t RNA

JISHNU K.
Assistant Professor
Dept. of Zoology
MES Keveeyam College, Valanchery

tRNA

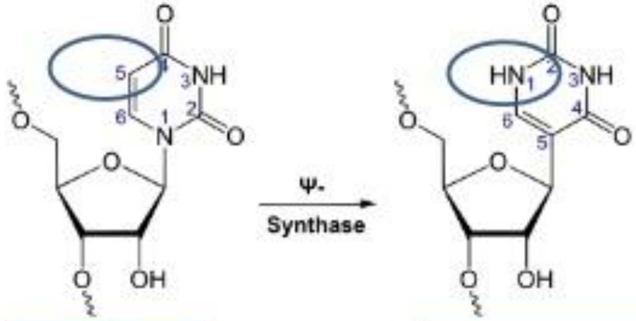
- t-RNA (transfer RNA) is also named as S-RNA (soluble or supernatant RNA) and adaptor RNA.
- t-RNA is a family of nearly 60 small sized ribonucleic acids.
- 10 – 15% of total cellular RNA is t-RNA.
- t-RNAs are small molecules with about 74 – 95 ribonucleotides.
- Sedimentation constant – 3.8S
- Molecular weight – nearly 25,000 – 30,000 Dalton
- t-RNAs are made up of a single stranded polynucleotide chain

Unique feature of tRNA

- **Presence of un usual base pairs**

- In addition to usual N-bases (A,U,G,C) tRNA contains number of unusual bases.
- These unusual bases are important as they **protect t-RNA molecules from dehydration by Rnase**, when tRNAs are floating freely in cytoplasm.
- **Protects mainly by methylation**

- Inosine (I) – Adenine
- Pseudouracil (ψ) - Uracil
- Dihydroxyuridine- urdine

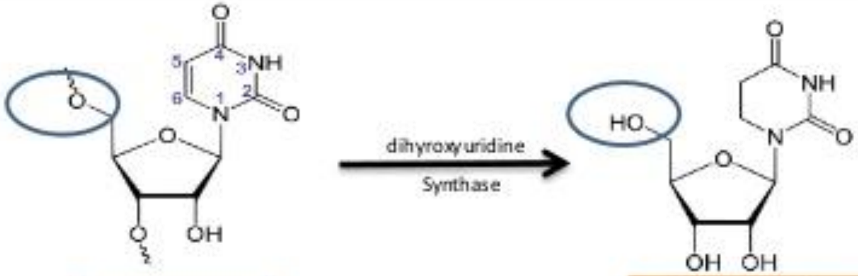


uridine

Psuedouridine

Adenosine

Inosine



uridine

dihyroxyuridine

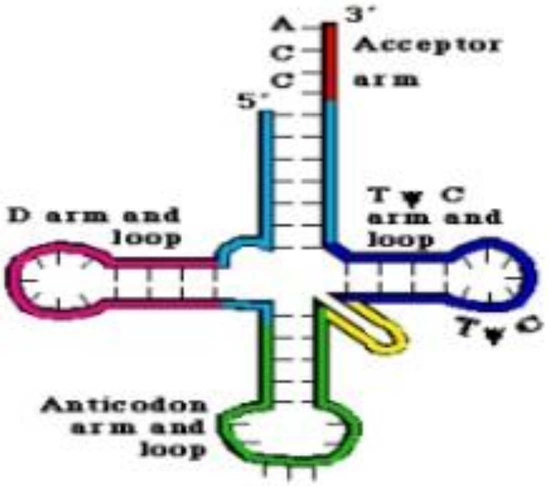
Structure of tRNA

- **Primary structure**- linear sequence of nucleotides
- **Secondary structure**-Clover leaf model
- **Tertiary structure**- 3-D structure of tRNA , L shape, Helix stacking

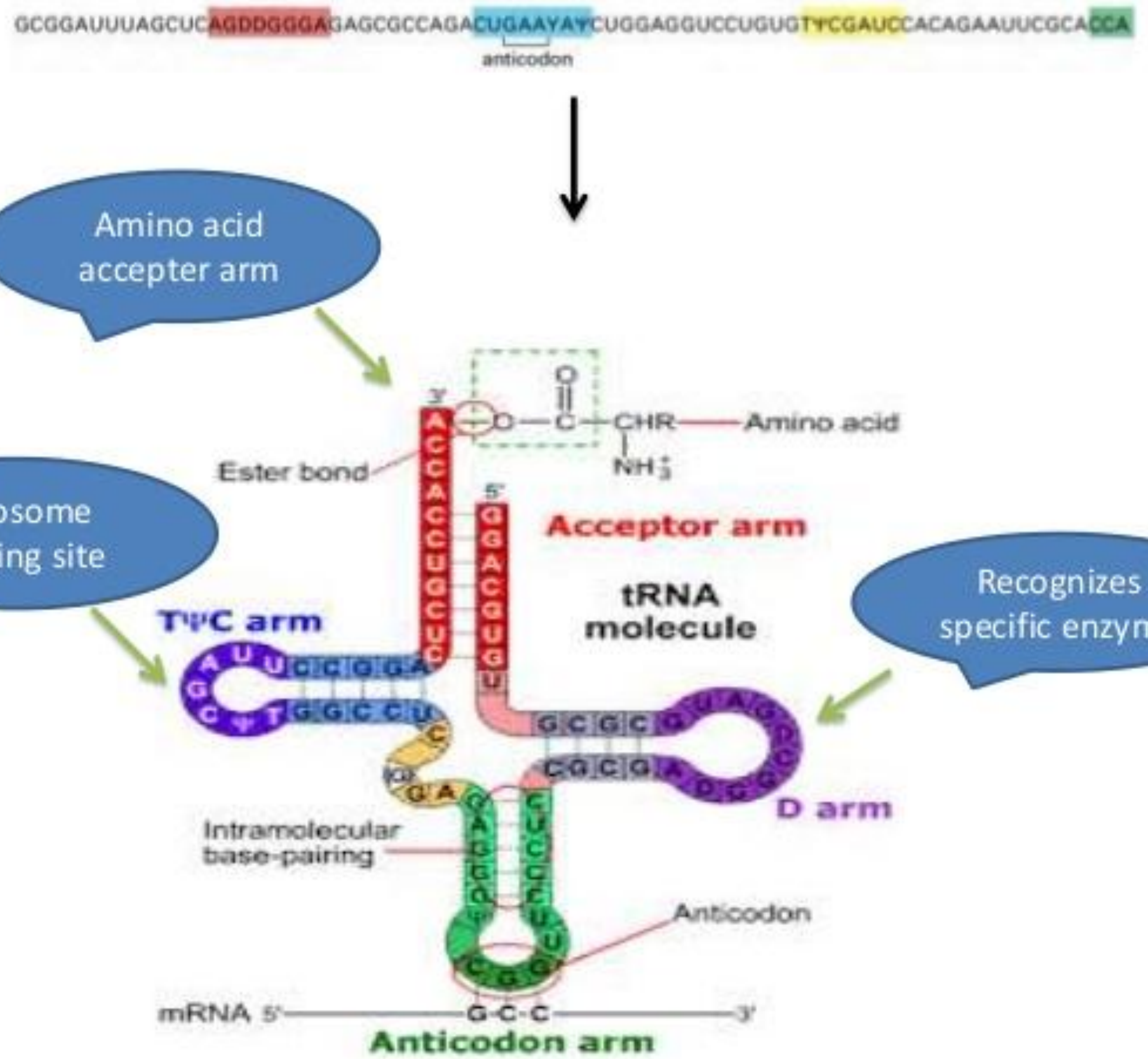
Primary Structure

- Linear sequence of nucleotides is 60-90 in nt long but most commonly 76
- Many **modified bases**, sometimes accounting for **20%** of the total bases in any one tRNA molecules
- All of them are created post transcriptionally.

Secondary structure/ clover leaf model



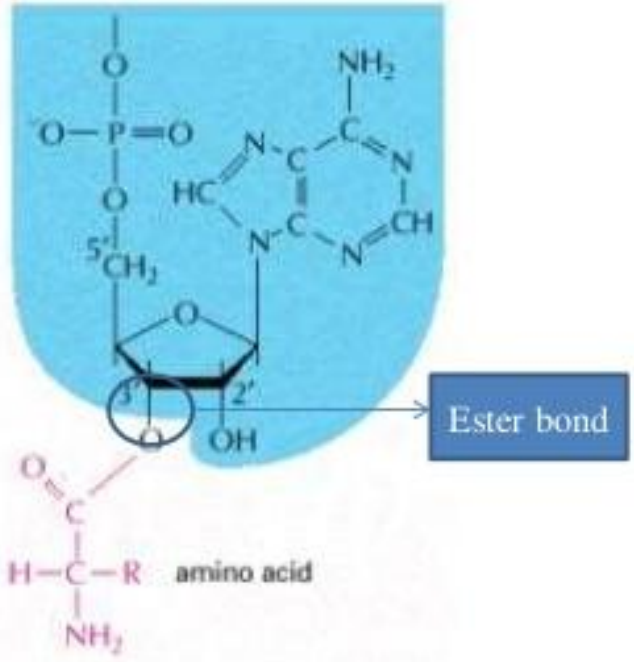
- Robert Holley proposed clover leaf model for the first time in 1968.
- It is a two dimensional description of the t-RNA.



Amino acid accepter arm

Ribosome binding site

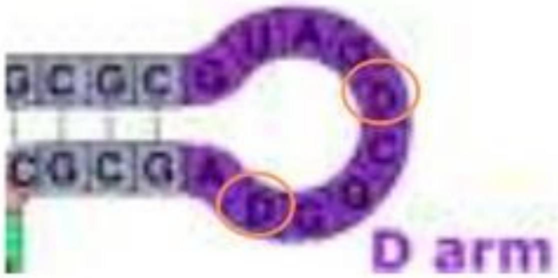
Recognizes specific enzyme



Ester bond

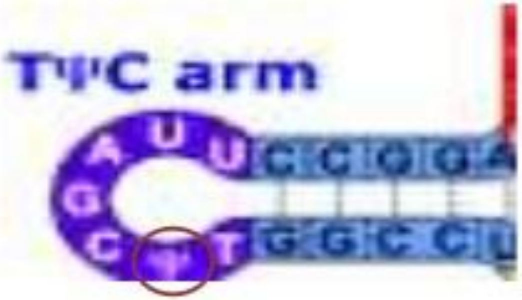
Amino acid acceptor arm

- Double helical (both 5’ and 3’ ends of tRNA)
- 7 base pairs unpaired
- At 3’ end, **5’CCA3’** protrudes with –OH at the tip
- Site for **attachment of amino acid**
- -COOH of specific amino acid joins with –OH of A in CCA to form amino acyl tRNA



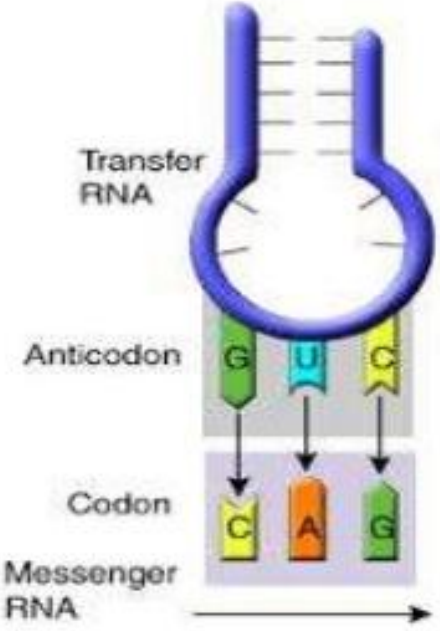
D arm

- **DHU or D arm** – This arm consists of stem and loop with unusual pyrimidine nucleotide **dihydrouracil**.
- 4 bp stem with a loop contain dihydrouridine
- Recognition site for the **specific enzyme aminoacyl-tRNA synthetase** that activate the amino acid
- Play a important role in the stabilization of the tRNA's tertiary structure.



T ψ C arm

- **TψC arm is named for the presence of sequence TψC (thymine – pseudouridine (ψ) – cytosine), where pseudouridine is unusual base.**
- **This arm also consists of stem and loop.**
- **Stem contains 5 base pairs; outermost of these pairs is C-G. Loop contains 7 unpaired nucleotides**
- **This loop contains a ribosome recognition site.**



Anticodon loop

- **This arm also contains stem and loop.**
- **Stem consists of 5 base pairs and loop (called as anticodon loop or loop II) contains 7 unpaired nucleotides.**
- **Out of these 7 unpaired nucleotides the middle three form anticodon.**
- **Anticodon recognizes and codon of mRNA and binds to it.**

Variable arm

- The variable arm has between 3 and 21 nucleotides, depending on which amino acid the tRNA encodes.
- Between anticodon loop and TΨU loop
- This tRNA's variable arm is very short so it looks quite different from the other arms of the molecule.
- May present or absent, it depends on species.
- The length of the variable arm is important in the recognition of the aminoacyl tRNA synthetase for the tRNA.
- Variable arm helps is stability of tRNA
- tRNAs are called class 1 if they lack it, and class 2 if they have it.

Tertiary structure : 3D structure

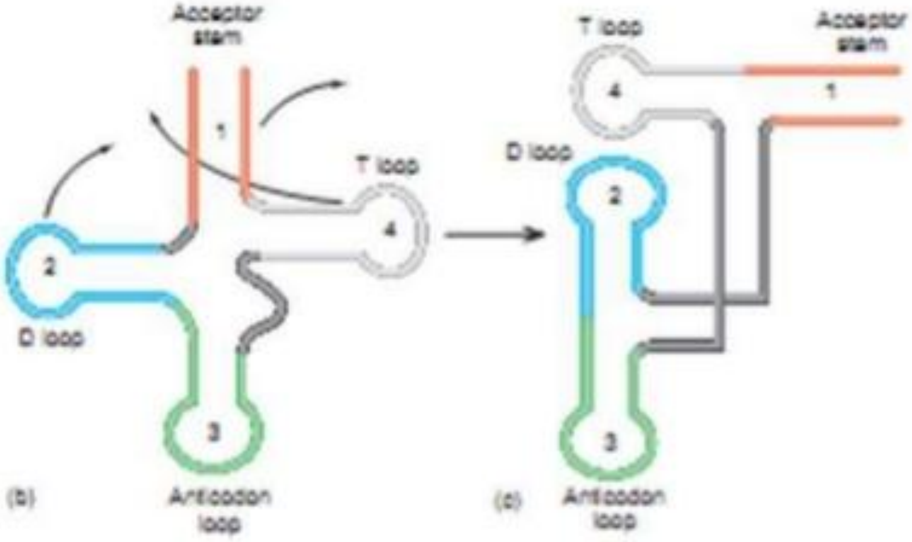
L-Shaped structure

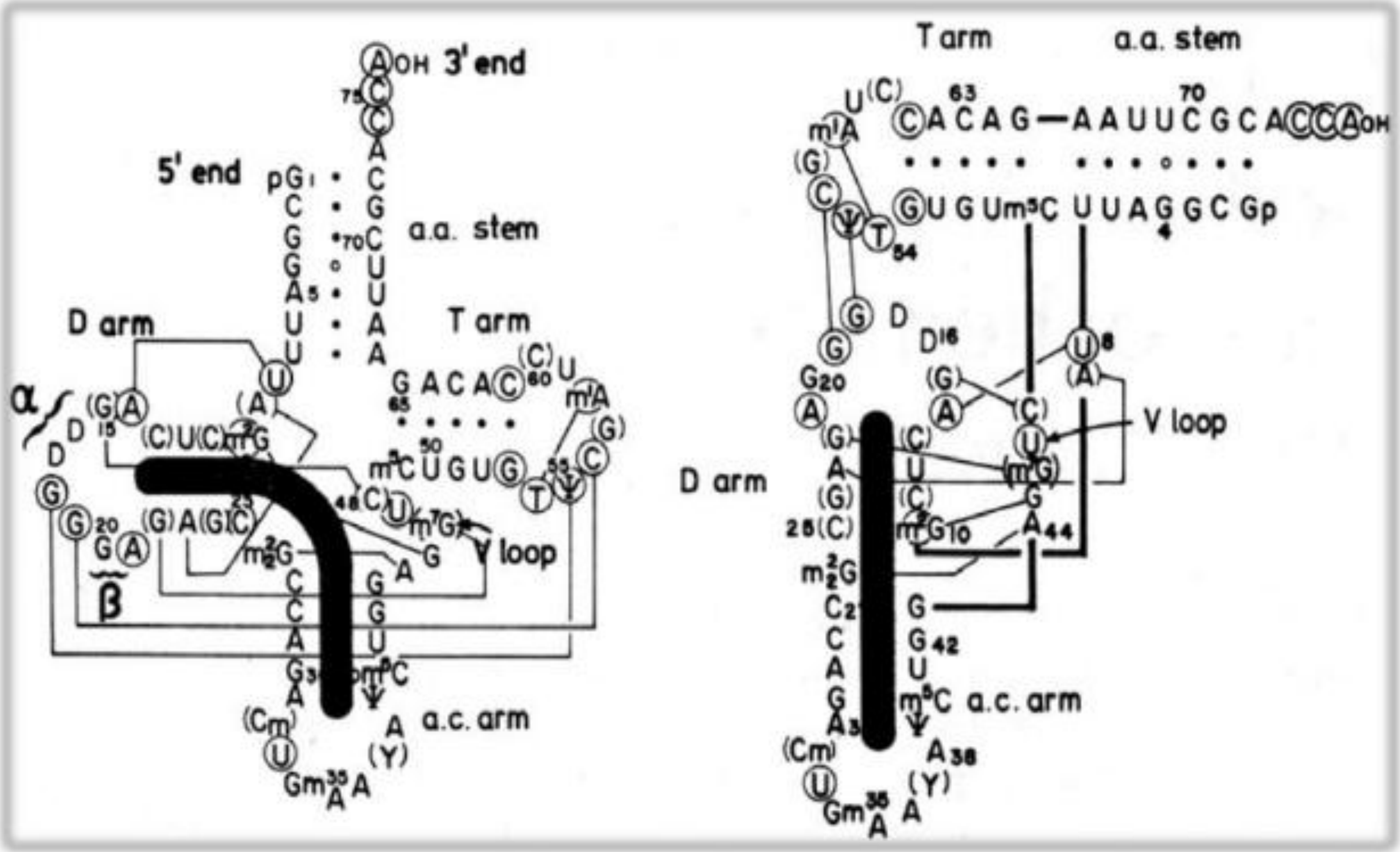
(i) Acceptor stem and ΨU stem form extended helix

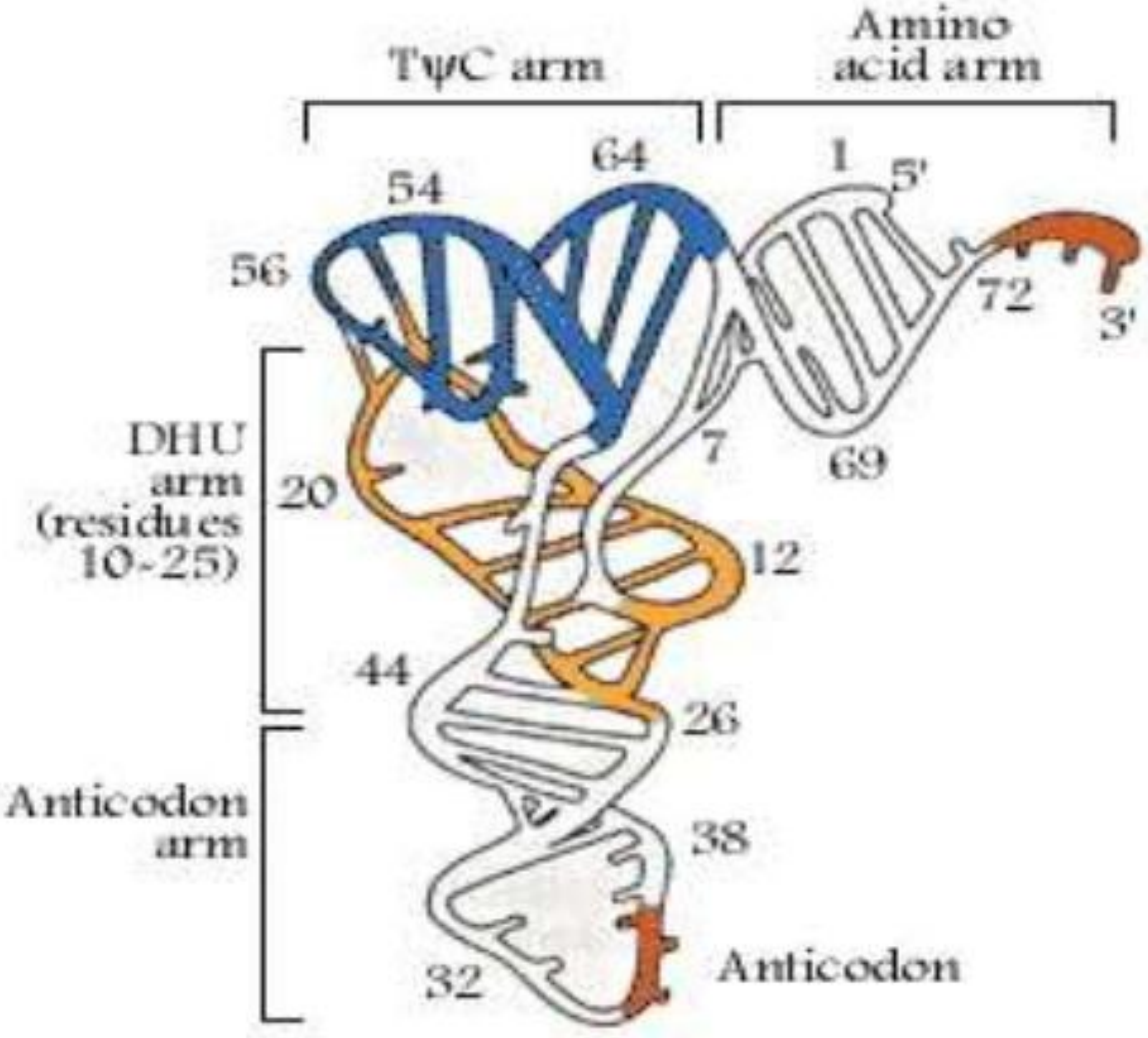
(ii) Anticodon stem and D-loop stem form extended helix

(iii) D-loop and T loop align together

(iv) Both extended helices align at right angle




3' end
5' end
a.a. stem
D arm
T arm
V loop
a.c. arm
α
β
T arm
a.a. stem
D arm
V loop
a.c. arm


TψC arm
Amino acid arm
64
54
1
5'
56
72
3'
DHU arm (residues 10-25)
20
7
69
12
44
26
Anticodon arm
38
Anticodon
32

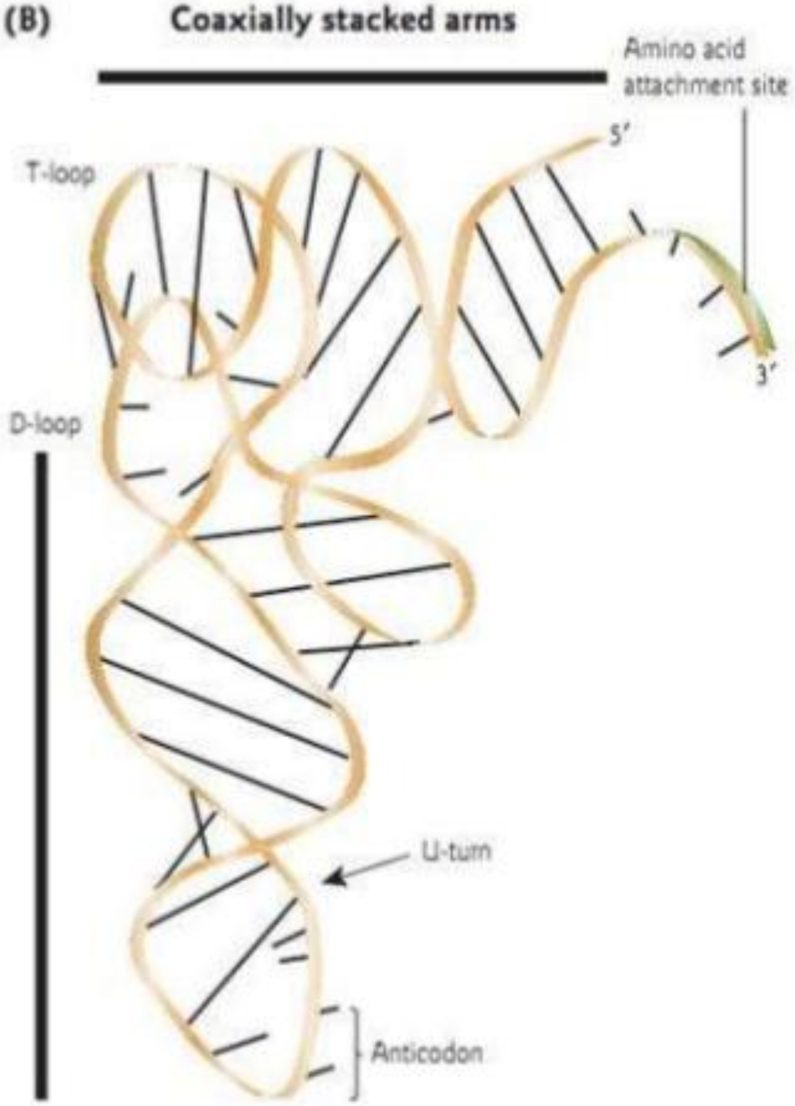
Stability of L-structure

- Tertiary structure of t-RNA is produced by hydrogen bonding –

✓ Between N-bases

✓ Between N-bases and ribose-phosphate backbone

✓ Between ribose-phosphate backbone



- Precursors of DNA and RNA.
- · Activated intermediates in many biosyntheses: e.g UDP-glucose ® glycogen, S-adenosylmathionine as methyl donor, etc.
- · Nucleotside triphosphates, especially ATP, as the universal currency of energy in biological systems.
- · Adenine nucleotides are components of the coenzymes, $NAD(P)^+$, FAD, and CoA.
- · Metabolic regulators: **(a)** c-AMP is the mediator of hormonal actions; **(b)** ATP-dependent protein phosphorylation - activates phosphorylase and inactivates glycogen synthase; **(c)** adenylation of a Tyr of bacterial glutamine synthetase - more sensitive to feedback inhibition and less active; **(d)** allosteric regulator - glycogen phosphorylase activated by ATP and inactivated by AMP.