

General Structure of RNA

The secondary structure of RNA refers to the local folding patterns that occur within a single RNA strand. Unlike DNA, which typically forms a double helix, RNA is single-stranded, allowing it to fold back on itself and form intricate secondary structures. These structures result from complementary base pairing between different regions of the same RNA molecule. The most common type of secondary structure in RNA is the stem-loop or hairpin structure. In a stem-loop, a segment of the RNA strand pairs with a complementary segment further downstream, forming a "stem" of base pairs, while a loop of unpaired bases forms at the end of the stem. The base pairing in the stem is stabilized by hydrogen bonds between complementary bases, while the unpaired loop region remains flexible. Secondary structures are essential for RNA function, stability, and regulation. They play a crucial role in various cellular processes, including mRNA stability and localization, RNA splicing, ribosome binding, and microRNA-mediated gene regulation. Additionally, secondary structures are important for the catalytic activity of certain RNAs, known as ribozymes, which can perform enzymatic functions without the need for protein cofactors. Predicting and understanding the secondary structure of RNA molecules is a fundamental area of RNA research. Computational methods and experimental techniques like chemical probing and RNA footprinting are used to study and characterize these structures. Secondary structure analysis helps researchers decipher the complex roles of RNA in gene expression, regulation, and other cellular processes, and it has significant implications for biotechnology, drug design, and therapeutic applications.

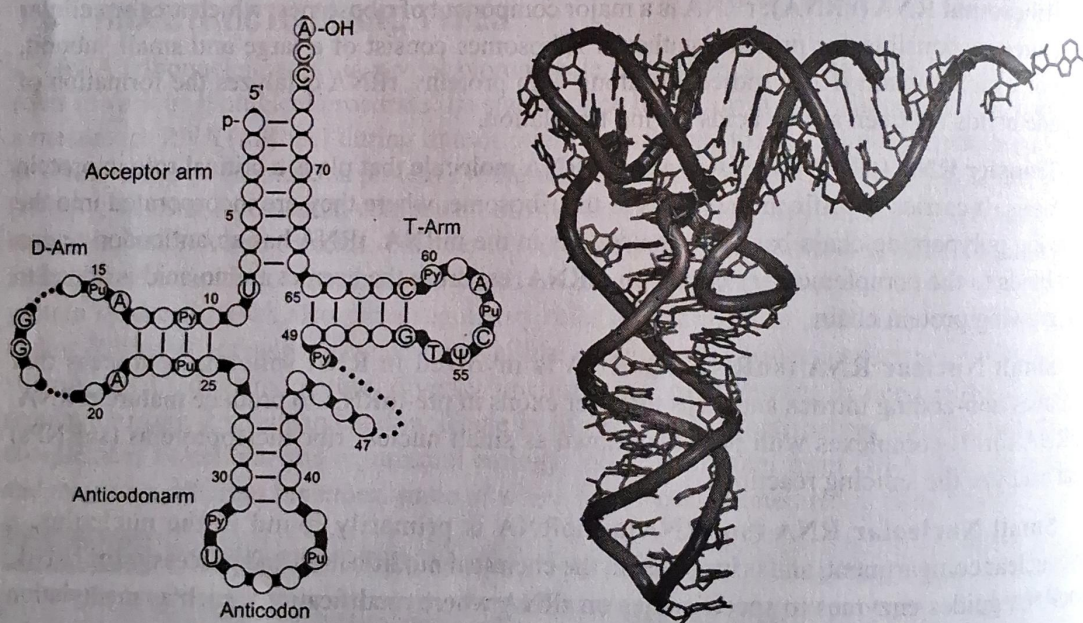


Fig. 1.5. Structure of t-RNA a. Secondary Structure, b. Tertiary structure.

The secondary structure of t-RNA was first described in detail by R. Holly and became popular as clover-leaf model. The secondary structure of tRNA is characterized by its unique L-shaped three-dimensional configuration, which arises from extensive base pairing between complementary regions within the single RNA strand. The secondary structure of tRNA consists of four main regions namely, acceptor stem, D-loop, psi loop and anticodon loop. The **acceptor stem** is a short double-stranded region at the 3' end of tRNA. It contains the sequence 5'-CCA-3', where the 3' end of the tRNA binds to the amino acid covalently. The acceptor stem is essential for recognizing the correct amino acid and attaching it to the tRNA during

the charging process. The **D-loop** contains modified nucleotides, including dihydrouridine, which help stabilize the overall structure of tRNA. This loop is important for the accurate recognition of tRNA by specific enzymes involved in charging it with the correct amino acid. The **anticodon loop** is located at the opposite end of the acceptor stem and contains a sequence of three nucleotides known as the anticodon. The anticodon is complementary to a specific codon on the mRNA, allowing tRNA to recognize the appropriate codon and deliver the corresponding amino acid during translation. The **TYC (thymidine-pseudouridine-cytosine) loop** contains modified nucleotides, including pseudouridine. It is involved in the accurate folding of tRNA and contributes to its stability.

Ribosomal RNA (rRNA) is a major component of ribosomes, the cellular machinery responsible for protein synthesis. The secondary structure of rRNA is highly complex and involves extensive base pairing and folding within a single RNA strand. rRNA forms the core structure of the ribosome, providing a scaffold for the binding of ribosomal proteins and playing a central role in catalyzing peptide bond formation during translation. The secondary structure of rRNA consists of several domains and helices. The most well-known rRNA secondary structure is the 16S rRNA in the small ribosomal subunit (in prokaryotes) and the 18S rRNA in the small ribosomal subunit (in eukaryotes). These domains are involved in the binding and decoding of mRNA during translation. Additionally, rRNA contains extensive secondary structure elements throughout its length, contributing to the overall stability and function of the ribosome. The complex secondary structure of rRNA is crucial for coordinating interactions with ribosomal proteins, tRNA molecules, and mRNA during translation, making it an essential component of the translation process. Both tRNA and rRNA exemplify the importance of secondary structure in RNA molecules. These structures allow tRNA to accurately transport amino acids to the ribosome and rRNA to play a central role in the translation of mRNA into proteins, contributing to the intricate molecular dance of cellular life.

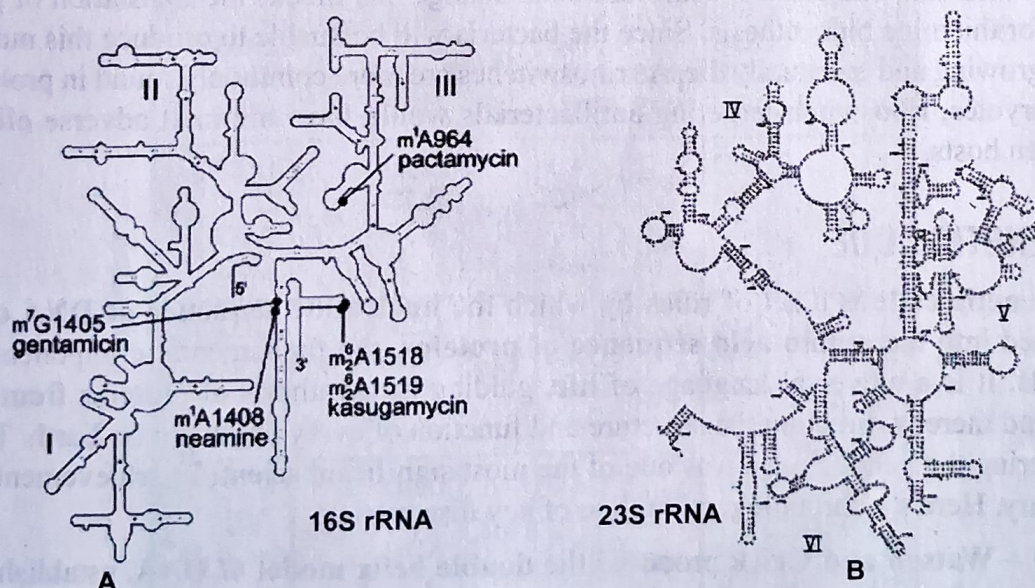


Fig. 1.6. Typical rRNA structure. A. 16S rRNA, b. 23S rRNA.