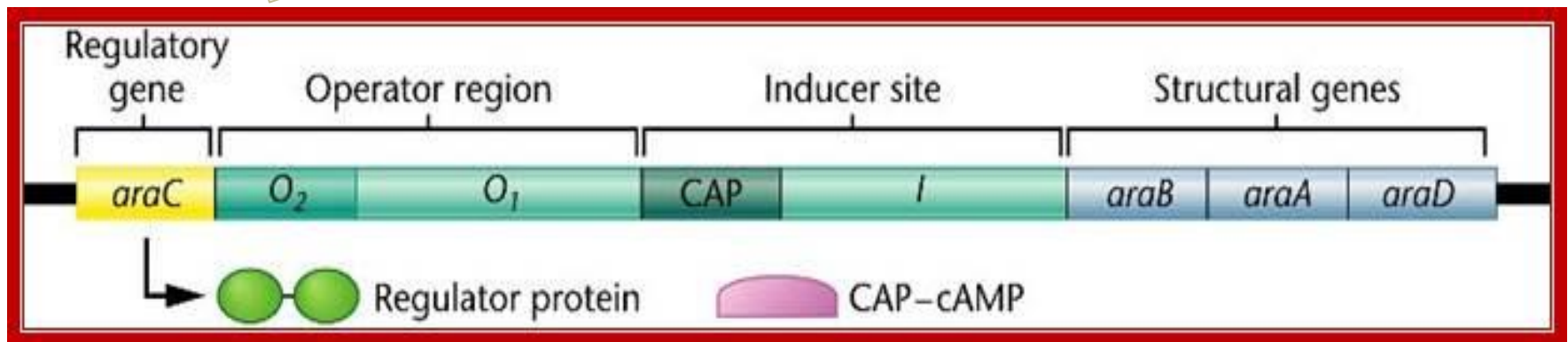
Department of Zoology
Patna University

THE ARABINOSE OPERON: AN INDUCIBLE OPERON

- The arabinose operon is a catabolic operon similar to the lac operon and comprises of 3 structural genes (*ara B*, *ara A*, *ara D*) which encode for arabinose metabolizing enzymes and are transcribed rightward from their promoter Ara P_{BAD}.
- One gene, *ara C*, encodes the regulator protein Ara C which is transcribed leftward from its promoter Ara P_C.

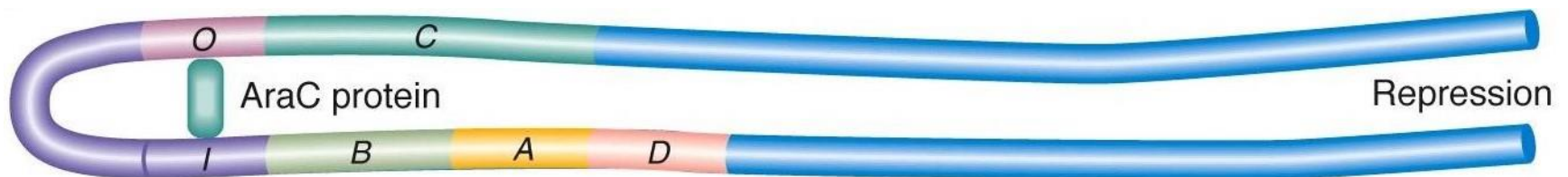


- Although an inducible operon, it differs from lac operon in several respects.
 - i. The ara operon consists of 2 operators namely ara O_1 and O_2 . The former regulates transcription of a regulator gene *ara C* while the other operator is located far upstream of the promoter it controls (P_{BAD}).
 - ii. The CAP binding site is about 200 base pairs upstream of ara promoter, yet it can stimulate transcription.
 - iii. The operon has a unique system of negative regulation mediated by *ara C* protein which is the major regulatory protein and exhibits both positive and negative regulatory effects on transcription of structural genes depending on certain environmental conditions.



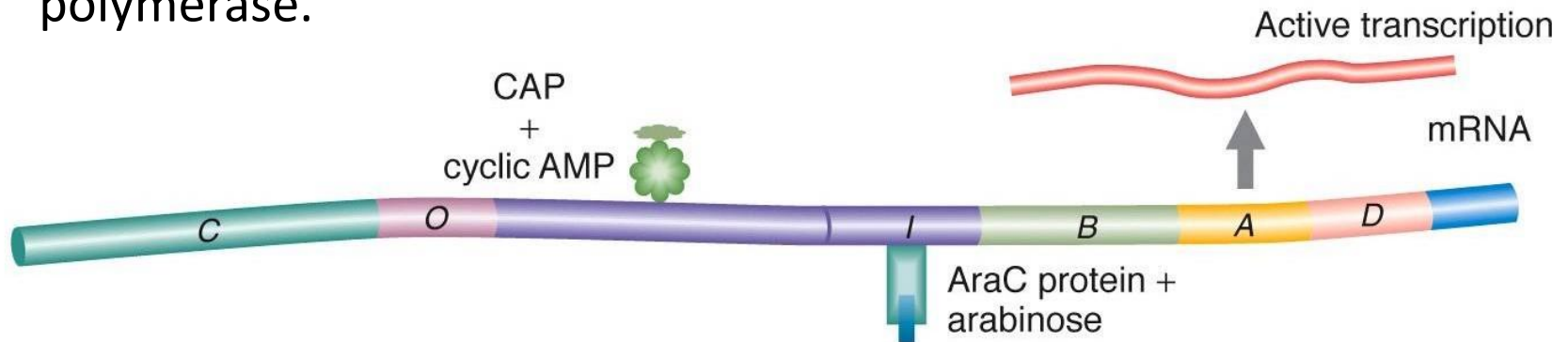
IN THE ABSENCE OF ARABINOSE

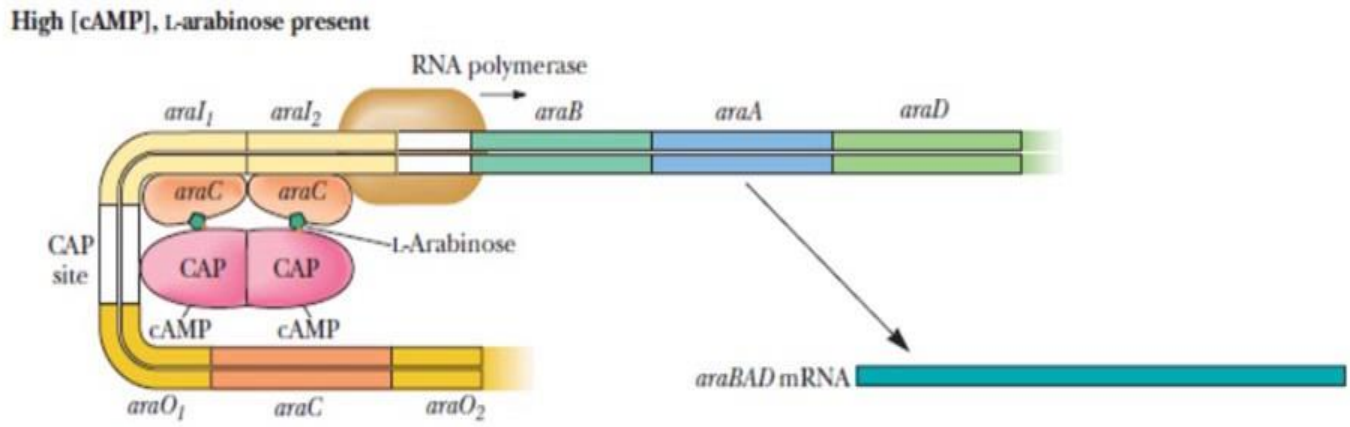
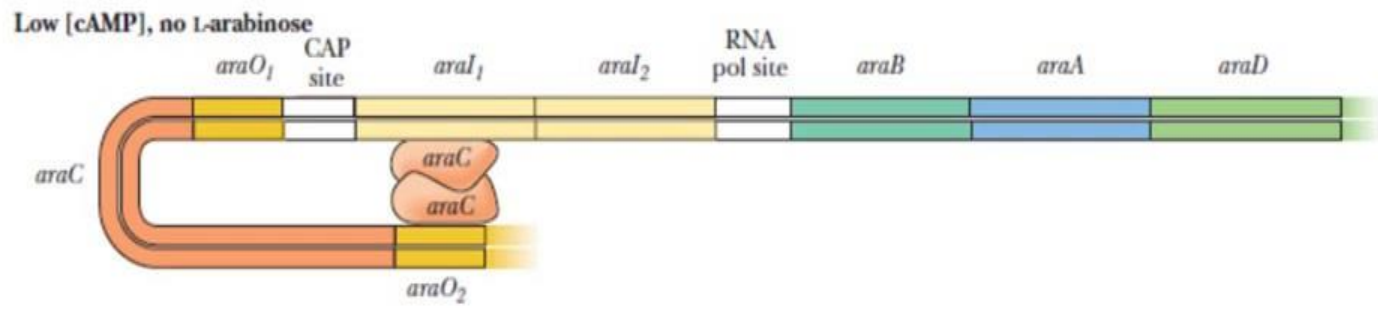
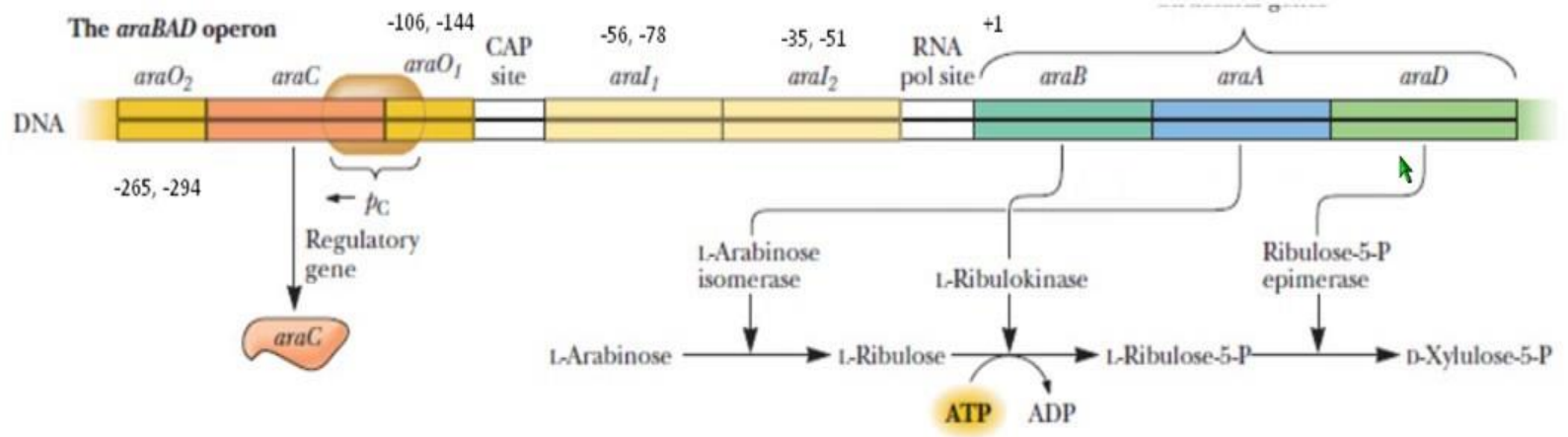
- Lobell and Schleif found that the Ara C protein has 3 binding sites for Ara O₁, Ara O₂ and Ara I; each of which can bind one monomer of Ara C.
- In the absence of arabinose and cAMP, no Ara BAD products are required and so Ara C exerts negative control by binding to Ara O₂ and Ara I₁, looping out the DNA in between and repressing the operon through blocking access to promoter (P_{BAD}) by RNA polymerase.
- The double stranded DNA can loop out and bring 2 protein binding sites together as long as these sites are located on same face of the double helix.



IN THE PRESENCE OF ARABINOSE

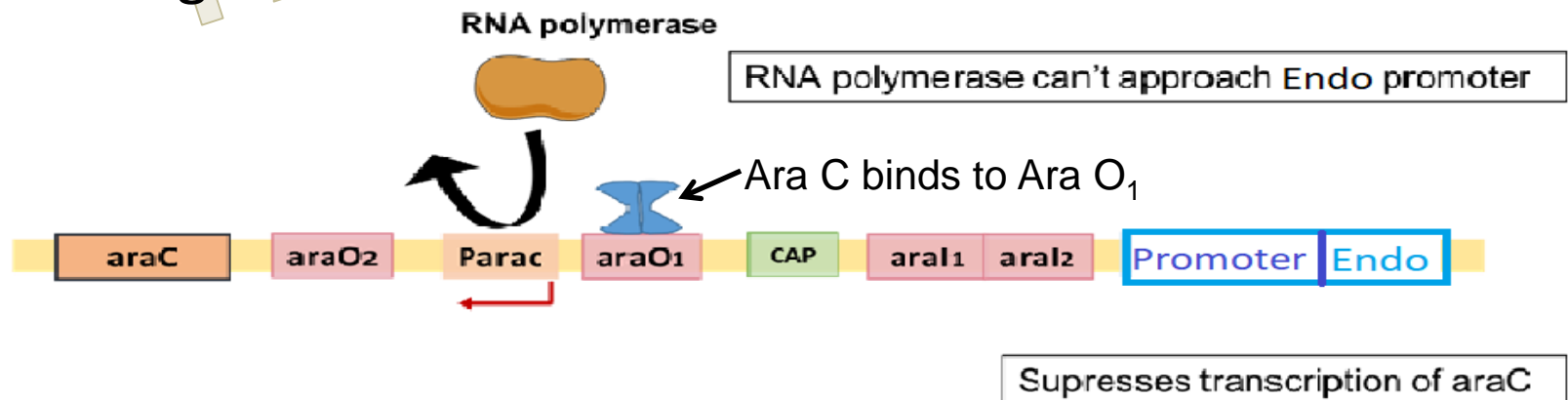
- When both arabinose and cAMP are present, arabinose binds to Ara C, changing its shape so it prefers to bind as a dimer to Ara I₁ and Ara I₂ instead of Ara O₂.
- This opens up the promoter to binding by RNA polymerase, breaks the repression loop and transcription ensues.
- Positive control mediated by CAP and cAMP also occurs in the absence of glucose which stimulates formation of cAMP.
- Once sufficient concentration of CAP/cAMP complex is attained, it occupies the CAP site which further stimulates polymerase binding to promoter (P_{BAD}) and facilitates transcription.
- The binding of CAP/cAMP complex at a remote site upstream from Ara P_{BAD} and still being able to control transcription can also be explained by DNA looping which could allow Cap to contact RNA polymerase.





AUTOREGULATION OF ARA C

- The operator Ara O_1 doesn't take part in regulation of Ara BAD transcription, instead it allows Ara C to regulate its own synthesis.
- The *ara C* gene is transcribed from Ara P_C in leftward direction which puts Ara O_1 in a position to control its transcription.
- As the level of Ara C rises, it binds to Ara O_1 and inhibits leftward transcription.
- It, thus, prevents an accumulation of excess repressor. This mechanism where Ara C controls its own synthesis is called autoregulation.



PARIMAL K. KHAN

THANK YOU