The University of Burdwan
Three year UG course in Zoology under CBCS
Core T11 (Molecular Biology)

RNA

STRUCTURE AND SALIENT FEATURES

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RNA

- The full form of RNA is Ribonucleic Acid
- In RNA, ribose sugar is present, instead of deoxyribose sugar in DNA. Some studies have also concluded that this chemical liability of RNA due to extra OH- the group has led to DNA being the genetic storehouse as it lacks OH group in 2'Carbon making it more stable to hold information.
- In RNA, Uracil (U) is present instead of thymine, although some other kinds of nitrogenous bases are also found in RNA.
- RNA is a single-stranded molecule; it does not follow Chargaff's rule.
- Being single-stranded, it can form a diverse kind of conformations.
- The RNA is of two kinds:
  - Genomic RNA
  - Non-genomic RNA

Genomic RNA

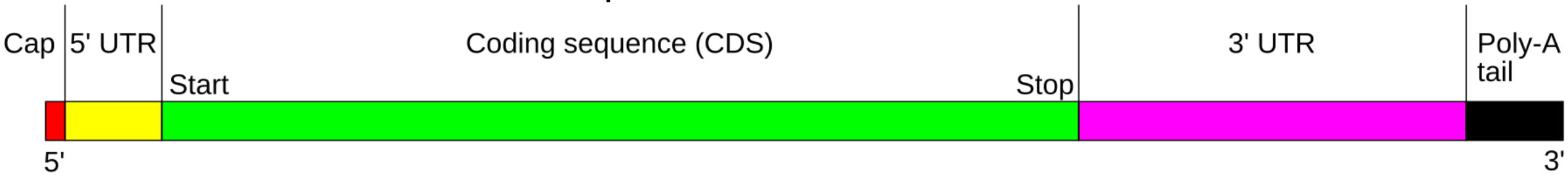
- It occurs in riboviruses and viroids.
- It is single stranded in TMV, HIV, Influenza viruses etc. while double stranded in Reovirus.
- In TMV genetic RNA is (+) RNA strand that directs the synthesis of a (-) RNA strand. Then the (-) RNA strand serves as the template for the synthesis of a large number of (+) RNA strands.
- In retroviruses like HIV, Rous sarcoma viruses the genetic RNA is the (+) strand that directs the synthesis of DNA by reverse transcription.

Non-genomic RNA

- Where DNA is the genetic material RNA is said to be non-genetic
- Such RNA is synthesized from DNA template by the process called transcription.
- Transcription is catalyzed by RNA polymerase. In prokaryotes a single type of RNA polymerase can transcribe all types of RNA while in eukaryotes three different types of RNA polymerases (RNA Pol 1, RNA Pol II and RNA Pol III) do the same job.
- The non-genetic RNA is mainly of 3 types – m RNA, tRNA and rRNA. The other types are hnRNA, snRNA, scRNA etc

mRNA

- mRNA (messenger RNA) are transcripted from the DNA and carries genetic information for the sequence of amino acids. They vary considerably in size.
- It constitutes about 5- 10% of total cellular RNA.
- INFORMOSOME = mRNA + protein



- mRNA has three parts:
  - Coding regions
  - Untranslated regions
  - Poly-A tail

Coding regions

- This region is composed of **codons** decoded and translated into proteins by the ribosomes.
- It starts with the initiation codon: **AUG**
- It stops with termination codons: **UAG** (amber), **UAA** (ochre) and **UGA** (opal or umber). These names of the stop codons historically correspond to different mutations of T4 and lambda phage used in experiments against *Escherichia coli*.
- The coding regions tend to be stabilized by internal base pairs; this impedes degradation.
- In addition to being protein-coding, portions of coding regions may serve as regulatory sequences in the pre-mRNA as exonic splicing enhancers or exonic splicing silencers.

Untranslated regions

- These are sections of the mRNA before the start codon and after the stop codon that are not translated, termed the **five prime untranslated regions (5' UTR) or leader sequence** and **three prime untranslated regions (3' UTR) or trailer sequence**, respectively.
- 5’ end of the eukaryotic mRNA bears a special type of guanine called 7-methyl guanosine (m^7G), called **cap**.
  - Cap 0 (found in unicellular eukaryotes)
  - Cap1 & 2 (found in all multicellular eukaryotes)
- Cap is essential for binding of mRNA to small subunit of ribosome during protein synthesis.
- In prokaryotes and phage, leader sequence contains a special sequence 5’-AGG AGG – 3’, which binds to 16s rRNA of small 30s ribosomal subunit, called Shine Dalgarno sequence.

Untranslated regions

- Several roles in gene expression have been attributed to the untranslated regions, including mRNA stability, mRNA localization, and translational efficiency.
- Genetic variants in 3' UTR have also been implicated in disease susceptibility because of the change in RNA structure and protein translation.
- The stability of mRNAs may be controlled by the 5' UTR and/or 3' UTR due to varying affinity for RNA degrading enzymes called ribonucleases and for ancillary proteins that can promote or inhibit RNA degradation.

Untranslated regions

- Translational efficiency, including sometimes the complete inhibition of translation, can be controlled by UTRs. Proteins that bind to either the 3' or 5' UTR may affect translation by influencing the ribosome's ability to bind to the mRNA. MicroRNAs bound to the 3' UTR also may affect translational efficiency or mRNA stability.
- Cytoplasmic localization of mRNA is thought to be a function of the 3' UTR.
- UTRs also form secondary structures that regulate levels of translation along with associated proteins.

Poly-A tail

- Poly-A tail is a long stretch of adenine sequences at the 3’ end of mature mRNA.
- It is not a transcriptional product and is added to pre-mRNA after transcription at the 3’ end.
- This tail promotes export from the nucleus and translation, and protects the mRNA from degradation.

tRNA

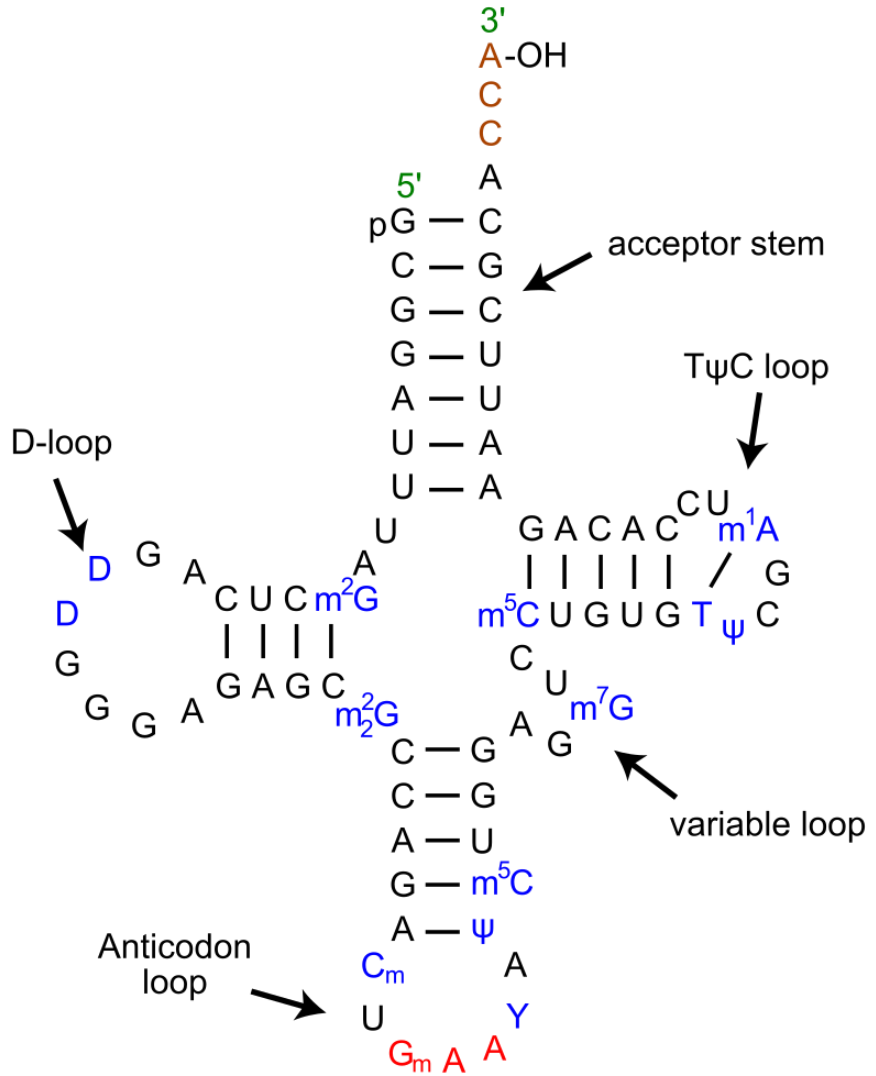
- Transfer RNA (tRNA) is the smallest RNA, also known as adaptor RNA and soluble RNA (sRNA).
- It constitutes 10-15% of the total cellular RNA.
- Each three-nucleotide codon in mRNA is complemented by a three-nucleotide anticodon in tRNA.
- Each tRNA corresponds to a particular amino acid.
- Multiple tRNAs representing the same amino acid are called **isoaccepting** tRNAs.
- The tRNA without amino acid is called **uncharged tRNA.** The tRNA attached to amino acid is called **charged or aminoacyl tRNA**.
- The tRNAs function as **translational adaptors** because at one hand they recognize specific codons of mRNA through anticodons and on the other hand deliver amino acids to the ribosome.

tRNA Structure

- The primary structure of tRNA is 74 to 95 nucleotides long.
- Their molecular weight is about 25,000 to 30,000.
- Except for the usual A, G, C and U, they contain many unusual bases such as pseudouridine (Ψ), dihydrouridine (D), inositol (I), ribothymidine (T), isopentenyladenosine (i^6A), thiouridine (s^4U) and methylguanosine (M^1G). All these unusual bases are the modifications of one of the four bases created post-transcriptionally.
- The 5’ end of tRNA always ends in phosphorylated guanine (pG), whiles the 3’ end always ends in the – CCA sequence.

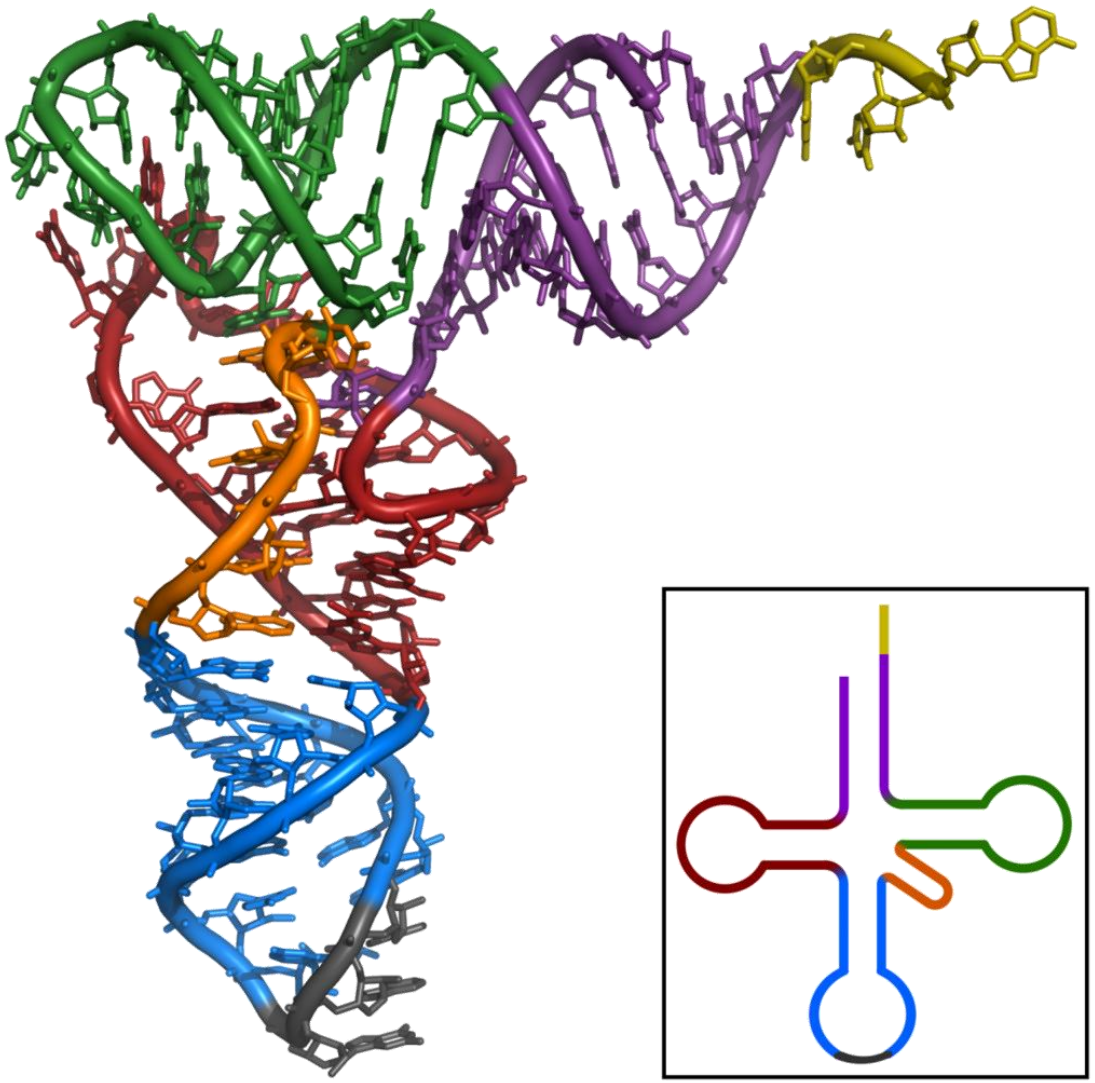
tRNA secondary structure

- All tRNAs have a common secondary structure that appears like **cloverleaf** due to base pairing between short complementary regions.
- The secondary cloverleaf model contains four major arms and one variable arm
  - **Acceptor arm** composed about 7bp stem that ends in an unpaired sequence (5'-CCA-3').
  - **D arm** consists of a stem (3 or 4 bp) and a loop called D-loop (DHU – loop) that contains the base dihydrouridine.
  - **Anticodon arm** consists of a stem (5 bp) and a 7 residues loop having anticodon triplet complementary to the codon.
  - **TΨC arm (T arm)** or **ribosomal recognition arm** composed of a 5 bp and a loop containing the triplets base sequence TΨC.
  - **Variable arm** lies between TΨC and anticodon arms, named dure to its highly variable base composition. On the basis of extra arm, tRNAs are of 2 types-
    - **Class 1 tRNAs** have small extra arm (3-5 bp long) and constitute 75% of all tRNAs.
    - **Class 2 tRNAs** have a large extra arm (13-21 bp) and often have a stem-loop structure.



tRNA tertiary structure

- The tRNA is functional in its tertiary structure and appears L-shaped.
- It is formed by the folding of cloverleaf structure and is stabilized by nine hydrogen bonds (tertiary hydrogen bonds) occurs between residues of D-arm and TΨC arm.



rRNA

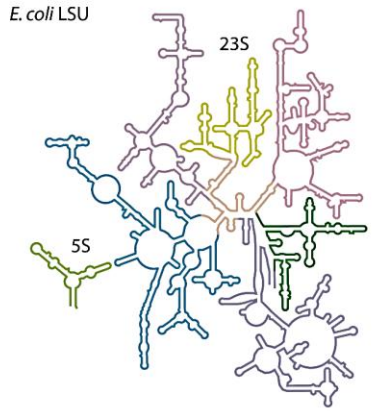
- The RNA which is found in ribosomes is called ribosomal RNA (rRNA).
- It is most abundant and constitutes about 80% of the total cellular RNA.
- The rRNA molecule is highly coiled. In combination with proteins, it forms small and large subunits of the ribosomes, hence its name.
- Ribosomal RNA is synthesize from nucleolar DNA in eukaryotes and forms a part of DNA in prokaryotes.
- rRNA is a ribozyme which carries out protein synthesis in ribosomes.
- The rRNA genes and their sequences are conserved through billion years of evolutionary divergences. Hence, by comparing the sequences of rRNA genes the possible phylogeny of organisms can be ascertained.

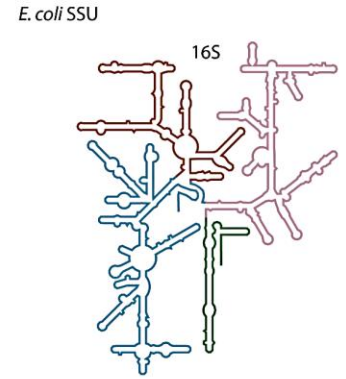
rRNA

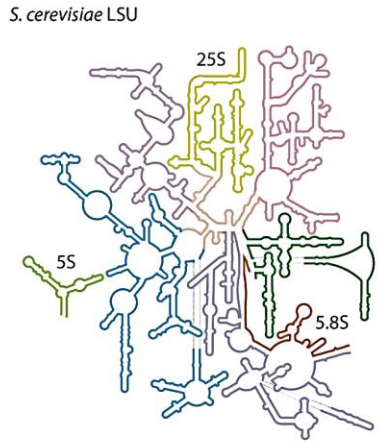
- In prokaryotes three types of rRNAs are available:
  - 16S rRNA
  - 23S rRNA
  - 5S rRNA

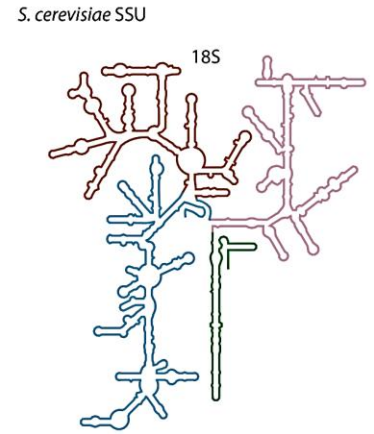
  → Large subunit
- In eukaryotes four types of rRNAs are available
  - 18S rRNA
  - 28S rRNA
  - 5.8S rRNA
  - 5S rRNA

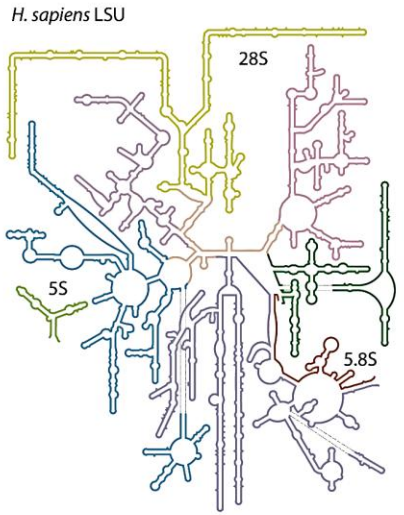
  → Large subunit

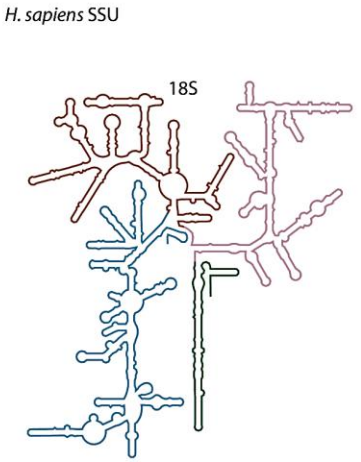












Some special RNA

Heterogenous nuclear RNA (hnRNA)

- These are large precursors of mRNA before processing found in the nucleus.
- About 25% of these are converted into mRNA.

Small nuclear RNA (snRNA)

- They are small nuclear RNA composed of 100 to 200 nucleotides.
- They are often associated with proteins and form small ribonucleoproteins.
- They are rich in uridine residues.
- They have enzymatic proteries.

Home work

- Moncistronic vs polycistronic mRNA?
- Intron vs exon?
- Difference between RNA and DNA?