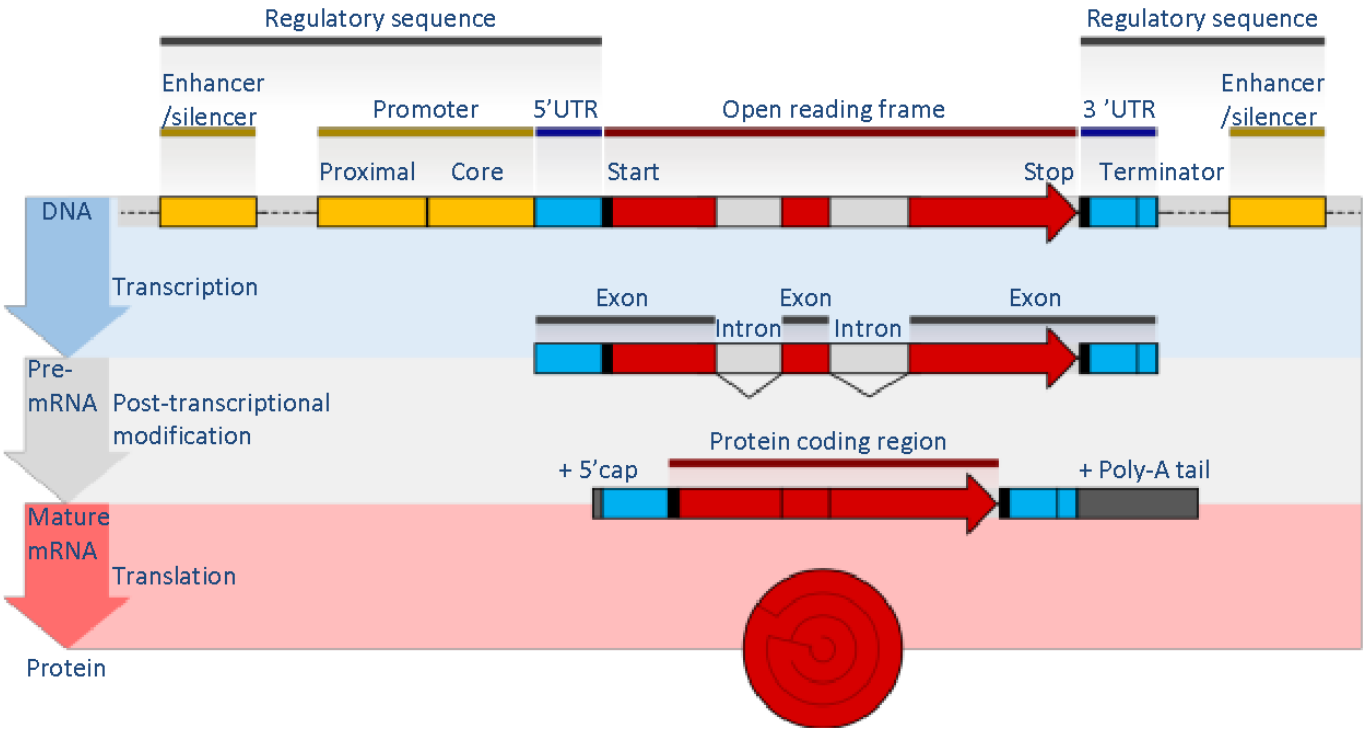
Bikram Ghosh
Contact : 9831756144, 9804993221

- **Structure of prokaryotic gene**

The overall organisation of prokaryotic genes is markedly different from that of the eukaryotes . The most obvious difference is that prokaryotic ORFs are often grouped into a polycistronic operon under the control of a shared set of regulatory sequences. These ORFs are all transcribed onto the same mRNA and so are co-regulated and often serve related functions. Each ORF typically has its own ribosome binding site (RBS) so that ribosomes simultaneously translate ORFs on the same mRNA. Some operons also display translational coupling, where the translation rates of multiple ORFs within an operon are linked. This can occur when the ribosome remains attached at the end of an ORF and simply translocates along to the next without the need for a new RBS. Translational coupling is also observed when translation of an ORF affects the accessibility of the next RBS through changes in RNA secondary structure. Having multiple ORFs on a single mRNA is only possible in prokaryotes because their transcription and translation take place at the same time and in the same subcellular location. The operator sequence next to the promoter is the main regulatory element in prokaryotes. Repressor proteins bound to the operator sequence physically obstructs the RNA polymerase enzyme, preventing transcription. Riboswitches are another important regulatory sequence commonly present in prokaryotic UTRs. These sequences switch between alternative secondary structures in the RNA depending on the concentration of key metabolites. The secondary structures then either block or reveal important sequence regions such as RBSs. Introns are extremely rare in prokaryotes and therefore do not play a significant role in prokaryotic gene regulation.



- **Episome:** An **episome** is a special type of plasmid, which remains part of the eukaryotic genome without integration. Episomes manage this by replicating together with the rest of the genome and subsequently associating with metaphase chromosomes during mitosis. Episomes do not degrade unlike standard plasmids and are not epigenetically silenced inside eukaryotic cell nucleus. DNA in some lysogenic bacteriophages acts as episomes, integrating into the genome and persisting as prophages.

➢ Genome organisation in prokaryotes

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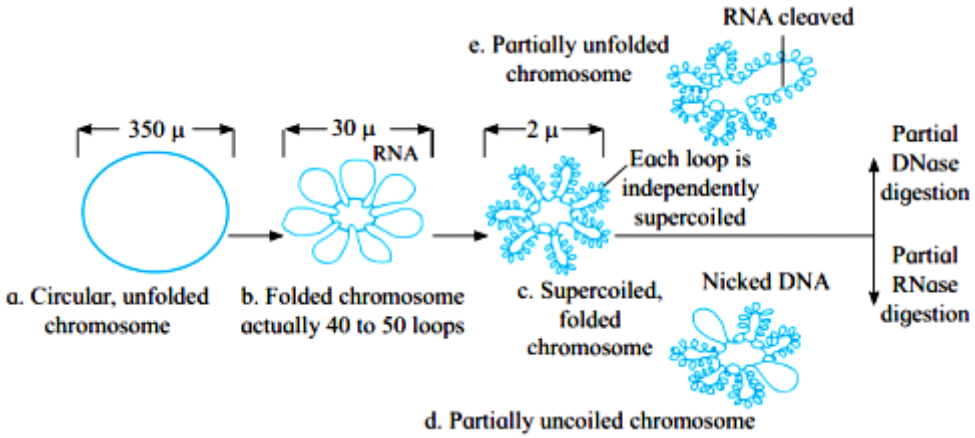
Thus, one way prokaryotes compress their DNA into smaller spaces is through Imagine supercoiling. Most bacterial genomes are negatively supercoiled during normal growth. During the 1980s and 1990s, researchers discovered that multiple proteins act together to fold and condense prokaryotic DNA. In one protein called **HU** , which is the most abundant protein in the nucleoid, works with an enzyme called topoisomerase I to bind DNA and introduce sharp bends in the chromosome, generating the tension necessary for negative supercoiling. Recent studies have also shown that other proteins, including **integration host factor (IHF)** , can bind to specific sequences within the genome and introduce additional bends (Rice The folded DNA is then organized into a variety of conformations and wound around tetramers of the HU that are supercoiled protein, much like eukaryotic chromosomes are wrapped around histones (Murphy & Zimmerman, 1997). Once the prokaryotic genome has been condensed, **DNA topoisomerase I**, maintain the supercoils. One of these maintenance proteins is **H-NS**, that plays an active role in transcription modulating the expression of the genes involved in the response to environmental stimuli. Another factor for maintenance protein, inversion stimulation (FIS), by is abundant during exponential growth and regulates the expression of more than 231 genes, including DNA topoisomerase I.



- **Plasmids copy No**: In cellular biology, the plasmid copy number is the number of copies of a given plasmid in a cell. To ensure survival and thus the continued propagation of the plasmid, they must regulate their copy number. If a plasmid has too high of a copy number, they may excessively burden their host by occupying too much cellular machinery and using too much energy. On the other hand, too low of a copy number may result in the plasmid not being present in all of their host's progeny. Plasmids may be either low, medium or high copy number plasmids; the regulation mechanisms between low and medium copy number plasmids are different.
- **Compatibility:** Plasmid compatibility is defined as the ability of different plasmids to be maintained in one bacterial cell. Plasmids with the different replicon are compatible because they do not compete for the same replication control machinery within the cell. but if they have the same replicon then they competes and becomes incompatible.